

SEQUENCE LISTING

<110> HUIGENE THERAPEUTICS CO., LTD.

<120> RNA ADENO-ASSOCIATED VIRUS (RAAV) VECTOR AND USES THEREOF

<130> 132045-00619

<150> PCT/CN2021/075874

<151> 2021-02-07

<160> 104

<170> PatentIn version 3.5

<210> 1

<211> 145

<212> DNA

<213> Adeno-associated virus - 2

<400> 1

ttggccactc cctctctgcg cgctcgctcg ctactgagg ccgcccgggc aaagcccggg 60

cgtcgggcga cctttggtcg ccggcctca gtgagcgagc gagcgcgag agagggagtg 120

gccaactcca tcactagggg ttcct 145

<210> 2

<211> 113

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 2

tccctctctg cgcgctcgct cgctcactga ggccgcccgg gcaaagcccg ggcgtcgggc 60

gacctttggt cgcccggcct cagtgagcga gcgagcgcg agagagggag tgg 113

<210> 3

<211> 138

<212> DNA

<213> Artificial Sequence

<220>

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 3
 tccctctctg cgcgctcgct cgctcactga ggccgcccgg gcaaagcccg ggcgtcgggc 60
 gaccttttgt cgcccgccct cagtgagcga gcgagcgcg agagagggag tggactagct 120
 ccatcactag gggttcct 138

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"

<400> 4
 ctccatcact aggggttcct 20

<210> 5
 <211> 145
 <212> DNA
 <213> Adeno-associated virus - 2

<400> 5
 aggaacccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctactgagg 60
 ccgcccgggc aaagcccggg cgtcgggcga cctttggtcg cccggcctca gtgagcgagc 120
 gagcgcgag agagggagtg gccaa 145

<210> 6
 <211> 736
 <212> PRT
 <213> Adeno-associated virus - 1

<400> 6
 Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
 1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro

30

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
 260 265 270

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

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

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

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
 325 330 335

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

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

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
 405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp

420	425	430
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg		
435	440	445
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser		
450	455	460
Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro		
465	470	480
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn		
485	490	495
Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn		
500	505	510
Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys		
515	520	525
Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly		
530	535	540
Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile		
545	550	555
Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg		
565	570	575
Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala		
580	585	590
Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln		
595	600	605
Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His		
610	615	620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

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

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 7

<211> 735

<212> PRT

<213> Adeno-associated virus - 2

<400> 7

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

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

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

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

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

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

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

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

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

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

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

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

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr

260		265		270
Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His	275	280	285	
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp	290	295	300	
Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val	305	310	315	320
Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu	325	330	335	
Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr	340	345	350	
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp	355	360	365	
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser	370	375	380	
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser	385	390	395	400
Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu	405	410	415	
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg	420	425	430	
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr	435	440	445	
Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln	450	455	460	

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

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

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

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln

660

665

670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
 675 680 685

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

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
 705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 8

<211> 736

<212> PRT

<213> Adeno-associated virus - 3

<400> 8

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

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

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
 35 40 45

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

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

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

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

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

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

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

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

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

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

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
435 440 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
450 455 460

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

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
485 490 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn

500	505	510																	
Gly	Arg	Asp	Ser	Leu	Val	Asn	Pro	Gly	Pro	Ala	Met	Ala	Ser	His	Lys				
	515						520					525							
Asp	Asp	Glu	Glu	Lys	Phe	Phe	Pro	Met	His	Gly	Asn	Leu	Ile	Phe	Gly				
	530					535					540								
Lys	Glu	Gly	Thr	Thr	Ala	Ser	Asn	Ala	Glu	Leu	Asp	Asn	Val	Met	Ile				
545					550					555					560				
Thr	Asp	Glu	Glu	Glu	Ile	Arg	Thr	Thr	Asn	Pro	Val	Ala	Thr	Glu	Gln				
				565					570					575					
Tyr	Gly	Thr	Val	Ala	Asn	Asn	Leu	Gln	Ser	Ser	Asn	Thr	Ala	Pro	Thr				
			580					585					590						
Thr	Gly	Thr	Val	Asn	His	Gln	Gly	Ala	Leu	Pro	Gly	Met	Val	Trp	Gln				
	595						600					605							
Asp	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His				
	610					615					620								
Thr	Asp	Gly	His	Phe	His	Pro	Ser	Pro	Leu	Met	Gly	Gly	Phe	Gly	Leu				
625					630					635					640				
Lys	His	Pro	Pro	Pro	Gln	Ile	Met	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala				
				645					650					655					
Asn	Pro	Pro	Thr	Thr	Phe	Ser	Pro	Ala	Lys	Phe	Ala	Ser	Phe	Ile	Thr				
			660					665					670						
Gln	Tyr	Ser	Thr	Gly	Gln	Val	Ser	Val	Glu	Ile	Glu	Trp	Glu	Leu	Gln				
	675						680					685							
Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Ser	Asn				
	690					695					700								

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 9

<211> 736

<212> PRT

<213> Adeno-associated virus - 3

<400> 9

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

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

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

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

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

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

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

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

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

Pro Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
 145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
 180 185 190

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

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270

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

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

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

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

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr

340	345	350
Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp		
355	360	365
Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser		
370	375	380
Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser		
385	390	400
Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu		
405	410	415
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg		
420	425	430
Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr		
435	440	445
Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser		
450	455	460
Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro		
465	470	475
Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn		
485	490	495
Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn		
500	505	510
Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys		
515	520	525
Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly		
530	535	540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
565 570 575

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

Thr Arg Thr Val Asn Asp Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

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

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 10

<211> 734

<212> PRT

<213> Adeno-associated virus - 4

<400> 10

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

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

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

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

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

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

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

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

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145 150 155 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
165 170 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser

180	185	190
Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly		
195	200	205
Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys		
210	215	220
Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr		
225	230	235
Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu		
245	250	255
Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr		
260	265	270
Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln		
275	280	285
Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val		
290	295	300
Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu		
305	310	315
Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp		
325	330	335
Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser		
340	345	350
Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr		
355	360	365
Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn		
370	375	380

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

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

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
 420 425 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
 435 440 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
 450 455 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
 465 470 475 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
 485 490 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
 500 505 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
 515 520 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
 530 535 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
 545 550 555 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
 565 570 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp

580

585

590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
 595 600 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
 610 615 620

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

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
 645 650 655

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

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
 675 680 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
 690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
 705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
 725 730

<210> 11

<211> 724

<212> PRT

<213> Adeno-associated virus - 5

<400> 11

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
 1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys

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

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

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

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

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

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

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

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

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

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

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

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

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

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp

420		425		430
Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln				
435		440		445
Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp				
450		455		460
Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly				
465		470		480
Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu				
	485		490	495
Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr				
	500		505	510
Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile				
	515		520	525
Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu				
	530		535	540
Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg				
545		550		560
Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser				
	565		570	575
Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro				
	580		585	590
Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp				
	595		600	605
Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met				
610		615		620

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

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

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

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

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

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

Thr Arg Pro Leu

<210> 12

<211> 736

<212> PRT

<213> Adeno-associated virus - 6

<400> 12

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45

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

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

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

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

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

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

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His

260	265	270
Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe		
275	280	285
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn		
290	295	300
Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln		
305	310	315
Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn		
325	330	335
Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro		
340	345	350
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala		
355	360	365
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly		
370	375	380
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro		
385	390	395
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe		
405	410	415
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp		
420	425	430
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg		
435	440	445
Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser		
450	455	460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
515 520 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr

660

665

670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685

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

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
 705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
 725 730 735

<210> 13

<211> 737

<212> PRT

<213> Adeno-associated virus - 7

<400> 13

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
 20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
 35 40 45

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

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

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

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

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

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
305 310 315 320

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

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
340 345 350

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

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

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

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

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

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
435 440 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
450 455 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His

500	505	510
Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr		
515	520	525
His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile		
530	535	540
Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu		
545	550	555
Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu		
565	570	575
Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala		
580	585	590
Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp		
595	600	605
Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro		
610	615	620
His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly		
625	630	635
Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro		
645	650	655
Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile		
660	665	670
Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu		
675	680	685
Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser		
690	695	700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
 705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735

Leu

<210> 14

<211> 738

<212> PRT

<213> Adeno-associated virus - 8

<400> 14

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

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

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
 35 40 45

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

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

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

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

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

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

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
260 265 270

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

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

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

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

325	330	335
Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln		
340	345	350
Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe		
355	360	365
Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn		
370	375	380
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr		
385	390	400
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr		
405	410	415
Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser		
420	425	430
Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu		
435	440	445
Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly		
450	455	460
Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp		
465	470	480
Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly		
485	490	495
Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His		
500	505	510
Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr		
515	520	525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
530 535 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

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

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

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

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg

725

730

735

Asn Leu

<210> 15

<211> 736

<212> PRT

<213> Adeno-associated virus - 9

<400> 15

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

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

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
 35 40 45

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

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

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

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

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

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

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly

145		150		155		160									
Lys	Ser	Gly	Ala	Gln	Pro	Ala	Lys	Lys	Arg	Leu	Asn	Phe	Gly	Gln	Thr
				165					170					175	
Gly	Asp	Thr	Glu	Ser	Val	Pro	Asp	Pro	Gln	Pro	Ile	Gly	Glu	Pro	Pro
			180					185					190		
Ala	Ala	Pro	Ser	Gly	Val	Gly	Ser	Leu	Thr	Met	Ala	Ser	Gly	Gly	Gly
		195					200					205			
Ala	Pro	Val	Ala	Asp	Asn	Asn	Glu	Gly	Ala	Asp	Gly	Val	Gly	Ser	Ser
	210					215					220				
Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Gln	Trp	Leu	Gly	Asp	Arg	Val	Ile
225					230					235					240
Thr	Thr	Ser	Thr	Arg	Thr	Trp	Ala	Leu	Pro	Thr	Tyr	Asn	Asn	His	Leu
				245					250					255	
Tyr	Lys	Gln	Ile	Ser	Asn	Ser	Thr	Ser	Gly	Gly	Ser	Ser	Asn	Asp	Asn
		260						265					270		
Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg
		275					280					285			
Phe	His	Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn
	290					295					300				
Asn	Trp	Gly	Phe	Arg	Pro	Lys	Arg	Leu	Asn	Phe	Lys	Leu	Phe	Asn	Ile
305					310					315					320
Gln	Val	Lys	Glu	Val	Thr	Asp	Asn	Asn	Gly	Val	Lys	Thr	Ile	Ala	Asn
				325					330					335	
Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Ser	Asp	Tyr	Gln	Leu
			340					345					350		

