

Sequence listing

<110> LLC "ANABION"

<120> ISOLATED MODIFIED VP1 CAPSID PROTEIN OF AAV5

<160> 18

<170> BiSSAP 1.3.6

<210> 1

<211> 724

<212> PRT

<213> Natural sequence

<223> The natural sequence of the VP1 protein of the wild-type AAV5 capsid

<400> 1

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Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
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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        80
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       160
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

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		275					280				285				
Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly	Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val
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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
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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					475					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					555					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> 2
<211> 724
<212> PRT
<213> Artificial sequence

<223> The isolated altered VP1 protein of the AAV5 capsid, which
includes one substitution in S651A position

<400> 2
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 80
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
145 150 155 160
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
 465 470 475 480
 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
 545 550 555 560
 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 Ala 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
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 Thr Arg Pro Leu

<210> 3
 <211> 724
 <212> PRT
 <213> Artificial sequence

<223> The isolated altered VP1 protein of the AAV5 capsid, which includes S2A and T711S substitutions

<400> 3
 Met Ala 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 80
 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
 145 150 155 160
 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

Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys
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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
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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					475					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	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					555					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	Ser	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu
705					710					715					720
Thr	Arg	Pro	Leu												

<211> 724
 <212> PRT
 <213> Artificial sequence

<223> The isolated altered VP1 protein of the AAV5 capsid protein, which includes 2A, S651A and T711S substitutions

<400>

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Met Ala 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     80
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    160
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

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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					475					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					555					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	Ala	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	Ser	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu
705					710					715					720
Thr	Arg	Pro	Leu												

<210> 5

<211> 2175

<212> DNA

<213> Artificial sequence

<223> The nucleic acid encoding the altered capsid protein of adeno-associated virus serotype 5 (AAV5) with S651A amino acid substitution

<400> 5

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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga	180
ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag	240
cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag	300
gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc	360
aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc	420
ggaaagcggg tagacgacca ctttccaaaa agaaagaagg ctccggaccga agaggactcc	480
aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaadc	540
ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca	600
ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc	660
gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc	720
agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc	780
aacgcctact ttggatacag caccctctgg gggtactttg actttaaccg cttccacagc	840
cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccg	900
tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc	960
accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag	1020
ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc	1080
tttacgctgc cgagctacgg ttacgcgacg ctgaaccgag acaacacaga aaatcccacc	1140
gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac	1200
aactttgagt ttacctaca ctttgaggag gtgcccttcc actccagctt cgctcccagt	1260
cagaacctgt tcaagctggc caaccgctg gtggaccagt acttgtagcg cttcgtgagc	1320
acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc	1380
tacaaaaact gggtcccggg gcccatgggc cgaaccagg gctggaacct gggctccggg	1440

gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg	1500
agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc	1560
tatgccttgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc	1620
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gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgcccc	1740
gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac	1800
gtgtacctcc aaggacccat ctgggccaaag atcccagaga cgggggcgca ctttcacccc	1860
tctccggcca tgggcggatt cggactcaaa caccaccgc ccatgatgct catcaagaac	1920
acgcctgtgc ccggaaatat caccagcttc gcggacgtgc ccgtcagcag cttcatcacc	1980
cagtacagca ccgggcaggc caccgtggag atggagtggg agctcaagaa ggaaaactcc	2040
aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac	2100
tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaac ccgatacctt	2160
acccgacccc tttaa	2175

<210> 6

<211> 2175

<212> DNA

<213> Artificial sequence

<223> The nucleic acid encoding the altered capsid protein of adeno-associated virus serotype 5 (AAV5) with S2A and T711S amino acid substitutions