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

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

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

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

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

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile

545		550		555		560									
Thr	Asn	Glu	Glu	Glu	Ile	Lys	Thr	Thr	Asn	Pro	Val	Ala	Thr	Glu	Ser
				565					570					575	
Tyr	Gly	Gln	Val	Ala	Thr	Asn	His	Gln	Ser	Ala	Gln	Ala	Gln	Ala	Gln
			580					585					590		
Thr	Gly	Trp	Val	Gln	Asn	Gln	Gly	Ile	Leu	Pro	Gly	Met	Val	Trp	Gln
		595					600					605			
Asp	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	His
	610					615					620				
Thr	Asp	Gly	Asn	Phe	His	Pro	Ser	Pro	Leu	Met	Gly	Gly	Phe	Gly	Met
625					630					635					640
Lys	His	Pro	Pro	Pro	Gln	Ile	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Ala
				645					650					655	
Asp	Pro	Pro	Thr	Ala	Phe	Asn	Lys	Asp	Lys	Leu	Asn	Ser	Phe	Ile	Thr
			660					665					670		
Gln	Tyr	Ser	Thr	Gly	Gln	Val	Ser	Val	Glu	Ile	Glu	Trp	Glu	Leu	Gln
		675					680					685			
Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Ser	Asn
	690					695					700				
Tyr	Tyr	Lys	Ser	Asn	Asn	Val	Glu	Phe	Ala	Val	Asn	Thr	Glu	Gly	Val
705					710					715					720
Tyr	Ser	Glu	Pro	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Asn	Leu
				725					730					735	

<210> 16
 <211> 738
 <212> PRT

<213> Adeno-associated virus - 10

<400> 16

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

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

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

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

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

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

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

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145 150 155 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Glu Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

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

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

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

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

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

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr

385		390		395		400									
Phe	Pro	Ser	Gln	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu	Phe	Ser	Tyr
				405					410					415	
Thr	Phe	Glu	Asp	Val	Pro	Phe	His	Ser	Ser	Tyr	Ala	His	Ser	Gln	Ser
			420					425					430		
Leu	Asp	Arg	Leu	Met	Asn	Pro	Leu	Ile	Asp	Gln	Tyr	Leu	Tyr	Tyr	Leu
		435					440					445			
Ser	Arg	Thr	Gln	Ser	Thr	Gly	Gly	Thr	Gln	Gly	Thr	Gln	Gln	Leu	Leu
	450					455					460				
Phe	Ser	Gln	Ala	Gly	Pro	Ala	Asn	Met	Ser	Ala	Gln	Ala	Lys	Asn	Trp
465					470					475					480
Leu	Pro	Gly	Pro	Cys	Tyr	Arg	Gln	Gln	Arg	Val	Ser	Thr	Thr	Leu	Ser
				485					490					495	
Gln	Asn	Asn	Asn	Ser	Asn	Phe	Ala	Trp	Thr	Gly	Ala	Thr	Lys	Tyr	His
			500					505					510		
Leu	Asn	Gly	Arg	Asp	Ser	Leu	Val	Asn	Pro	Gly	Val	Ala	Met	Ala	Thr
		515					520					525			
His	Lys	Asp	Asp	Glu	Glu	Arg	Phe	Phe	Pro	Ser	Ser	Gly	Val	Leu	Met
	530					535					540				
Phe	Gly	Lys	Gln	Gly	Ala	Gly	Arg	Asp	Asn	Val	Asp	Tyr	Ser	Ser	Val
545					550					555					560
Met	Leu	Thr	Ser	Glu	Glu	Glu	Ile	Lys	Thr	Thr	Asn	Pro	Val	Ala	Thr
				565					570					575	
Glu	Gln	Tyr	Gly	Val	Val	Ala	Asp	Asn	Leu	Gln	Gln	Ala	Asn	Thr	Gly
			580					585					590		

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

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

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 17

<211> 733

<212> PRT

<213> Adeno-associated virus - 11

<400> 17

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

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

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

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

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

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

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

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145 150 155 160

Lys Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Glu Glu Asp Thr
165 170 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
180 185 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
195 200 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys

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

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Leu Asp
420 425 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
435 440 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
450 455 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465 470 475 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
485 490 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
500 505 510

Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
515 520 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
530 535 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545 550 555 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
565 570 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
580 585 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
595 600 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly

610

615

620

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

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ala
 645 650 655

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

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
 675 680 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly Asn
 690 695 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
 705 710 715 720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
 725 730

<210> 18

<211> 742

<212> PRT

<213> Adeno-associated virus - 12

<400> 18

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

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

Lys Ala Asn Gln Gln His Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro

50

55

60

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

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

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

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

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

Pro Leu Glu Lys Thr Pro Asn Arg Pro Thr Asn Pro Asp Ser Gly Lys
145 150 155 160

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

Arg Arg Thr Leu Asp Phe Glu Asp Ser Gly Ala Gly Asp Gly Pro Pro
180 185 190

Glu Gly Ser Ser Ser Gly Glu Met Ser His Asp Ala Glu Met Arg Ala
195 200 205

Ala Pro Gly Gly Asn Ala Val Glu Ala Gly Gln Gly Ala Asp Gly Val
210 215 220

Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp Ser Glu Gly
225 230 235 240

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

Asn His Leu Tyr Leu Arg Ile Gly Thr Thr Ala Asn Ser Asn Thr Tyr
260 265 270

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

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

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

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

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

Val Met Asp Ala Gly Gln Glu Gly Ser Phe Pro Pro Phe Pro Asn Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Cys Gly Val Val Thr Gly Lys
370 375 380

Asn Gln Asn Gln Thr Asp Arg Asn Ala Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

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

Phe Glu Lys Val Pro Phe His Ser Met Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Met Met Asn Pro Leu Leu Asp Gln Tyr Leu Trp His Leu Gln
435 440 445

Ser Thr Thr Thr Gly Asn Ser Leu Asn Gln Gly Thr Ala Thr Thr Thr

450

455

460

Tyr Gly Lys Ile Thr Thr Gly Asp Phe Ala Tyr Tyr Arg Lys Asn Trp
 465 470 475 480

Leu Pro Gly Ala Cys Ile Lys Gln Gln Lys Phe Ser Lys Asn Ala Asn
 485 490 495

Gln Asn Tyr Lys Ile Pro Ala Ser Gly Gly Asp Ala Leu Leu Lys Tyr
 500 505 510

Asp Thr His Thr Thr Leu Asn Gly Arg Trp Ser Asn Met Ala Pro Gly
 515 520 525

Pro Pro Met Ala Thr Ala Gly Ala Gly Asp Ser Asp Phe Ser Asn Ser
 530 535 540

Gln Leu Ile Phe Ala Gly Pro Asn Pro Ser Gly Asn Thr Thr Thr Ser
 545 550 555 560

Ser Asn Asn Leu Leu Phe Thr Ser Glu Glu Glu Ile Ala Thr Thr Asn
 565 570 575

Pro Arg Asp Thr Asp Met Phe Gly Gln Ile Ala Asp Asn Asn Gln Asn
 580 585 590

Ala Thr Thr Ala Pro His Ile Ala Asn Leu Asp Ala Met Gly Ile Val
 595 600 605

Pro Gly Met Val Trp Gln Asn Arg Asp Ile Tyr Tyr Gln Gly Pro Ile
 610 615 620

Trp Ala Lys Val Pro His Thr Asp Gly His Phe His Pro Ser Pro Leu
 625 630 635 640

Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile Phe Ile Lys
 645 650 655

Asn Thr Pro Val Pro Ala Asn Pro Asn Thr Thr Phe Ser Ala Ala Arg
660 665 670

Ile Asn Ser Phe Leu Thr Gln Tyr Ser Thr Gly Gln Val Ala Val Gln
675 680 685

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

Val Gln Phe Thr Ser Asn Tyr Gly Thr Gln Asn Ser Met Leu Trp Ala
705 710 715 720

Pro Asp Asn Ala Gly Asn Tyr His Glu Leu Arg Ala Ile Gly Ser Arg
725 730 735

Phe Leu Thr His His Leu
740

<210> 19

<211> 733

<212> PRT

<213> Adeno-associated virus - 13

<400> 19

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

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

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

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

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

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

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

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

Val Glu Gln Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145 150 155 160

Ser Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr Gly
165 170 175

Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro Ala
180 185 190

Ala Pro Ser Gly Val Gly Ser Thr Thr Met Ala Ser Gly Gly Gly Ala
195 200 205

Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser Ser
210 215 220

Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr
225 230 235 240

Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr
245 250 255

Lys Gln Ile Ser Ser Gln Ser Gly Ala Thr Asn Asp Asn His Tyr Phe
260 265 270

Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys

275

280

285

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

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

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

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

Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp Val
 355 360 365

Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser Gln
 370 375 380

Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln
 385 390 395 400

Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu Asp
 405 410 415

Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu
 420 425 430

Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr Gln
 435 440 445

Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala Gly
 450 455 460

Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro Cys
 465 470 475 480

Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn Ser
485 490 495

Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly Arg Asp
500 505 510

Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp Lys
515 520 525

Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu Gly
530 535 540

Thr Asn Ala Asn Asn Ala Asp Leu Glu Asn Val Met Ile Thr Asp Glu
545 550 555 560

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

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

Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg Asp
595 600 605

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

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

Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Pro
645 650 655

Thr Asn Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser
660 665 670

Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn

675

680

685

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

Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu
 705 710 715 720

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

<210> 20

<211> 737

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 20

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

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

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

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

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

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

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

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

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

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ala Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

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

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

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

Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu
340 345 350

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

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

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

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

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

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Arg Thr Gln Thr Thr Gly Gly Thr Thr Asn Thr Gln Thr Leu Gly Phe
450 455 460

Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp Leu
465 470 475 480

Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp
485 490 495

Asn Asn Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu
500 505 510

Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His
515 520 525

Lys Asp Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe
530 535 540

Gly Lys Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met
545 550 555 560

Ile Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu
565 570 575

Gln Tyr Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala
580 585 590

Ala Thr Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp
595 600 605

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

His Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

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

Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu Gly
 705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
 725 730 735

Leu

<210> 21

<211> 743

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 21

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

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

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
 35 40 45

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

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

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

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

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

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

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

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

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

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

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

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn

500	505	510
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys		
515	520	525
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly		
530	535	540
Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile		
545	550	560
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser		
565	570	575
Tyr Gly Gln Val Ala Thr Asn His Gln Ser Asp Gly Thr Leu Ala Val		
580	585	590
Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile		
595	600	605
Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro		
610	615	620
Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro		
625	630	635
Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile		
645	650	655
Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp		
660	665	670
Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val		
675	680	685
Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro		
690	695	700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705 710 715 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
725 730 735

Arg Tyr Leu Thr Arg Asn Leu
740

<210> 22

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 22

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

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

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

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

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

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

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

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
260 265 270

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

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

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

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn
 325 330 335

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

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

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
 370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
 385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe
 405 410 415

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

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg
 435 440 445

Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser
 450 455 460

Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro
 465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn
 485 490 495

Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn
 500 505 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys
515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
530 535 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

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

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

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

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 23

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 23

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

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

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

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

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

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

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

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145 150 155 160

Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Asn Thr Met Ala Ala Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Gly Ser Thr Asn Asp Asn Thr
260 265 270

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

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

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

Val Lys Glu Val Thr Thr Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn

325	330	335
Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro		
340	345	350
Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala		
355	360	365
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly		
370	375	380
Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro		
385	390	400
Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe		
405	410	415
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp		
420	425	430
Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg		
435	440	445
Thr Gln Thr Thr Ser Gly Thr Ala Gly Asn Arg Thr Leu Gln Phe Ser		
450	455	460
Gln Ala Gly Pro Ser Ser Met Ala Asn Gln Ala Lys Asn Trp Leu Pro		
465	470	480
Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Thr Asn Gln Asn		
485	490	495
Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu Asn		
500	505	510
Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Thr His Lys		
515	520	525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Leu Ile Phe Gly
530 535 540

Lys Gln Gly Ala Gly Asn Ser Asn Val Asp Leu Asp Asn Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Glu
565 570 575

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

Thr Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

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

Tyr Asn Lys Ser Thr Asn Val Asp Phe Ala Val Asp Thr Asn Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu

725

730

735

<210> 24

<211> 745

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 24

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

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

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

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

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

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

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

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

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

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

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

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

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Thr
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

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

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

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

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

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

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385 390 395 400

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

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Leu Ala Leu Gly Glu
580 585 590

Thr Thr Arg Pro Ala Arg Gln Ala Ala Thr Ala Asp Val Asn Thr Gln
595 600 605

Gly Val Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln
610 615 620

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly His Phe His Pro
625 630 635 640

Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His Pro Pro Pro Gln Ile
645 650 655

Leu Ile Lys Asn Thr Pro Val Pro Ala Asn Pro Ser Thr Thr Phe Ser
660 665 670

Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
675 680 685

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
690 695 700

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn Lys Ser Ile Asn Val
705 710 715 720

Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser Glu Pro Arg Pro Ile
725 730 735

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745

<210> 25
 <211> 143
 <212> DNA
 <213> Adeno-associated virus - 1

<400> 25
 ttgccactc cctctctgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60
 agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcag agagggagtg 120
 ggcaactcca tcactagggg taa 143

<210> 26
 <211> 143
 <212> DNA
 <213> Adeno-associated virus - 1

<400> 26
 ttaccacctag tgatggagtt gccactccc tctctgcgcg ctcgctcgct cgggtggggcc 60
 tgcggaccaa aggtccgcag acggcagagc tctgctctgc cggccccacc gagcgagcga 120
 gcgcgcagag agggagtggg caa 143

<210> 27
 <211> 145
 <212> DNA
 <213> Adeno-associated virus - 2

<400> 27
 ttggccactc cctctctgcg cgctcgctcg ctactgagg ccgggcgacc aaaggtcgcc 60
 cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgcag agagggagtg 120
 gccaaactcca tcactagggg ttcct 145

<210> 28
 <211> 145
 <212> DNA
 <213> Adeno-associated virus - 2

<400> 28
 aggaaccctt agtgatggag ttggccactc cctctctgcg cgctcgctcg ctactgagg 60
 ccgggcgacc aaaggtcgcc cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc 120

gagcgcgcag agagggagtg gccaa 145

<210> 29

<211> 143

<212> DNA

<213> Adeno-associated virus - 3

<400> 29

ttggccactc cctctatgcg cactcgctcg ctcggtgggg cctggcgacc aaaggtcgcc 60

agacggacgt gctttgcacg tccggcccca ccgagcgagc gagtgcgcat agagggagtg 120

gccaaactcca tcactagagg tat 143

<210> 30

<211> 143

<212> DNA

<213> Adeno-associated virus - 3

<400> 30

atacctctag tgatggagtt ggccactccc tctatgcgca ctgctcgct cgggtggggcc 60

tggcgaccaa aggtcgccag acggacgtgc tttgcacgtc cggccccacc gagcgagcga 120

gtgcgcatag agggagtggc caa 143

<210> 31

<211> 146

<212> DNA

<213> Adeno-associated virus - 4

<400> 31

ttggccactc cctctatgcg cgctcgctca ctactcggc cctggagacc aaaggtctcc 60

agactgccgg cctctggccg gcagggccga gtgagtgagc gagcgcgcat agagggagtg 120

gccaaactcca tcacttaggt ttgccc 146

<210> 32

<211> 144

<212> DNA

<213> Adeno-associated virus - 4

<400> 32

ggcaaaccag atgatggagt tggccacatt agctatgcgc gctcgtcac tcactcgccc 60

ctggagacca aaggtctcca gactgccggc ctctggccgg cagggccgag tgagtgagcg	120
agcgcgcata gagggagtgg ccaa	144

<210> 33
 <211> 167
 <212> DNA
 <213> Adeno-associated virus - 5

<400> 33	
ctctcccccc tgtcgcgttc gctcgctcgc tggctcgttt ggggggggtgg cagctcaaag	60
agctgccaga cgacggccct ctggccgtcg ccccccaaa cgagccagcg agcgagcgaa	120
cgcgacaggg gggagagtgc cacactctca agcaaggggg ttttcta	167

<210> 34
 <211> 167
 <212> DNA
 <213> Adeno-associated virus - 5

<400> 34	
tacaaaacct ctttgcttga gagtgtggca ctctcccccc tgtcgcgttc gctcgctcgc	60
tggctcgttt ggggggggtgg cagctcaaag agctgccaga cgacggccct ctggccgtcg	120
cccccccaaa cgagccagcg agcgagcgaa cgcgacaggg gggagag	167

<210> 35
 <211> 145
 <212> DNA
 <213> Adeno-associated virus - 6

<400> 35	
ttggccactc cctctctgcg cgctcgctcg ctactgagg cggggcgacc aaaggtcgcc	60
cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgag agagggagtg	120
gccaactcca tcactagggg ttcct	145

<210> 36
 <211> 143
 <212> DNA
 <213> Adeno-associated virus - 6

<400> 36
 atacccttag tgatggagtt gccactccc tctatgcgcg ctgctcgct cggtagggcc 60
 ggagagcag agctctgccg tctgcggacc tttggtccgc agggcccacc gagcgagcga 120
 gcgcgcatag agggagtggg caa 143

<210> 37
 <211> 145
 <212> DNA
 <213> Adeno-associated virus - 7

<400> 37
 ttggcactc cctctatgcg cgctcgctcg ctcggtgggg cctgcggacc aaaggtccgc 60
 agacggcaga gctctgctct gccggcccca ccgagcgagc gagcgcgcat agagggagtg 120
 gccaaactcca tcactagggg taccg 145

<210> 38
 <211> 145
 <212> DNA
 <213> Adeno-associated virus - 7

<400> 38
 cggtacccct agtgatggag ttggcactc cctctatgcg cgctcgctcg ctcggtgggg 60
 cctgcggacc aaaggtccgc agacggcaga gctctgctct gccggcccca ccgagcgagc 120
 gagcgcgcat agagggagtg gccaa 145

<210> 39
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 39
 gccacggcgg aactcatcgc cgctgcctt gccgctgct ggacaggggc tcggctgttg 60
 ggactgaca attccgtggt 80

<210> 40
<211> 289
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 40
Met Pro Leu Ile Phe Lys Ile Gly Tyr Asn Val Ile Pro Leu Gln Asp
1 5 10 15