<400> 6

atggcttttg ttgatcacc tccagattgg ttggaagaag ttggtgaagg tcttcgcgag	60
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gcccgtggtc ttgtgctgcc tggttataac tatctcggac ccggaaacgg tctcgatcga	180
ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag	240
cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag	300
gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc	360
aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc	420
ggaaagcgga tagacgacca ctttcaaaa agaaagaagg ctcggaccga agaggactcc	480

aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaatc	540
ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca	600
ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc	660
gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc	720
agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc	780
aacgcctact ttggatacag cacccttggt ggggtactttg actttaaccg cttccacagc	840
cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccg	900
tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacgggtgca ggactccacc	960
accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag	1020
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tttacgctgc cgcagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc	1140
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aactttgagt ttacctaca ctttgaggag gtgcccttcc actccagctt cgctcccagt	1260
cagaacctct tcaagctggc caaccgctg gtggaccagt acttgtagcg cttcgtgagc	1320
acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc	1380
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gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg	1500
agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc	1560
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acgtacctcg agggcaacat gtcatacacc agcgagagcg agacgcagcc ggtgaaccgc	1680
gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgcccc	1740
gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac	1800
gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc	1860
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cagtacagca ccgggcaggc caccgtggag atggagtggg agctcaagaa ggaaaaactcc	2040
aagagggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac	2100

tttgcctcgg acagcaccgg ggaatacaga agcaccagac ctatcggaac ccgatacctt	2160
acccgacccc tttaa	2175

<210> 7
 <211> 2175
 <212> DNA
 <213> Artificial sequence

<223> The nucleic acid encoding the altered capsid protein of adeno-associated virus serotype 5 (AAV5) with S2A, S651A and T711S amino acid substitutions

<400> 7	
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gcccgtgggtc ttgtgctgcc tgggtataac tatctcggac ccggaaacgg tctcgatcga	180
ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag	240
cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag	300
gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc	360
aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggccccctacc	420
ggaaagcggg tagacgacca ctttcaaaa agaaagaagg ctcggaccga agaggactcc	480
aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaata	540
ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca	600
ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc	660
gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc	720
agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc	780
aacgcctact ttggatacag cccccctgg ggggtactttg actttaaccg cttccacagc	840
cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccgg	900
tccctcagag tcaaaatctt caacattcaa gtcaaagagg tcacggtgca ggactccacc	960
accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag	1020
ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc	1080
tttacgtgc cgcagtagcg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc	1140

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gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac      1200
aactttgagt ttacctacaa ctttgaggag gtgcccttcc actccagctt cgctcccagt      1260
cagaacctct tcaagctggc caacccgctg gtggaccagt acttgtaccg cttcgtgagc      1320
acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc      1380
tacaaaaact ggttcccggg gcccatgggc cgaacccagg gctggaacct gggctccggg      1440
gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg      1500
agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc      1560
tatgccctgg agaacactat gatcttcaac agccagccgg cgaacccggg caccaccgcc      1620
acgtacctcg agggcaacat gtcctcacc agcgagagcg agacgcagcc ggtgaaccgc      1680
gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgcccc      1740
gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac      1800
gtgtacctcc aaggacccat ctgggccaag atcccagaga cgggggcgca ctttcacccc      1860
tctccggcca tgggcggatt cggactcaaa caccaccgc ccatgatgct catcaagaac      1920
acgcctgtgc ccggaatat caccagcttc gcggacgtgc ccgtcagcag cttcatcacc      1980
cagtacagca ccgggcaggt caccgtggag atggagtggg agctcaagaa ggaaaactcc      2040
aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccca gtttgtggac      2100
tttgccccgg acagcaccgg ggaatacaga agcaccagac ctatcggaac ccgatacctt      2160
acccgacccc tttaa                                                    2175

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<210> 8

<211> 588

<212> PRT

<213> Natural sequence

<223> The isolated amino acid sequence of the VP2 protein of the wild-type AAV5 capsid

<400> 8

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Lys Ala Arg Thr Glu Glu Asp Ser Lys Pro Ser Thr Ser Ser Asp Ala
          20          25          30
Glu Ala Gly Pro Ser Gly Ser Gln Gln Leu Gln Ile Pro Ala Gln Pro