Val Ile Leu Pro Thr Pro Ser Ser Lys Val Leu Lys Tyr Leu Ile Gln
20 25 30

Ser Gly Lys Leu Ile Pro Ser Leu Lys Asp Leu Ile Thr Ser Arg Asp
35 40 45

Lys Tyr Lys Pro Ile Phe Ile Ser His Leu Gly Phe Asn Gln Arg Arg
50 55 60

Ile Phe Gln Thr Asn Gly Asn Leu Lys Thr Ile Thr Lys Gly Ser Arg
65 70 75 80

Leu Ser Ser Ile Ile Ala Phe Ser Thr Gln Ala Asn Val Leu Ser Glu
85 90 95

Val Ala Asp Glu Gly Ile Phe Glu Thr Val Tyr Gly Lys Phe His Ile
100 105 110

Met Ile Glu Ser Ile Glu Ile Val Glu Val Glu Lys Leu Lys Glu Glu
115 120 125

Val Glu Lys His Met Asn Asp Asn Ile Arg Val Arg Phe Val Ser Pro
130 135 140

Thr Leu Leu Ser Ser Lys Val Leu Leu Pro Pro Ser Leu Ser Glu Arg
145 150 155 160

Tyr Lys Lys Ile His Ala Gly Tyr Ser Thr Leu Pro Ser Val Gly Leu
165 170 175

Ile Val Ala Tyr Ala Tyr Asn Val Tyr Cys Asn Leu Ile Gly Lys Lys
180 185 190

Glu Val Glu Val Arg Ala Phe Lys Phe Gly Ile Leu Ser Asn Ala Leu
195 200 205

Ser Arg Ile Ile Gly Tyr Asp Leu His Pro Val Thr Val Ala Ile Gly
210 215 220

Glu Asp Ser Lys Gly Asn Leu Arg Lys Ala Arg Gly Val Met Gly Trp
225 230 235 240

Ile Glu Phe Asp Ile Pro Asp Glu Arg Leu Lys Arg Arg Ala Leu Asn
245 250 255

Tyr Leu Leu Thr Ser Ser Tyr Leu Gly Ile Gly Arg Ser Arg Gly Ile
260 265 270

Gly Phe Gly Glu Ile Arg Leu Glu Phe Arg Lys Ile Glu Glu Lys Glu
275 280 285

Gly

<210> 41

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 41

Met Asp Leu Glu Tyr Met His Ile Ser Tyr Pro Asn Ile Leu Leu Asn
1 5 10 15

Met Arg Asp Gly Ser Lys Leu Arg Gly Tyr Phe Ala Lys Lys Tyr Ile
20 25 30

Asp Glu Glu Ile Val His Asn His Arg Asp Asn Ala Phe Val Tyr Lys
35 40 45

Tyr Pro Gln Ile Gln Phe Lys Ile Ile Asp Arg Ser Pro Leu Ile Ile
50 55 60

Gly Ile Gly Ser Leu Gly Ile Asn Phe Leu Glu Ser Lys Arg Ile Phe
65 70 75 80

Phe Glu Lys Glu Leu Ile Ile Ser Asn Asp Thr Asn Asp Ile Thr Glu
85 90 95

Val Asn Val His Lys Asp Met Asp His Phe Gly Thr Thr Asp Lys Ile
100 105 110

Leu Lys Tyr Gln Phe Lys Thr Pro Trp Met Ala Leu Asn Ala Lys Asn
115 120 125

Ser Glu Ile Tyr Lys Asn Ser Asp Glu Ile Asp Arg Glu Glu Phe Leu
130 135 140

Lys Arg Val Leu Ile Gly Asn Ile Leu Ser Met Ser Lys Ser Leu Gly
145 150 155 160

Tyr Thr Ile Glu Glu Lys Leu Lys Val Lys Ile Asn Leu Lys Glu Val
165 170 175

Pro Val Lys Phe Lys Asn Gln Asn Met Val Gly Phe Arg Gly Glu Phe
180 185 190

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

Ser Arg Gly Phe Gly Thr Val Val Lys Val
210 215

<210> 42

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 42

Met Tyr Arg Ser Arg Asp Phe Tyr Val Arg Val Ser Gly Gln Arg Ala
1 5 10 15

Leu Phe Thr Asn Pro Ala Thr Lys Gly Gly Ser Glu Arg Ser Ser Tyr
20 25 30

Ser Val Pro Thr Arg Gln Ala Leu Asn Gly Ile Val Asp Ala Ile Tyr
35 40 45

Tyr Lys Pro Thr Phe Thr Asn Ile Val Thr Glu Val Lys Val Ile Asn
50 55 60

Gln Ile Gln Thr Glu Leu Gln Gly Val Arg Ala Leu Leu His Asp Tyr
65 70 75 80

Ser Ala Asp Leu Ser Tyr Val Ser Tyr Leu Ser Asp Val Val Tyr Leu
85 90 95

Ile Lys Phe His Phe Val Trp Asn Glu Asp Arg Lys Asp Leu Asn Ser
100 105 110

Asp Arg Leu Pro Ala Lys His Glu Ala Ile Met Glu Arg Ser Ile Arg
115 120 125

Lys Gly Gly Arg Arg Asp Val Phe Leu Gly Thr Arg Glu Cys Leu Gly
130 135 140

Leu Leu Asp Asp Ile Ser Gln Glu Glu Tyr Glu Thr Thr Val Ser Tyr
 145 150 155 160

Tyr Asn Gly Val Asn Ile Asp Leu Gly Ile Met Phe His Ser Phe Ala
 165 170 175

Tyr Pro Lys Asp Lys Lys Thr Pro Leu Lys Ser Tyr Phe Thr Lys Thr
 180 185 190

Val Met Lys Asn Gly Val Ile Thr Phe Lys Ala Gln Ser Glu Cys Asp
 195 200 205

Ile Val Asn Thr Leu Ser Ser Tyr Ala Phe Lys Ala Pro Glu Glu Ile
 210 215 220

Lys Ser Val Asn Asp Glu Cys Met Glu Tyr Asp Ala Met Glu Lys Gly
 225 230 235 240

Glu Asn

<210> 43

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 43

Met Arg Asn Glu Val Gln Phe Glu Leu Phe Gly Asp Tyr Ala Leu Phe
 1 5 10 15

Thr Asp Pro Leu Thr Lys Ile Gly Gly Glu Lys Leu Ser Tyr Ser Val
 20 25 30

Pro Thr Tyr Gln Ala Leu Lys Gly Ile Ala Glu Ser Ile Tyr Trp Lys
 35 40 45

Pro Thr Ile Val Phe Val Ile Asp Glu Leu Arg Val Met Lys Pro Ile
50 55 60

Gln Met Glu Ser Lys Gly Val Arg Pro Ile Glu Tyr Gly Gly Gly Asn
65 70 75 80

Thr Leu Ala His Tyr Thr Tyr Leu Lys Asp Val His Tyr Gln Val Lys
85 90 95

Ala His Phe Glu Phe Asn Leu His Arg Pro Asp Leu Ala Phe Asp Arg
100 105 110

Asn Glu Gly Lys His Tyr Ser Ile Leu Gln Arg Ser Leu Lys Ala Gly
115 120 125

Gly Arg Arg Asp Ile Phe Leu Gly Ala Arg Glu Cys Gln Gly Tyr Val
130 135 140

Ala Pro Cys Glu Phe Gly Ser Gly Asp Gly Phe Tyr Asp Gly Gln Gly
145 150 155 160

Lys Tyr His Leu Gly Thr Met Val His Gly Phe Asn Tyr Pro Asp Glu
165 170 175

Thr Gly Gln His Gln Leu Asp Val Arg Leu Trp Ser Ala Val Met Glu
180 185 190

Asn Gly Tyr Ile Gln Phe Pro Arg Pro Glu Asp Cys Pro Ile Val Arg
195 200 205

Pro Val Lys Glu Met Glu Pro Lys Ile Phe Asn Pro Asp Asn Val Gln
210 215 220

Ser Ala Glu Gln Leu Leu His Asp Leu Gly Gly Glu
225 230 235

<210> 44
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 44
Met Pro Asn Asp Pro Tyr Ser Leu Tyr Ser Ile Val Ile Glu Leu Gly
1 5 10 15

Ala Ala Glu Lys Gly Phe Pro Thr Gly Ile Leu Gly Arg Ser Leu His
20 25 30

Ser Gln Val Leu Gln Trp Phe Lys Gln Asp Asn Pro Phe Leu Ala Thr
35 40 45

Glu Leu His Gln Ser Gln Ile Ser Pro Phe Ser Ile Ser Pro Leu Met
50 55 60

Gly Lys Arg His Ala Lys Leu Thr Lys Ala Gly Asp Arg Leu Phe Phe
65 70 75 80

Arg Ile Cys Leu Leu Arg Gly Asp Leu Leu Gln Pro Leu Leu Asn Gly
85 90 95

Ile Glu Gln Thr Val Asn Gln Ser Val Cys Leu Asp Lys Phe Arg Phe
100 105 110

Arg Leu Cys Gln Thr His Ile Leu Pro Gly Ser His Pro Leu Ala Gly
115 120 125

Ala Ser His Tyr Ser Leu Ile Ser Gln Thr Pro Val Ser Ser Lys Ile
130 135 140

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

Ile Gln Val Phe Pro Leu Gly Glu His Val Phe Asn Ser Leu Leu Arg
165 170 175

Arg Trp Asn Asn Phe Ala Pro Glu Asp Leu His Phe Ser Gln Val Asp
180 185 190

Trp Ser Ile Pro Ile Ala Ala Phe Asp Val Lys Thr Ile Pro Ile His
195 200 205

Leu Lys Lys Val Glu Ile Gly Ala Gln Gly Trp Val Thr Tyr Ile Phe
210 215 220

Pro Asn Thr Glu Gln Ala Lys Ile Ala Ser Val Leu Ser Glu Phe Ala
225 230 235 240

Phe Phe Ser Gly Val Gly Arg Lys Thr Thr Met Gly Met Gly Gln Val
245 250 255

Gln Val Arg Ser
260

<210> 45
<211> 199
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 45
Met Tyr Leu Ser Lys Val Ile Ile Ala Arg Ala Trp Ser Arg Asp Leu
1 5 10 15

Tyr Gln Leu His Gln Gly Leu Trp His Leu Phe Pro Asn Arg Pro Asp
20 25 30

Ala Ala Arg Asp Phe Leu Phe His Val Glu Lys Arg Asn Thr Pro Glu
35 40 45

Gly Cys His Val Leu Leu Gln Ser Ala Gln Met Pro Val Ser Thr Ala
50 55 60

Val Ala Thr Val Ile Lys Thr Lys Gln Val Glu Phe Gln Leu Gln Val
65 70 75 80

Gly Val Pro Leu Tyr Phe Arg Leu Arg Ala Asn Pro Ile Lys Thr Ile
85 90 95

Leu Asp Asn Gln Lys Arg Leu Asp Ser Lys Gly Asn Ile Lys Arg Cys
100 105 110

Arg Val Pro Leu Ile Lys Glu Ala Glu Gln Ile Ala Trp Leu Gln Arg
115 120 125

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

Arg Pro Gln Tyr Phe Ser Gly Asp Gly Lys Ser Gly Lys Ile Gln Thr
145 150 155 160

Val Cys Phe Glu Gly Val Leu Thr Ile Asn Asp Ala Pro Ala Leu Ile
165 170 175

Asp Leu Val Gln Gln Gly Ile Gly Pro Ala Lys Ser Met Gly Cys Gly
180 185 190

Leu Leu Ser Leu Ala Pro Leu
195

<210> 46

<211> 187

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 46

Met Asp His Tyr Leu Asp Ile Arg Leu Arg Pro Asp Pro Glu Phe Pro
1 5 10 15

Pro Ala Gln Leu Met Ser Val Leu Phe Gly Lys Leu His Gln Ala Leu
20 25 30

Val Ala Gln Gly Gly Asp Arg Ile Gly Val Ser Phe Pro Asp Leu Asp
35 40 45

Glu Ser Arg Ser Arg Leu Gly Glu Arg Leu Arg Ile His Ala Ser Ala
50 55 60

Asp Asp Leu Arg Ala Leu Leu Ala Arg Pro Trp Leu Glu Gly Leu Arg
65 70 75 80

Asp His Leu Gln Phe Gly Glu Pro Ala Val Val Pro His Pro Thr Pro
85 90 95

Tyr Arg Gln Val Ser Arg Val Gln Ala Lys Ser Asn Pro Glu Arg Leu
100 105 110

Arg Arg Arg Leu Met Arg Arg His Asp Leu Ser Glu Glu Glu Ala Arg
115 120 125

Lys Arg Ile Pro Asp Thr Val Ala Arg Ala Leu Asp Leu Pro Phe Val
130 135 140

Thr Leu Arg Ser Gln Ser Thr Gly Gln His Phe Arg Leu Phe Ile Arg
145 150 155 160

His Gly Pro Leu Gln Val Thr Ala Glu Glu Gly Gly Phe Thr Cys Tyr
165 170 175

Gly Leu Ser Lys Gly Gly Phe Val Pro Trp Phe
180 185

<210> 47

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 47

Met Ala Ala Arg Arg Gly Gly Ile Arg Arg Thr Asp Leu Leu Arg Arg
1 5 10 15

Ser Gly Gln Pro Arg Gly Arg His Arg Ala Ser Ala Ala Glu Ser Gly
20 25 30

Leu Thr Trp Ile Ser Pro Thr Leu Ile Leu Val Gly Phe Ser His Arg
35 40 45

Gly Asp Arg Arg Met Thr Glu His Leu Ser Arg Leu Thr Leu Thr Leu
50 55 60

Glu Val Asp Ala Pro Leu Glu Arg Ala Arg Val Ala Thr Leu Gly Pro
65 70 75 80

His Leu His Gly Val Leu Met Glu Ser Ile Pro Ala Asp Tyr Val Gln
85 90 95

Thr Leu His Thr Val Pro Val Asn Pro Tyr Ser Gln Tyr Ala Leu Ala
100 105 110

Arg Ser Thr Thr Ser Leu Glu Trp Lys Ile Ser Thr Leu Thr Asn Glu
115 120 125

Ala Arg Gln Gln Ile Val Gly Pro Ile Asn Asp Ala Ala Phe Ala Gly
130 135 140

Phe Arg Leu Arg Ala Ser Gly Ile Ala Thr Gln Val Thr Ser Arg Ser
145 150 155 160

Leu Glu Gln Asn Pro Leu Ser Gln Phe Ala Arg Ile Phe Tyr Ala Arg
165 170 175

Pro Glu Thr Arg Lys Phe Arg Val Glu Phe Leu Thr Pro Thr Ala Phe
180 185 190

Lys Gln Ser Gly Glu Tyr Val Phe Trp Pro Asp Pro Arg Leu Val Phe
195 200 205

Gln Ser Leu Ala Gln Lys Tyr Gly Ala Ile Val Asp Gly Glu Glu Pro
210 215 220

Asp Pro Gly Leu Ile Ala Glu Phe Gly Gln Ser Val Arg Leu Ser Ala
225 230 235 240

Phe Arg Val Ala Ser Ala Pro Phe Ala Val Gly Ala Ala Arg Val Pro
245 250 255

Gly Phe Thr Gly Ser Ala Thr Phe Thr Val Arg Gly Val Asp Thr Phe
260 265 270

Ala Ser Tyr Ile Ala Ala Leu Leu Trp Phe Gly Glu Phe Ser Gly Cys
275 280 285

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

Ala Pro Arg Glu Lys Cys Val Pro Lys Pro
305 310

<210> 48

<211> 264

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 48

Met Arg Phe Leu Ile Arg Leu Val Pro Glu Asp Lys Asp Arg Ala Phe
1 5 10 15

Lys Val Pro Tyr Asn His Gln Tyr Tyr Leu Gln Gly Leu Ile Tyr Asn
20 25 30

Ala Ile Lys Ser Ser Asn Pro Lys Leu Ala Thr Tyr Leu His Glu Val
35 40 45

Lys Gly Pro Lys Leu Phe Thr Tyr Ser Leu Phe Met Ala Glu Lys Arg
50 55 60

Glu His Pro Lys Gly Leu Pro Tyr Phe Leu Gly Tyr Lys Lys Gly Phe
65 70 75 80

Phe Tyr Phe Ser Thr Cys Val Pro Glu Ile Ala Glu Ala Leu Val Asn
85 90 95

Gly Leu Leu Met Asn Pro Glu Val Arg Leu Trp Asp Glu Arg Phe Tyr
100 105 110

Leu His Glu Ile Lys Val Leu Arg Glu Pro Lys Lys Phe Asn Gly Ser
115 120 125

Thr Phe Val Thr Leu Ser Pro Ile Ala Val Thr Val Val Arg Lys Gly
130 135 140

Lys Ser Tyr Asp Val Pro Pro Met Glu Lys Glu Phe Tyr Ser Ile Ile
145 150 155 160

Lys Asp Asp Leu Gln Asp Lys Tyr Val Met Ala Tyr Gly Asp Lys Pro
165 170 175

Pro Ser Glu Phe Glu Met Glu Val Leu Ile Ala Lys Pro Lys Arg Phe
180 185 190

Arg Ile Lys Pro Gly Ile Tyr Gln Thr Ala Trp His Leu Val Phe Arg
195 200 205

Ala Tyr Gly Asn Asp Asp Leu Leu Lys Val Gly Tyr Glu Val Gly Phe
210 215 220

Gly Glu Lys Asn Ser Leu Gly Phe Gly Met Val Lys Val Glu Gly Asn
225 230 235 240

Lys Thr Thr Lys Glu Ala Glu Glu Gln Glu Lys Ile Thr Phe Asn Ser
245 250 255

Arg Glu Glu Leu Lys Thr Gly Val
260

<210> 49
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 49
Met Phe Val Thr Gln Val Ile Phe Asn Ile Gly Glu Arg Thr Tyr Pro
1 5 10 15

Asp Arg Ala Arg Ala Met Val Ala Glu Leu Met Asp Gly Val Gln Pro
20 25 30

Gly Leu Val Ala Thr Leu Met Asn Tyr Ile Pro Gly Thr Ser Thr Ser
35 40 45

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

Cys Leu Leu Gly Phe Gly Asp Gly Gly Gly Ala Ile Val Arg Asp Ala
65 70 75 80

Val Pro Leu Ile His Ala Ala Leu Ala Arg Arg Met Pro Asp Arg Ile
85 90 95

Ile Gln Val Glu His Lys Glu His Ser Leu Ser Ala Glu Ala Arg Pro
100 105 110

Tyr Val Leu Ser Tyr Thr Val Pro Arg Met Val Val Gln Lys Lys Gln
115 120 125

Arg His Ala Glu Arg Leu Leu His Glu Ala Glu Gly Lys Ala His Leu
130 135 140

Glu Gly Leu Phe Leu Arg Ser Leu Gln Arg Gln Ala Ala Ala Val Gly
145 150 155 160

Leu Pro Leu Pro Glu Asn Leu Glu Val Glu Phe Lys Gly Ala Val Gly
165 170 175

Asp Phe Ala Ala Lys His Asn Pro Asn Ser Lys Val Ala Tyr Arg Gly
180 185 190

Leu Arg Gly Ala Val Phe Asp Val Asn Ala Arg Leu Gly Gly Ile Trp
195 200 205

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

His Gln Leu Ser Gly Ala Val Asn Ala Leu Ser Glu
225 230 235

<210> 50

<211> 259

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 50

Met His Gln Thr Leu Ile Arg Ile Asn Trp Pro Lys Gly Phe Lys Cys
1 5 10 15

Pro Pro Ala Glu Phe Arg Glu Lys Leu Ala Lys Ser Glu Met Phe Pro
20 25 30

Pro Glu Phe Phe His Tyr Gly Thr Glu Leu Ala Val Trp Asp Lys Gln
35 40 45

Thr Ala Glu Val Glu Gly Lys Ile Lys Thr Val Ser Lys Glu Lys Ile
50 55 60

Ile Lys Thr Phe Asp Lys Pro Ile Pro Leu Asn Gly Arg Ala Pro Val
65 70 75 80

Arg Val Ile Gly Gly Gln Ala Trp Ala Gly Val Ile Ala Asp Pro Glu
85 90 95

Met Glu Gly Met Leu Ile Pro His Leu Gly Ser Ile Leu Lys Val Ala
100 105 110

Ser Ser Ala Ala Gly Cys Ala Val Lys Ile Glu Leu Glu Gln Arg Lys
115 120 125

Phe Gly Ile Ser Tyr Thr Glu Tyr Pro Val Lys Tyr Asn Leu Arg Glu
130 135 140

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

Ser Leu Ile Ala Asp Arg Ile Trp Gly Gly Val Ser Gly Glu Ser Tyr
165 170 175

Tyr Gly Ile Asp Gly Thr Cys Ala Lys Phe Gly Phe Glu Pro Pro Ser
180 185 190

Arg Glu Gln Leu Glu Leu Arg Ile Phe Pro Met Lys Asn Ile Gly Leu
195 200 205

His Met Lys Ser Ser Asp Gly Leu Ser Lys Glu Tyr Met Ser Leu Ile
210 215 220

Asp Ala Glu Val Trp Met Asn Ala Lys Leu Glu Gly Val Trp Gln Val
225 230 235 240

Gly Asn Leu Ile Ser Arg Gly Tyr Gly Arg Phe Ile Lys Ser Ile Gly
245 250 255

Ala Gln Ser

<210> 51
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 51
gataatctct tatagaattg aaag 24

<210> 52
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 52
ctaaaagaat aacttgcaaa ataacaagca ttgaaac 37

<210> 53

<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 53
gtctcaccct tcatgggtga gtggattgaa at 32

<210> 54
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 54
gtcgcactct tcatgggtgc gtggattgaa at 32

<210> 55
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 55
gtttcagtcc cgtagtcggg atttagtggt tggaaag 37

<210> 56
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 56
gagttccccg cgccagcggg gataaacg 29

<210> 57
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 57
gttcactgcc gtataggcag ctaagaa 28

<210> 58
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 58
gtcgtcagac ccaaaacccc gagaggggac ggaaac 36

<210> 59
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 59
gttacaataa gactaaaata gaattgaaag 30

<210> 60
<211> 29
<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 60

gtatttccccg cgtgcgcggg ggtgagcgg

29

<210> 61

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 61

tattggatac acccactcat tggtaggtgg ttagaac

37

<210> 62

<211> 24

<212> RNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 62

gauaaucucu uauagaauug aaag

24

<210> 63

<211> 37

<212> RNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 63

cuaaaagaau aacuugcaaa auaacaagca uugaaac 37

<210> 64
<211> 32
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 64
gucucacccu ucauggguga guggauugaa au 32

<210> 65
<211> 32
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 65
gucgcacucu ucaugggugc guggauugaa au 32

<210> 66
<211> 37
<212> RNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 66
guuucagucc cguagucggg auuuaguggu uggaaag 37

<210> 67
<211> 29
<212> RNA
<213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

 <400> 67
 gaguuccccg cgccagcggg gauaaaccg 29

<210> 68
 <211> 28
 <212> RNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

 <400> 68
 guucacugcc guauaggcag cuaagaaa 28

<210> 69
 <211> 36
 <212> RNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

 <400> 69
 gucgucagac ccaaaacccc gagaggggac ggaaac 36

<210> 70
 <211> 30
 <212> RNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

 <400> 70
 guuacaauaa gacuaaaaaua gaauugaaag 30

<210> 71
 <211> 29
 <212> RNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

 <400> 71
 guauuucccg cgugcgcggg ggugagcgg 29

 <210> 72
 <211> 37
 <212> RNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

 <400> 72
 uauuggauac acccacucau uggugggugg uuagaac 37

 <210> 73
 <211> 2133
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

 <400> 73
 atgcccaaga agaagcggaa ggtgatgcct ctgatcttca agatcggcta taacgtgatc 60
 cccctgcagg acgtgatcct gccacccct tccagcaagg tgctgaagta cctgatccag 120
 agcggcaagc tgatccccag cctgaaggac ctgatacaca gccgggacaa gtacaagcca 180
 atcttcatct cccacctggg cttcaaccag cggaggattt tccagaccaa cggcaatctg 240
 aaaaccatca ccaagggcag tagactgagc tccatcatcg ccttcagcac ccaggccaac 300

gtgctgtccg aggtggccga tgaagggatc ttcgaaaccg tgtacggaaa gttccacatc	360
atgatcgaaa gcatcgagat cgtggagggtg gaaaagctga aggaggaggt ggagaagcac	420
atgaacgaca acatcagagt gagattcgtg tctccacac tgctgagctc caaggtgctg	480
ctgcccccca gcctgtccga aagatacaag aagatccacg ccgggtacag caccctgccc	540
agcgtgggcc tgatcgtggc ctacgcctac aacgtgtact gcaatctgat cggcaagaag	600
gaagtggaag tgcgggcctt caagtttggga atcctgagca acgccctgtc cagaatcatc	660
ggctacgacc tgcaccctgt gaccgtggcc atcggcgagg acagcaaggg gaatctgaga	720
aaggctcggg gcgtgatggg ctggatcgag ttcgacatcc ccgacgaaag actgaagcgg	780
cgggccctga actatctgct gaccagcagc tacctgggca tcgggagatc tcggggcatc	840
ggcttcggcg agatccggct ggagttccgg aagattgaag agaaggaggg acccaagaag	900
aagcgggaagg tgggtggagg cggaggttct gggggaggag gtagtggcgg tgggtggttca	960
ggaggcggcg gaagccagct gcattttaccg caggttttag ctgacgctgt ctcacgcctg	1020
gtcataggta agtttggtga cctgaccgac aacttctcct cccctcacgc tcgcagaata	1080
ggtctggctg gagtcgtcat gacaacaggc acagatgtta aagatgccaa ggtgatatgt	1140
gtttctacag gagcaaaatg tattaatggg gaatacctaa gtgatcgtgg ctttgcatta	1200
aatgactgcc atgcagaaat agtatctcgg agatccttgc tcagatttct ttatacacia	1260
cttgagcttt acttaaataa cgaggatgat caaaaaagat ccatctttca gaaatcagag	1320
cgaggggggt ttaggctgaa ggagaatata cagtttcatc tgtacatcag cacctctccc	1380
tgtggagatg ccagaatctt ctcaccacat gaggcaatcc tggaagaacc agcagataga	1440
cacccaaatc gtaaagcaag aggacagcta cggaccaaaa tagaggctgg tcaggggacg	1500
attccagtgc gcaacaatgc gagcatccaa acgtgggacg gggtgctgca aggggagcgg	1560
ctgctacca tgtcctgcag tgacaagatt gcacgctgga acgtggtggg catccaggga	1620
tcactgctca gcattttcgt ggagcccatt tacttctcga gcatcatcct gggcagcctt	1680
taccacgggg accacctttc cagggccatg taccagcgga tctccaacat agaggacctg	1740
ccacctctct acaccctcaa caagcctttg ctcacaggca tcagcaatgc agaagcacgg	1800