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Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro Glu Thr Gly Ala
 465 470 475 480
 His Phe His Pro Ser Pro Ala Met Gly Gly Phe Gly Leu Lys His Pro
 485 490 495
 Pro Pro Met Met Leu Ile Lys Asn Thr Pro Val Pro Gly Asn Ile Thr
 500 505 510
 Ser Phe Ser Asp Val Pro Val Ser Ser Phe Ile Thr Gln Tyr Ser Thr
 515 520 525
 Gly Gln Val Thr Val Glu Met Glu Trp Glu Leu Lys Lys Glu Asn Ser
 530 535 540
 Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Asn Asn Tyr Asn Asp Pro
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 Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
 580 585

<210> 9

<211> 588

<212> PRT

<213> Artificial sequence

<223> The isolated altered VP2 protein of the AAV5 capsid, which includes T575S substitution

<400> 9

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 Glu Ala Gly Pro Ser Gly Ser Gln Gln Leu Gln Ile Pro Ala Gln Pro
 35 40 45
 Ala Ser Ser Leu Gly Ala Asp Thr Met Ser Ala Gly Gly Gly Gly Pro
 50 55 60
 Leu Gly Asp Asn Asn Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly
 65 70 75 80
 Asp Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val Thr Lys
 85 90 95
 Ser Thr Arg Thr Trp Val Leu Pro Ser Tyr Asn Asn His Gln Tyr Arg
 100 105 110
 Glu Ile Lys Ser Gly Ser Val Asp Gly Ser Asn Ala Asn Ala Tyr Phe
 115 120 125
 Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Ser
 130 135 140
 His Trp Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Tyr Trp Gly
 145 150 155 160
 Phe Arg Pro Arg Ser Leu Arg Val Lys Ile Phe Asn Ile Gln Val Lys
 165 170 175
 Glu Val Thr Val Gln Asp Ser Thr Thr Thr Ile Ala Asn Asn Leu Thr
 180 185 190
 Ser Thr Val Gln Val Phe Thr Asp Asp Asp Tyr Gln Leu Pro Tyr Val
 195 200 205

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225					230					235					240
Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro
				245					250					255	
Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe
			260					265					270		
Glu	Glu	Val	Pro	Phe	His	Ser	Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe
		275					280					285			
Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp	Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser
	290					295					300				
Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln	Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg
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Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp	Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr
				325					330					335	
Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly	Val	Asn	Arg	Ala	Ser	Val	Ser	Ala
			340					345					350		
Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu	Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val
			355				360					365			
Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr	Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr
	370					375					380				
Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile	Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro
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Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu	Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu
				405					410					415	
Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg	Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln
			420					425					430		
Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser	Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr
			435				440					445			
Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro	Gly	Ser	Val	Trp	Met	Glu	Arg	Asp
	450					455					460				
Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala
465					470					475					480
His	Phe	His	Pro	Ser	Pro	Ala	Met	Gly	Gly	Phe	Gly	Leu	Lys	His	Pro
				485					490					495	
Pro	Pro	Met	Met	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr
			500					505					510		
Ser	Phe	Ser	Asp	Val	Pro	Val	Ser	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr
			515				520					525			
Gly	Gln	Val	Thr	Val	Glu	Met	Glu	Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser
						535					540				
Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro
545					550					555					560
Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp	Ser	Thr	Gly	Glu	Tyr	Arg	Ser	Thr
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Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Pro	Leu				
			580					585							

<210> 10

<211> 588

<212> PRT

<213> Artificial sequence

<223> The isolated altered VP2 protein of the AAV5 capsid, which includes S515A and T575S substitutions