cagccagggga agggcccccattt	attcagtgtc aactggacgg	taggcgactc cgctattgag	1860
gtcatcaacg ccacgactgg	gaagggagag ctggggccg	cgccccgcct gtgtaagcac	1920
gcgttggtact gtcgctggat	gcgtgtgcac ggcaaggttc	cctcccactt actacgtcc	1980
aagattacca agcccaacgt	gtaccatgag acaaagctgg	cggcaaagga gtaccaggcc	2040
gccaaggcgc gtctgttcac	agccttcac aaggcggggc	tgggggcctg ggtggagaag	2100
cccaccgagc aggaccagtt	ctcactcacg taa		2133

<210> 74

<211> 1920

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 74

atgcccgaaga agaagcggaa	ggtgatggac ctggagtaca	tgcacatctc ctaccctaac	60
atcctgctga acatgcggga	cggcagcaag ctgcggggct	acttcgcaa gaagtacatc	120
gacgaagaga ttgtgcacaa	ccacagagac aacgcctttg	tgtacaagta ccccagatc	180
cagtttaaga tcatcgatag	aagccccctg atcatcggca	ttggctctct gggcatcaat	240
ttcctggaga gcaagcggat	cttcttcgag aaggaactga	ttatcagcaa cgacaccaac	300
gacatcaccg aggtgaacgt	gcacaaggac atggatcact	tcggcacgac cgacaagatc	360
ctgaagtacc agttcaagac	cccttgatg gcactgaacg	ccaagaatag cgagatctac	420
aagaactctg acgagatcga	ccgggaggag ttcctgaaga	gagtgtgat tgggaatatc	480
ctgagcatgt ctaagagcct	gggctatacc atcgaagaaa	agctgaaggt gaagattaac	540
ctgaagggaag tgcccgtgaa	gttcaagaac cagaacatgg	tgggctttcg gggcgagttc	600
tacatcaact tcgacatccc	tcagtatctg ggcacggcc	ggaatgtgtc ccggggattc	660
ggcacagtgg tgaaggtgcc	caagaagaag cggaaggtgg	gtggaggcgg aggttctggg	720
ggaggaggta gtggcggtgg	tggttcagga ggcggcgga	gccagctgca tttaccgcag	780

gttttagctg acgctgtctc acgcctggtc ataggtaagt ttggtgacct gaccgacaac	840
ttctcctccc ctacgctcg cagaataggt ctggctggag tcgtcatgac aacaggcaca	900
gatgttaaag atgccaaggt gatatgtgtt tctacaggag caaaatgtat taatggtgaa	960
tacctaagtg atcgtggcct tgcattaaat gactgccatg cagaaatagt atctcggaga	1020
tccttgctca gatttcttta tacacaactt gagctttact taaataacga ggatgatcaa	1080
aaaagatcca tctttcagaa atcagagcga ggggggttta ggctgaagga gaatatacag	1140
tttcatctgt acatcagcac ctctccctgt ggagatgcca gaatcttctc accacatgag	1200
gcaatcctgg aagaaccagc agatagacac ccaaatcgta aagcaagagg acagctacgg	1260
acaaaaatag aggctggatc ggggacgatt ccagtgcgca acaatgcgag catccaaacg	1320
tgggacgggg tgctgcaagg ggagcggctg ctcacatgt cctgcagtga caagattgca	1380
cgctggaacg tgggtggcat ccagggatca ctgctcagca ttttcgtgga gcccatttac	1440
ttctcgagca tcatcctggg cagcctttac cacggggacc acctttccag ggccatgtac	1500
cagcggatct ccaacataga ggacctgcca cctctctaca ccctcaacaa gcctttgctc	1560
acaggcatca gcaatgcaga agcacggcag ccagggaagg ccccatatt cagtgtcaac	1620
tggacggtag gcgactccgc tattgaggtc atcaacgcca cgactgggaa gggagagctg	1680
ggccgcgcgt cccgcctgtg taagcacgcg ttgtactgtc gctggatgcg tgtgcacggc	1740
aaggttccct cccacttact acgctccaag attaccaagc ccaacgtgta ccatgagaca	1800
aagctggcgg caaaggagta ccaggccgcc aaggcgcgtc tgttcacagc cttcatcaag	1860
gcggggctgg gggcctgggt ggagaagccc accgagcagg accagttctc actcacgtaa	1920

<210> 75

<211> 1974

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 75

atgccaaga agaagcggaa ggtgatgaga aatgaagtgc agttcgagct gttcggcgac	60
tacgccctgt tcaccgaccc cctgaccaag atcggcggcg aaaagctgag ctacagcgtg	120
cctacctacc aggccctgaa gggcatcgcc gagagcatct actggaagcc caccatcgtg	180
ttcgtgatcg acgaactgcg ggtcatgaag ccattcaga tggagtctaa gggcgtgagg	240
cccatcgagt acggcggcgg caacaccctg gccactaca cctacctgaa ggatgtgcac	300
taccaggtga aggccactt cgagttcaac ctgcaccggc ccgacctggc cttcgataga	360
aacgagggca agcactactc catcctgcag agaagcctga aggccggcgg cagaagagat	420
attttcctgg gcgcccggga gtgccagggc tacgtggccc cctgcgagtt cggcagcggc	480
gacggcttct acgacggcca gggcaagtac cacctgggaa ccatggtgca cggtttcaac	540
taccccgacg aaaccggaca gcaccagctg gatgtgagac tgtggtctgc cgtcatggaa	600
aacggctaca tccagttccc ccgccctgag gactgcccc a tcgtgcggcc tgtgaaggag	660
atggaacca agatcttcaa ccccgacaac gtgcagtccg ccgaacagct gctgcacgac	720
ctgggcggcg aaccaagaa gaagcgggaag gtgggtggag gcggaggttc tgggggagga	780
ggtagtggcg gtggtggttc aggaggcggc ggaagccagc tgcatttacc gcaggtttta	840
gctgacgctg tctcacgcct ggtcataggt aagtttggtg acctgaccga caacttctcc	900
tcccctcacg ctgcagaat aggtctggct ggagtcgtca tgacaacagg cacagatgtt	960
aaagatgcca aggtgatatg tgtttctaca ggagcaaaat gtattaatgg tgaataccta	1020
agtgatcgtg gccttgcat aaatgactgc catgcagaaa tagtatctcg gagatccttg	1080
ctcagatttc ttatacaca acttgagctt tacttaaata acgaggatga tcaaaaaaga	1140
tccatctttc agaaatcaga gcgagggggg tttaggctga aggagaatat acagtttcat	1200
ctgtacatca gcacctctcc ctgtggagat gccagaatct tctcaccaca tgaggcaatc	1260
ctggaagaac cagcagatag acacccaaat cgtaaagcaa gaggacagct acggaccaaa	1320
atagaggctg gtcaggggac gattccagtg cgacaacatg cgagcatcca aacgtgggac	1380
ggggtgctgc aaggggagcg gctgctcacc atgtcctgca gtgacaagat tgcacgctgg	1440
aacgtggtgg gcatccaggg atcactgctc agcattttcg tggagcccat ttacttctcg	1500

agcatcatcc tgggcagcct ttaccacggg gaccaccttt ccagggccat gtaccagcgg	1560
atctccaaca tagaggacct gccacctctc tacacctca acaagccttt gctcacaggc	1620
atcagcaatg cagaagcacg gcagccaggg aaggccccc tattcagtgt caactggacg	1680
gtaggcgact ccgctattga ggtcatcaac gccacgactg ggaagggaga gctgggccgc	1740
gcgtcccgcc tgtgtaagca cgcgttgtag tgctgctgga tgctgtgca cggcaaggtt	1800
ccctcccact tactacgctc caagattacc aagcccaacg tgtaccatga gacaaagctg	1860
gcggcaaagg agtaccaggc cgccaaggcg cgtctgttca cagccttcat caaggcgggg	1920
ctgggggcct ggggtggagaa gcccaccgag caggaccagt tctcactcac gtaa	1974

<210> 76

<211> 1992

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 76

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tcactcacgt aa	1992

<210> 77
 <211> 2046
 <212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 77

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<210> 78

<211> 1860

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 78

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aagaccatcc tggacaacca gaagcggctg gacagcaagg gcaacatcaa gaggtgcaga	360
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<210> 79

<211> 1824

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 79

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<210> 80

<211> 2208

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 80

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<210> 81

<211> 2058

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 81

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<210> 82

<211> 1971

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 82

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ctggtggcca ccctgatgaa ctacatcccc ggcaccagca cgagccggac agagttcccc	180
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agtggcggtg gtggttcagg aggcggcgga agccagctgc atttaccgca ggtttttagct	840
gacgctgtct cacgcctggt cataggtaag tttggtgacc tgaccgacaa cttctcctcc	900
cctcacgctc gcagaatagg tctggctgga gtcgtcatga caacaggcac agatgttaaa	960
gatgccaagg tgatatgtgt ttctacagga gcaaaatgta ttaatggtga atacctaagt	1020
gatcgtggcc ttgcattaaa tgactgccat gcagaaatag tatctcggag atccttgctc	1080
agatttcttt atacacaact tgagctttac ttaaataacg aggatgatca aaaaagatcc	1140
atctttcaga aatcagagcg agggggggtt aggctgaagg agaataataca gtttcatctg	1200
tacatcagca cctctccctg tggagatgcc agaatcttct caccacatga ggcaatcctg	1260
gaagaaccag cagatagaca ccaaatcgt aaagcaagag gacagctacg gaccaaata	1320

gaggctggtc aggggacgat tccagtgcgc aacaatgcga gcatccaaac gtgggacggg	1380
gtgctgcaag gggagcggct gtcaccatg tcctgcagtg acaagattgc acgctggaac	1440
gtggtgggca tccagggatc actgctcagc attttcgtgg agccattta cttctcgagc	1500
atcatcctgg gcagccttta ccacggggac cacctttcca gggccatgta ccagcggatc	1560
tccaacatag aggacctgcc acctctctac accctcaaca agcctttgct cacaggcatc	1620
agcaatgcag aagcacggca gccagggaag gccccatat tcagtgtcaa ctggacggta	1680
ggcgactccg ctattgaggt catcaacgcc acgactggga agggagagct gggccgcgcg	1740
tccgcctgt gtaagcacgc gttgtactgt cgctggatgc gtgtgcacgg caaggttccc	1800
tcccacttac tacgctcaa gattaccaag cccaacgtgt accatgagac aaagctggcg	1860
gcaaaggagt accaggccgc caaggcgcgt ctgttcacag cttcatcaa ggcggggctg	1920
ggggcctggg tggagaagcc caccgagcag gaccagttct cactcacgta a	1971