<400> 10

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Glu	Ala	Gly	Pro	Ser	Gly	Ser	Gln	Gln	Leu	Gln	Ile	Pro	Ala	Gln	Pro
			35				40					45			
Ala	Ser	Ser	Leu	Gly	Ala	Asp	Thr	Met	Ser	Ala	Gly	Gly	Gly	Gly	Pro
	50					55				60					
Leu	Gly	Asp	Asn	Asn	Gln	Gly	Ala	Asp	Gly	Val	Gly	Asn	Ala	Ser	Gly
65					70				75					80	
Asp	Trp	His	Cys	Asp	Ser	Thr	Trp	Met	Gly	Asp	Arg	Val	Val	Thr	Lys
			85					90						95	
Ser	Thr	Arg	Thr	Trp	Val	Leu	Pro	Ser	Tyr	Asn	Asn	His	Gln	Tyr	Arg
			100					105					110		
Glu	Ile	Lys	Ser	Gly	Ser	Val	Asp	Gly	Ser	Asn	Ala	Asn	Ala	Tyr	Phe
		115					120					125			
Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg	Phe	His	Ser
	130					135					140				
His	Trp	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn	Tyr	Trp	Gly
145					150				155						160
Phe	Arg	Pro	Arg	Ser	Leu	Arg	Val	Lys	Ile	Phe	Asn	Ile	Gln	Val	Lys
				165				170						175	
Glu	Val	Thr	Val	Gln	Asp	Ser	Thr	Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr
			180					185					190		
Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val
		195					200					205			
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	210					215					220				
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225				230					235						240
Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser	Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro
				245				250						255	
Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn	Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe
			260					265					270		
Glu	Glu	Val	Pro	Phe	His	Ser	Ser	Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe
		275					280					285			
Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp	Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser
	290					295					300				
Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln	Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg
305				310					315						320
Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp	Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr
				325					330					335	
Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly	Val	Asn	Arg	Ala	Ser	Val	Ser	Ala
			340					345					350		
Phe	Ala	Thr	Asn	Arg	Met	Glu	Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	
		355				360						365			

Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr	Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr
	370					375					380				
Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile	Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro
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Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu	Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu
				405					410						415
Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg	Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln
			420					425					430		
Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser	Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr
		435					440					445			
Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro	Gly	Ser	Val	Trp	Met	Glu	Arg	Asp
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Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp	Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala
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Pro	Pro	Met	Met	Leu	Ile	Lys	Asn	Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr
			500					505					510		
Ser	Phe	Ala	Asp	Val	Pro	Val	Ser	Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr
		515					520					525			
Gly	Gln	Val	Thr	Val	Glu	Met	Glu	Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser
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Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln	Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro
545					550					555					560
Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp	Ser	Thr	Gly	Glu	Tyr	Arg	Ser	Thr
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Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu	Thr	Arg	Pro	Leu				
			580					585							

<210> 11

<211> 532

<212> PRT

<213> Natural sequence

<223> The amino acid sequence of the VP3 protein of the wild-type AAV5 capsid

<400> 11

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

		115					120				125				
Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp
	130						135				140				
Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys
145					150					155					160
Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr
			165						170					175	
Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser
			180					185					190		
Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn
		195					200					205			
Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser
	210					215					220				
Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp
225				230						235					240
Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln
			245						250					255	
Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp
		260					265						270		
Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly
		275					280					285			
Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu
	290					295					300				
Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr
305					310					315					320
Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile
			325						330					335	
Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu
			340					345					350		
Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg
		355					360					365			
Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser
	370				375						380				
Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr	Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro
385					390					395					400
Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp
			405					410						415	
Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met
			420				425						430		
Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn
		435				440						445			
Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ser	Asp	Val	Pro	Val	Ser
	450					455					460				
Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu
465					470					475					480
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln
			485					490						495	
Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp
			500					505					510		
Ser	Thr	Gly	Glu	Tyr	Arg	Thr	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu
		515					520					525			
Thr	Arg	Pro	Leu												
	530														

<210> 12
 <211> 532
 <212> PRT
 <213> Artificial sequence

<223> The isolated altered VP3 protein of the AAV5 capsid, which includes T519S substitution

<400> 12
 Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
 1 5 10 15
 Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
 20 25 30
 Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
 35 40 45
 Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
 50 55 60
 Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
 65 70 75 80
 Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
 85 90 95
 Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
 100 105 110
 Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
 115 120 125
 Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
 130 135 140
 Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
 145 150 155 160
 Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
 165 170 175
 Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
 180 185 190
 Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
 195 200 205
 Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
 210 215 220
 Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
 225 230 235 240
 Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
 245 250 255
 Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
 260 265 270
 Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
 275 280 285
 Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
 290 295 300
 Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
 305 310 315 320
 Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
 325 330 335