<210> 83

<211> 2040

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 83

atgcccaaga agaagagaaa ggtgcaccag accctgatcc ggatcaactg gccaaggga	60
ttcaagtgcc cccctgccga gttccgggaa aagctggcca agagcgagat gttcccccc	120
gagttcttcc actacggcac ggaactggcc gtgtgggaca agcagaccgc cgaggtggag	180
ggcaagatca agaccgtgtc caaggagaag atcatcaaga ctttgacaa gcccatcccc	240
ctgaatggcc gggccccggt cagagtgatc ggcggccagg cctgggccgg cgtgatcgcc	300
gaccccgaga tggagggcat gctgatcca cacctgggga gcatcctgaa ggtggccagc	360
agcgcggccg gatgcgcagt gaagatcgaa ctggaacaga gaaagttcgg catcagctac	420
accgagtacc ccgtgaagta caacctgcgg gagctggtgc tgaagagaag atgcgaggac	480

gccccgtcta ccgatatcga gaggcctgatt gccgatagaa tctggggcgg cgtgtccggc	540
gagagctact atggcatcga cggcacatgc gccaaagtttg gcttcgaacc cccagcaga	600
gagcagctgg agctgcggat cttcccatg aagaacatcg gactgcacat gaagtccagc	660
gacggactgt ccaaggagta catgagcctg attgacgccg aggtgtggat gaacgctaag	720
ctggaaggag tgtggcaggt gggcaacctg atcagcaggg gctacggccg gttcatcaag	780
tctatcggcg cccagtcccc caagaagaag cggaaggtgg gtggaggcgg aggttctggg	840
ggaggaggta gtggcggtag tggttcagga ggcggcgga gccagctgca tttaccgcag	900
gttttagctg acgctgtctc acgcctggtc ataggtaagt ttggtgacct gaccgacaac	960
ttctcctccc ctacgctcg cagaataggt ctggctggag tcgtcatgac aacaggcaca	1020
gatgttaaag atgccaaggt gatatgtgtt tctacaggag caaaatgtat taatggtgaa	1080
tacctaagtg atcgtggcct tgcattaaat gactgccatg cagaaatagt atctcggaga	1140
tccttgctca gatttcttta tacacaactt gagctttact taaataacga ggatgatcaa	1200
aaaagatcca tctttcagaa atcagagcga ggggggttta ggctgaagga gaatatacag	1260
tttcatctgt acatcagcac ctctccctgt ggagatgcca gaatcttctc accacatgag	1320
gcaatcctgg aagaaccagc agatagacac ccaaatcgta aagcaagagg acagctacgg	1380
acaaaaatag aggctggtca ggggacgatt ccagtgcga acaatgcgag catccaaacg	1440
tgggacgggg tgctgcaagg ggagcggctg ctcacatgt cctgcagtga caagattgca	1500
cgctggaacg tgggtggcat ccagggatca ctgctcagca ttttcgtgga gcccatttac	1560
ttctcgagca tcatcctggg cagcctttac cacggggacc acctttccag ggccatgtac	1620
cagcggatct ccaacataga ggacctgcca cctctctaca ccctcaacaa gcctttgctc	1680
acaggcatca gcaatgcaga agcacggcag ccagggaagg ccccatatt cagtgtcaac	1740
tggacggtag gcgactccgc tattgaggtc atcaacgcca cgactgggaa gggagagctg	1800
ggccgcgcgt cccgcctgtg taagcacgcg ttgtactgtc gctggatgcg tgtgcacggc	1860
aaggttccct cccacttact acgctccaag attaccaagc ccaacgtgta ccatgagaca	1920
aagctggcgg caaaggagta ccaggccgcc aaggcgcgtc tgttcacagc cttcatcaag	1980

gcggggctgg gggcctgggt ggagaagccc accgagcagg accagttctc actcacgtaa 2040

<210> 84

<211> 867

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 84

atgcctctga tcttcaagat cggctataac gtgatccccc tgcaggacgt gatcctgccc	60
accccttcca gcaaggtgct gaagtacctg atccagagcg gcaagctgat cccagcctg	120
aaggacctga tcaccagccg ggacaagtac aagccaatct tcattctcca cctgggcttc	180
aaccagcgga ggattttcca gaccaacggc aatctgaaaa ccatcaccaa gggcagtaga	240
ctgagctcca tcatcgcctt cagcaccag gccaacgtgc tgtccgaggt ggccgatgaa	300
gggatcttcg aaacctgtga cggaaagttc cacatcatga tcgaaagcat cgagatcgtg	360
gaggtggaaa agctgaagga ggaggtggag aagcacatga acgacaacat cagagtgaga	420
ttcgtgtctc ccacactgct gagctccaag gtgctgctgc ccccagcct gtccgaaaga	480
tacaagaaga tccacgccgg gtacagcacc ctgcccagcg tgggcctgat cgtggcctac	540
gcctacaacg tgtactgcaa tctgatcggc aagaaggaag tggaagtgcg ggccttcaag	600
tttggaatcc tgagcaacgc cctgtccaga atcatcggct acgacctgca ccctgtgacc	660
gtggccatcg gcgaggacag caaggggaat ctgagaaagg ctcggggcgt gatgggctgg	720
atcgagtctg acatccccga cgaaagactg aagcggcggg ccctgaacta tctgctgacc	780
agcagctacc tgggcatcgg gagatctcgg ggcacggct tcggcgagat ccggctggag	840
ttccggaaga ttgaagagaa ggaggga	867

<210> 85

<211> 654

<212> DNA

<213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 85
 atggacctgg agtacatgca catctcctac cctaacatcc tgctgaacat gcgggacggc 60
 agcaagctgc ggggctactt cgccaagaag tacatcgacg aagagattgt gcacaaccac 120
 agagacaacg cctttgtgta caagtacccc cagatccagt ttaagatcat cgatagaagc 180
 cccctgatca tcggcattgg ctctctgggc atcaatttcc tggagagcaa gcggatcttc 240
 ttcgagaagg aactgattat cagcaacgac accaacgaca tcaccgaggt gaacgtgcac 300
 aaggacatgg atcacttcgg cacgaccgac aagatcctga agtaccagtt caagaccctt 360
 tggatggcac tgaacgcaa gaatagcgag atctacaaga actctgacga gatcgaccgg 420
 gaggagtcc tgaagagagt gctgattggg aatatacctga gcatgtctaa gagcctgggc 480
 tataccatcg aagaaaagct gaaggtgaag attaacctga aggaagtgcc cgtgaagtcc 540
 aagaaccaga acatggtggg ctttcggggc gagttctaca tcaacttcga catccctcag 600
 tatctgggca tcggccggaa tgtgtcccgg ggattcggca cagtggtgaa ggtg 654

<210> 86
 <211> 708
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 86
 atgagaaatg aagtgcagtt cgagctgttc ggcgactacg ccctgttcac cgaccccctg 60
 accaagatcg gcggcgaaaa gctgagctac agcgtgccta cctaccaggc cctgaagggc 120
 atcgccgaga gcatctactg gaagcccacc atcgtgttcg tgatcgacga actgcgggtc 180
 atgaagccca ttcagatgga gtctaagggc gtgaggccca tcgagtacgg cggcgggaac 240
 accctggccc actacaccta cctgaaggat gtgcactacc aggtgaaggc ccacttcgag 300

ttcaacctgc accggcccgga cctggccttc gatagaaacg agggcaagca ctactccatc	360
ctgcagagaa gcctgaaggc cggcggcaga agagatattt tcctgggcg cggggagtgc	420
cagggctacg tggccccctg cgagttcggc agcggcgacg gcttctacga cggccagggc	480
aagtaccacc tgggaaccat ggtgcacggt ttcaactacc ccgacgaaac cggacagcac	540
cagctggatg tgagactgtg gtctgccgtc atggaaaacg gctacatcca gttccccgc	600
cctgaggact gccccatcgt gcggcctgtg aaggagatgg aaccaagat cttcaacccc	660
gacaacgtgc agtccgccga acagctgctg cacgacctgg gcggcgaa	708

<210> 87

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 87

atgtacagaa gccgggactt ctacgtgaga gtgtccggcc agcgggccct gttcaccaac	60
cccgccacca agggcggctc cgaacggagc tcctactccg tgcctaccg gcaggccctg	120
aacgggattg tggacgcat ctactacaag cccacgttca ccaacatcgt gaccgagggt	180
aaggtgatta accagatcca gaccgaactg cagggcgtgc gggccctgct gcatgactac	240
agcggcgacc tgagctacgt gtcctacctg agcgacgtgg tgtacctgat taagtttcat	300
ttcgtgtgga acgaggatag aaaggacctg aatagcgacc ggctgccagc caagcatgag	360
gccatcatgg agcgggtctat ccggaagggc ggcagacggg acgtgttcct gggcaccaga	420
gaatgcctgg gcctgctgga cgacatcagc caggaagaat acgaaaccac agtgagctat	480
tacaatgggg tgaacatcga cctgggcatc atgttccaca gcttcgctta cccaaggac	540
aagaaaaccc ccctgaagtc ctacttcaca aagaccgtga tgaagaacgg cgtgatcacc	600
ttcaaggccc agtccgaatg cgatattgtg aacaccctga gctcctacgc cttcaaggcc	660
cccgaggaga tcaagagcgt gaacgacgag tgcattggagt acgacgcat ggagaagggc	720

gaaaac

726

<210> 88

<211> 780

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 88

atgcccaacg atccctacag cctgtactcc atcgtgatcg aactgggcgc cgccgaaaag	60
ggattcccca caggcatcct gggcagaagc ctgcatagcc aggtgctgca gtggttcaag	120
caggataacc ctttcctggc caccgagctg caccagagcc agatctcccc cttctccatc	180
tctccactga tgggcaagcg gcacgccaag ctgaccaagg ccggcgaccg gctgttcttt	240
cggatctgcc tgctgagagg agatctgctg cagcccctgc tgaacggcat tgagcagacc	300
gtgaaccaga gcgtgtgcct ggacaagttc cggttcgggc tgtgccagac ccacatcctg	360
cccggcagcc accctctggc tggcgcctcc cactatagcc tgatcagcca gaccccagtg	420
agctccaaga ttaccctgga cttcaagagt tctacctcct tcaaggtgga ccggaagatc	480
atccaagtgt tccctctggg cgaacacgtg ttcaacagcc tgctcagacg ctggaataac	540
ttcgcccccg aggacctgca cttctctcag gtggactgga gcatcccat cgccgcattc	600
gacgtgaaaa ccatcccat ccacctgaag aaggtcgaga tcggcgcacg gggctgggtg	660
acctacatct tccccaacac agaacaggcc aagatcgctt ccgtgctgag cgaattcgcc	720
ttcttcagcg gagtgggacg gaaaaccacc atgggcatgg gccagggtgca ggtgcggtcc	780