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
 340 345 350
 Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
 355 360 365
 Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
 370 375 380
 Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
 385 390 395 400
 Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
 405 410 415
 Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
 420 425 430
 Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
 435 440 445
 Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
 450 455 460
 Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
 465 470 475 480
 Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
 485 490 495
 Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
 500 505 510
 Ser Thr Gly Glu Tyr Arg Ser Thr Arg Pro Ile Gly Thr Arg Tyr Leu
 515 520 525
 Thr Arg Pro Leu
 530

<210> 13

<211> 532

<212> PRT

<213> Artificial sequence

<223> The isolated altered VP3 protein of the AAV5 capsid, which includes S459A and T519S substitutions

<400> 13

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

		115					120				125				
Thr	Thr	Ile	Ala	Asn	Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp
	130						135				140				
Asp	Asp	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Gly	Asn	Gly	Thr	Glu	Gly	Cys
145					150					155					160
Leu	Pro	Ala	Phe	Pro	Pro	Gln	Val	Phe	Thr	Leu	Pro	Gln	Tyr	Gly	Tyr
				165					170					175	
Ala	Thr	Leu	Asn	Arg	Asp	Asn	Thr	Glu	Asn	Pro	Thr	Glu	Arg	Ser	Ser
			180					185					190		
Phe	Phe	Cys	Leu	Glu	Tyr	Phe	Pro	Ser	Lys	Met	Leu	Arg	Thr	Gly	Asn
		195					200					205			
Asn	Phe	Glu	Phe	Thr	Tyr	Asn	Phe	Glu	Glu	Val	Pro	Phe	His	Ser	Ser
	210					215					220				
Phe	Ala	Pro	Ser	Gln	Asn	Leu	Phe	Lys	Leu	Ala	Asn	Pro	Leu	Val	Asp
225				230						235					240
Gln	Tyr	Leu	Tyr	Arg	Phe	Val	Ser	Thr	Asn	Asn	Thr	Gly	Gly	Val	Gln
				245					250					255	
Phe	Asn	Lys	Asn	Leu	Ala	Gly	Arg	Tyr	Ala	Asn	Thr	Tyr	Lys	Asn	Trp
			260					265					270		
Phe	Pro	Gly	Pro	Met	Gly	Arg	Thr	Gln	Gly	Trp	Asn	Leu	Gly	Ser	Gly
		275					280					285			
Val	Asn	Arg	Ala	Ser	Val	Ser	Ala	Phe	Ala	Thr	Thr	Asn	Arg	Met	Glu
	290					295					300				
Leu	Glu	Gly	Ala	Ser	Tyr	Gln	Val	Pro	Pro	Gln	Pro	Asn	Gly	Met	Thr
305					310					315					320
Asn	Asn	Leu	Gln	Gly	Ser	Asn	Thr	Tyr	Ala	Leu	Glu	Asn	Thr	Met	Ile
				325					330					335	
Phe	Asn	Ser	Gln	Pro	Ala	Asn	Pro	Gly	Thr	Thr	Ala	Thr	Tyr	Leu	Glu
			340					345					350		
Gly	Asn	Met	Leu	Ile	Thr	Ser	Glu	Ser	Glu	Thr	Gln	Pro	Val	Asn	Arg
		355					360					365			
Val	Ala	Tyr	Asn	Val	Gly	Gly	Gln	Met	Ala	Thr	Asn	Asn	Gln	Ser	Ser
	370					375					380				
Thr	Thr	Ala	Pro	Ala	Thr	Gly	Thr	Tyr	Asn	Leu	Gln	Glu	Ile	Val	Pro
385					390					395					400
Gly	Ser	Val	Trp	Met	Glu	Arg	Asp	Val	Tyr	Leu	Gln	Gly	Pro	Ile	Trp
				405					410					415	
Ala	Lys	Ile	Pro	Glu	Thr	Gly	Ala	His	Phe	His	Pro	Ser	Pro	Ala	Met
			420					425					430		
Gly	Gly	Phe	Gly	Leu	Lys	His	Pro	Pro	Pro	Met	Met	Leu	Ile	Lys	Asn
		435					440					445			
Thr	Pro	Val	Pro	Gly	Asn	Ile	Thr	Ser	Phe	Ala	Asp	Val	Pro	Val	Ser
	450					455					460				
Ser	Phe	Ile	Thr	Gln	Tyr	Ser	Thr	Gly	Gln	Val	Thr	Val	Glu	Met	Glu
465					470					475					480
Trp	Glu	Leu	Lys	Lys	Glu	Asn	Ser	Lys	Arg	Trp	Asn	Pro	Glu	Ile	Gln
				485					490					495	
Tyr	Thr	Asn	Asn	Tyr	Asn	Asp	Pro	Gln	Phe	Val	Asp	Phe	Ala	Pro	Asp
			500					505					510		
Ser	Thr	Gly	Glu	Tyr	Arg	Ser	Thr	Arg	Pro	Ile	Gly	Thr	Arg	Tyr	Leu
		515					520					525			
Thr	Arg	Pro	Leu												
	530														

<210> 14
 <211> 2175
 <212> DNA
 <213> Artificial sequence

<223> The isolated nucleic acid encoding aforementioned VP1 of the capsid of the wild-type adeno-associated virus serotype 5 (AAV5)

<400> 14
 atgtcttttg ttgatcacc tccagattgg ttggaagaag ttggtgaagg tcttcgag 60
 tttttgggcc ttgaagcggg cccaccgaaa ccaaaacca atcagcagca tcaagatcaa 120
 gcccgtgggtc ttgtgctgcc tggttataac tatctcggac ccggaacgg tctcgatcga 180
 ggagagcctg tcaacagggc agacgaggtc gcgcgagagc acgacatctc gtacaacgag 240
 cagcttgagg cgggagacaa cccctacctc aagtacaacc acgcggacgc cgagtttcag 300
 gagaagctcg ccgacgacac atccttcggg ggaaacctcg gaaaggcagt ctttcaggcc 360
 aagaaaaggg ttctcgaacc ttttggcctg gttgaagagg gtgctaagac ggcccctacc 420
 ggaaagcggg tagacgacca ctttcaaaa agaaagaagg ctcggaccga agaggactcc 480
 aagccttcca cctcgtcaga cgccgaagct ggacccagcg gatcccagca gctgcaaadc 540
 ccagcccaac cagcctcaag tttgggagct gatacaatgt ctgcgggagg tggcggccca 600
 ttgggcgaca ataaccaagg tgccgatgga gtgggcaatg cctcgggaga ttggcattgc 660
 gattccacgt ggatggggga cagagtcgtc accaagtcca cccgaacctg ggtgctgccc 720
 agctacaaca accaccagta ccgagagatc aaaagcggct ccgtcgacgg aagcaacgcc 780
 aacgcctact ttggatacag cccccctgg gggtactttg actttaaccg cttccacagc 840
 cactggagcc cccgagactg gcaaagactc atcaacaact actggggctt cagaccccg 900
 tccctcagag tcaaatctt caacattcaa gtcaaagagg tcacgggtgca ggactccacc 960
 accaccatcg ccaacaacct cacctccacc gtccaagtgt ttacggacga cgactaccag 1020
 ctgccctacg tcgtcggcaa cgggaccgag ggatgcctgc cggccttccc tccgcaggtc 1080
 tttacgtgc cgagtacgg ttacgcgacg ctgaaccgcg acaacacaga aaatcccacc 1140
 gagaggagca gcttcttctg cctagagtac tttcccagca agatgctgag aacgggcaac 1200
 aactttgagt ttacctaca ctttgaggag gtgcccttcc actccagctt cgctcccagt 1260