<210> 89

<211> 597

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 89
atgtacctga gcaaggtgat catcgccaga gcctggagca gagacctgta ccagctgcac 60
cagggcctgt ggcacctgtt cccaaccgg cccgacgccg cccgggattt cctgttccac 120
gtggagaaga gaaacacccc ggaaggctgc cacgtgctgc tgcagagcgc acagatgcct 180
gtgagcaccg ccgtggccac cgtgatcaag accaagcagg tggagttcca gctgcaggtg 240
ggcgtgcccc tgtatttcag gctgcgggcg aatcccatca agaccatcct ggacaaccag 300
aagcggctgg acagcaaggg caacatcaag aggtgcagag tgcctctgat caaggaggcc 360
gaacagatcg cctggctgca gcggaagctg ggcaatgccg ccagagtgga ggacgtgcac 420
cccatcagcg agcggcccca gtacttctcc ggcgacggaa agagcggaaa gatccagacc 480
gtgtgcttcg agggcgtgct gaccatcaac gacgcaccg ccctgatcga cctcgtgcag 540
caggggatcg gccctgcaa gtccatgggc tgcggactgc tgtccctggc cccctg 597

<210> 90
<211> 561
<212> DNA
<213> Artificial Sequence
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 90
atggaccact acctggacat tagactgcgc cctgaccag agttccctcc tgcccagctg 60
atgtctgtgc tgtttgcaa gctgcaccag gccctggtgg cccagggcgg tgacagaatc 120
ggagtgtctt tccctgatct ggacgaatct agatctagac tgggagagag actgagaatc 180
cacgcgtctg ccgacgacct gagagctctg ctggccagac catggctgga aggactgcgc 240
gaccacctgc agttcggatga acctgccgtg gtgcctcacc caactccata cagacaggtg 300
agtagagtgc aggcaaagtc taatccagag agactgagac gcagactgat gagaaggcat 360
gacctgtccg aagaagaagc cagaaagaga atcccagaca cagtggccag agccctggat 420
ctgccttttg tgaccctgag aagccagtct accggccagc acttcagact gtttattcgc 480

cacggaccac tgcaggtgac cgccgaagag ggaggtttta cctgctacgg actgagcaag	540
ggaggtttcg tgccttggtt c	561

<210> 91
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 91	
atggccgcca gaagaggcgg aatccggaga accgacctgc tgcggaggtc tggccagcct	60
cggggcagac accgggcctc cgccgccgag agcggcctga catggatctc ccctaccctg	120
atcctgggtgg gcttcagcca caggggcgat aggagaatga ccgagcacct gtccagactg	180
accctgaccc tggaagtgga tgccccctg gagagagccc ggggtggccac cctgggcccc	240
cacctgcatg gcgtgctgat ggagtctatc cccgccgact acgtgcagac actgcacaca	300
gtgccggtga acccttacag ccagtagcgt ctggcccgga gcaccaccag cctggagtgg	360
aagatctcca ccctgacaaa tgaggcccgg cagcagatcg tcggcccat caacgacgcc	420
gccttcgccg gcttcgggt gcgggccagc ggcatcgcca ccaggtgac aagcagaagc	480
ctggagcaga accccctgtc ccagtttgcc agaatcttct acgccaggcc cgaaaccgcg	540
aagttcagag tggagttcct gacccccacc gccttcaagc agagcggcga gtacgtgttt	600
tggcccgatc ccagactggt gttccagtcc ctggcccaga agtacggcgc catcgtggac	660
ggagaagagc ccgaccccg cctgatcgcc gagtttggtc agtccgtgag actgagcgcc	720
ttcagagtgg ccagcgcccc ttttgccgtg ggcgccgcca gggtgcccgg attcaccggc	780
agcgccacct tcaccgtgcg gggagtggac accttcgcca gctacatcgc cgctctgctg	840
tggttcggcg agttcagcgg atgcggcatc aaggcctcca tgggaatggg cgccatccgg	900
gtgcagcctc tggcccccg ggagaagtgc gtgcccaagc cc	942

<210> 92

<211> 792
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 92
atgagattcc tgatcagact ggtgcccagag gacaaggaca gagccttcaa ggtgccttac 60
aaccaccagt actatctgca gggcctgata tacaacgcca tcaagtcctc caacccaag 120
ctggccacct acctgcacga ggtgaagggc cccaagctgt tcacctacag cctgttcattg 180
gccgaaaagc gggagcacc taagggcctg ccctactttc tgggctacaa gaagggttc 240
ttctacttca gcacctgcgt gcccagatc gccgaggccc tggatgaacgg cctgctgatg 300
aatcccaggg tgcggctgtg ggacgagaga ttctacctgc acgaaatcaa ggtcctgcgg 360
gagcccaaga agttcaacgg cagcaccttc gtgacctga gcccacatgc cgtgacctg 420
gtgagaaaagg gcaagtccta cgacgtgccc cccatggaaa aggagttcta cagcattatc 480
aaggatgacc tgcaggacaa gtacgtgatg gcctacggcg acaagcccc cagtgaattc 540
gagatggaag tgctgatcgc caagcccaag cggttcgga tcaagcccgg catctatcag 600
accgcctggc acctggtgtt tcgggcctac ggcaatgacg acctgctgaa ggtgggctac 660
gaagtgggat tcggggagaa gaactccctg ggattcggaa tggatcaagg gaggggcaac 720
aagaccacca aggaagccga agaacaggag aagatcacct tcaactccc ggaagagctg 780
aaaacaggcg tg 792

<210> 93
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 93

atgttcgtga cccaggtgat cttcaacatc ggcgaacgga cgtaccccga cagggtcgg	60
gctatggtgg ccgagctgat ggatggcgtc cagcctggcc tggtagggccac cctgatgaac	120
tacatccccg gcaccagcac gagccggaca gagttcccca ccgtgcagtt cggcggcgcc	180
agcgacggct tttgcctgct gggcttcggc gacggcggcg gcgccatcgt gagagatgcc	240
gtgcccctga tccacgccgc cctggcaagg cggatgcctg atcggatcat ccaggtggaa	300
cacaaggagc acagcctgtc cgccgaggcc cggccctacg tgctgagcta caccgtgcct	360
cggatggtgg tgcagaagaa gcagcggcac gccgagagac tgctgcacga agccgaggga	420
aaggctcacc tggagggcct gttcctgcgg agcctgcaga ggcaggccgc cgccgtgggc	480
ctgcccctgc ccgagaacct ggaggtggag ttcaaggag cgtggggcga cttcgccgca	540
aagcacaatc caaatagcaa ggtggcctac cggggactga gaggcgccgt gttcgatgtg	600
aacgccagac tgggcggcat ctggaccgcc ggattcatgc tgagcaaggg ctacggccag	660
tttaacgcca cccaccagct gagcggcgcc gtgaacgctc tgtccgaa	708

<210> 94

<211> 777

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 94

atgcaccaga ccctgatccg gatcaactgg cccaagggat tcaagtgcc ccctgccgag	60
ttccgggaaa agctggccaa gagcgagatg ttcccccccg agttcttcca ctacggcacg	120
gaactggccg tgtgggacaa gcagaccgcc gaggtggagg gcaagatcaa gaccgtgtcc	180
aaggagaaga tcatcaagac ctttgacaag cccatcccc tgaatggccg ggccccggtc	240
agagtgatcg gcggccaggc ctgggccggc gtgatcgccg accccgagat ggagggcattg	300
ctgatccac acctggggag catcctgaag gtggccagca gcgcggccgg atgcgcagtg	360
aagatcgaac tggaacagag aaagttcggc atcagctaca ccgagtacc cgtgaagtac	420

aacctgcggg agctgggtgct gaagagaaga tgcgaggacg cccggtctac cgatatcgag	480
agcctgattg ccgatagaat ctggggcggc gtgtccggcg agagctacta tggcatcgac	540
ggcacatgcg ccaagtttgg cttcgaaccc cccagcagag agcagctgga gctgcggatc	600
ttccccatga agaacatcgg actgcacatg aagtccagcg acggactgtc caaggagtac	660
atgagcctga ttgacgccga ggtgtggatg aacgctaagc tggaaggagt gtggcaggtg	720
ggcaacctga tcagcagggg ctacggccgg ttcatcaagt ctatcggcgc ccagtcc	777

<210> 95
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
 <221> VARIANT
 <222> (3)..(3)
 <223> /replace="Phe"

<220>
 <221> VARIANT
 <222> (4)..(4)
 <223> /replace="Tyr"

<220>
 <221> SITE
 <222> (1)..(6)
 <223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<400> 95
 Arg Asn Tyr Phe Ser His
 1 5

<210> 96
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 96
Arg Asn Tyr Phe Ser His
1 5

<210> 97
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 97
Arg Asn Phe Tyr Ser His
1 5

<210> 98
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> VARIANT
<222> (3)..(3)
<223> /replace="Lys"

<220>
<221> SITE
<222> (1)..(6)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<400> 98

Arg Asn Ala Ala Leu His
1 5

<210> 99
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 99
Arg Ala Phe Phe His His
1 5

<210> 100
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 100
Arg Arg Ala Phe Phe His
1 5

<210> 101
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<223> a, c, t, or g

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        preference with respect to those in the annotations
        for variant positions"

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agacggccgn gctctgcccc gccggcccca gcgagcgagc gagcgcgcad agagggagtg      120
gccaactcca tcactagggg tdcbb                                           145

<210> 102
<211> 144
<212> DNA
<213> Artificial Sequence

<220>
<221> source
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        polynucleotide"

<220>
<221> variation
<222> (1)..(1)
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<220>
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<223> a, c, t, or g

<220>
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        preference with respect to those in the annotations
        for variant positions"

<400> 102
rdtacccta gtgatggagt tggccactcc ctctatgcgc gctcgctcgc tcggtggggc      60

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ctgcvgacca aaggtcbcca gacggcvng ctctgchcgg ccggccccac cgagcgagcg 120

agcgcgcata gagggagtgg ccaa 144

<210> 103

<211> 22

<212> DNA

<213> Adeno-associated virus - 2

<400> 103

ctgcgcgctc gctcgctcac tg 22

<210> 104

<211> 22

<212> DNA

<213> Adeno-associated virus - 2

<400> 104

cagtgagcga gcgagcgcg ag 22