cagaacctct tcaagctggc caaccgctg gtggaccagt acttgtagcg cttcgtgagc	1320
acaaataaca ctggcggagt ccagttcaac aagaacctgg ccgggagata cgccaacacc	1380
tacaaaaact gggtcccggg gcccatgggc cgaaccagg gctggaacct gggctccggg	1440
gtcaaccgcg ccagtgtcag cgccttcgcc acgaccaata ggatggagct cgagggcgcg	1500
agttaccagg tgccccgca gccgaacggc atgaccaaca acctccaggg cagcaacacc	1560
tatgccctgg agaacactat gatcttcaac agccagccgg cgaaccggg caccaccgcc	1620
acgtacctcg agggcaacat gtcctcacc agcgagagcg agacgcagcc ggtgaaccgc	1680
gtggcgtaca acgtcggcgg gcagatggcc accaacaacc agagctccac cactgcccc	1740
gcgaccggca cgtacaacct ccaggaaatc gtgcccggca gcgtgtggat ggagagggac	1800
gtgtacctcc aaggacccat ctgggccaaag atcccagaga cgggggcgca ctttcacccc	1860
tctccggcca tgggcggatt cggactcaaa caccaccgc ccatgatgct catcaagaac	1920
acgcctgtgc ccggaaatat caccagcttc tcggacgtgc ccgtcagcag cttcatcacc	1980
cagtacagca ccgggcaggc caccgtggag atggagtggg agctcaagaa ggaaaactcc	2040
aagaggtgga acccagagat ccagtacaca aacaactaca acgaccccc gtttgtggac	2100
tttgccccgg acagcaccgg ggaatacaga accaccagac ctatcggaa ccgatacctt	2160
acccgacccc tttaa	2175

<210> 15

<211> 1767

<212> DNA

<213> Artificial sequence

<223> The isolated nucleic acid encoding altered VP2 protein of the
 adeno-associated virus serotype 5 (AAV5) capsid with amino acid T575S
 substitution

<400> 15

acggccccta ccggaaagcg gatagacgac cactttccaa aaagaaagaa ggctcggacc	60
gaagaggact ccaagccttc cacctcgtca gacgccgaag ctggacccag cggatcccag	120
cagctgcaaa tcccagccca accagcctca agtttgggag ctgatacaat gtctgcggga	180
ggtggcggcc cattgggcga caataacaa ggtgccgatg gagtgggcaa tgctcggga	240
gattggcatt gcgattccac gtggatgggg gacagagtcg tcaccaagtc caccgaacc	300

tgggtgctgc ccagctacaa caaccaccag taccgagaga tcaaaagcgg ctccgtcgac	360
ggaagcaacg ccaacgccta ctttggatac agcaccacct ggggggtactt tgactttaac	420
cgcttccaca gccactggag ccccgagac tggcaaagac tcatcaacaa ctactggggc	480
ttcagacccc ggtccctcag agtcaaaatc ttcaacattc aagtcaaaga ggtcacgggtg	540
caggactcca ccaccacat cgccaacaac ctcacctcca ccgtccaagt gtttacggac	600
gacgactacc agctgcccta cgctgctggc aacgggaccg agggatgcct gccggccttc	660
cctccgcagg tctttacgct gccgcagtac ggttacgcga cgctgaaccg cgacaacaca	720
gaaaatccca ccgagaggag cagcttcttc tgcctagagt actttcccag caagatgctg	780
agaacgggca acaactttga gtttacctac aactttgagg aggtgccctt ccactccagc	840
ttcgctccca gtcagaacct cttcaagctg gccaaaccgc tgggtggacca gtacttgtac	900
cgcttcgtga gcacaaataa cactggcgga gtccagttca acaagaacct ggccgggaga	960
tacgccaaca cctacaaaaa ctggttcccg gggcccatgg gccgaaccca gggctggaac	1020
ctgggctccg ggggtcaaccg cgccagtgtc agcgccttcg ccacgaccaa taggatggag	1080
ctcgagggcg cgagttacca ggtgcccccg cagccgaacg gcatgaccaa caacctccag	1140
ggcagcaaca cctatgccct ggagaacact atgatcttca acagccagcc ggccaacccg	1200
ggcaccaccg ccacgtacct cgagggaac atgctcatca ccagcgagag cgagacgcag	1260
ccggtgaacc gcgtggcgta caacgtcggc gggcagatgg ccaccaacaa ccagagctcc	1320
accactgccc ccgcgaccgg cacgtacaac ctccaggaaa tcgtgcccgg cagcgtgtgg	1380
atggagaggg acgtgtacct ccaaggacct atctgggcca agatcccaga gacgggggcg	1440
cactttcacc cctctccggc catgggcgga ttcggactca aacacccacc gcccatgatg	1500
ctcatcaaga acacgcctgt gcccggaaat atcaccagct tctcggacgt gcccgtcagc	1560
agcttcatca ccagtacag caccgggcag gtcaccgtgg agatggagtg ggagctcaag	1620
aaggaaaact ccaagagggtg gaaccagag atccagtaca caaacaacta caacgacccc	1680
cagtttgtgg actttgcccc ggacagcacc ggggaataca gaagcaccag acctatcgga	1740
acccgatacc ttaccgacc cctttaa	1767

<211> 1767
 <212> DNA
 <213> Artificial sequence

<223> The isolated nucleic acid encoding altered aforementioned VP2 of
 the adeno-associated virus serotype 5 (AAV5) capsid of the wild-type

<400> 16
 acggccccta ccggaagcg gatagacgac cactttccaa aaagaaagaa ggctcggacc 60
 gaagaggact ccaagccttc cacctcgtca gacgccgaag ctggacccag cggatcccag 120
 cagctgcaaa tcccagccca accagcctca agtttgggag ctgatacaat gtctgcggga 180
 ggtggcggcc cattgggcga caataaccaa ggtgccgatg gagtgggcaa tgcctcggga 240
 gattggcatt gcgattccac gtggatgggg gacagagtcg tcaccaagtc caccgaacc 300
 tgggtgctgc ccagctacaa caaccaccag taccgagaga tcaaaagcgg ctccgtcgac 360
 ggaagcaacg ccaacgccta ctttgatac agcaccacct ggggtactt tgactttaac 420
 cgcttcaca gccactggag ccccgagac tggcaaagac tcatcaacaa ctactggggc 480
 ttcagacccc ggtccctcag agtcaaaatc ttcaacattc aagtcaaaga ggtcacggtg 540
 caggactcca ccaccacat cgccaacaac ctcacctca ccgtccaagt gtttacggac 600
 gacgactacc agctgcccta cgtcgtcggc aacgggaccg agggatgcct gccggccttc 660
 cctccgcagg tctttacgct gccgcagtac gggttacgca cgctgaaccg cgacaacaca 720
 gaaaatccca ccgagaggag cagcttcttc tgcctagagt actttcccag caagatgctg 780
 agaacgggca acaactttga gtttacctac aactttgagg aggtgccctt ccactccagc 840
 ttcgctccca gtcagaacct cttcaagctg gccaaaccgc tggtagacca gtacttgtac 900
 cgcttcgtga gcacaaataa cactggcgga gtccagttca acaagaacct ggccgggaga 960
 tacgccaaca cctacaaaaa ctggttcccg gggcccatgg gccgaacca gggctggaac 1020
 ctgggctccg ggggtcaaccg cgccagtgtc agcgccttcg ccacgaccaa taggatggag 1080
 ctcgagggcg cgagttacca ggtgcccccg cagccgaacg gcatgaccaa caacctccag 1140
 ggcagcaaca cctatgccct ggagaacact atgatcttca acagccagcc ggcgaaccg 1200
 ggcaccaccg ccacgtacct cgagggaac atgctcatca ccagcgagag cgagacgcag 1260
 ccggtgaacc gcgtggcgta caacgtcggc gggcagatgg ccaccaacaa ccagagctcc 1320

accactgccc ccgcgaccgg cacgtacaac ctccaggaaa tcgtgcccgg cagcgtgtgg	1380
atggagaggg acgtgtacct ccaaggaccc atctgggcca agatcccaga gacggggggcg	1440
cactttcacc cctctccggc catgggcgga ttcggactca aacaccacc gcccatgatg	1500
ctcatcaaga acacgcctgt gcccggaaat atcaccagct tctcggacgt gcccgtcagc	1560
agcttcatca ccagttacag caccgggcag gtcaccgtgg agatggagtg ggagctcaag	1620
aaggaaaact ccaagaggtg gaaccagag atccagtaca caaacaacta caacgacccc	1680
cagtttgtgg actttgcccc ggacagcacc ggggaataca gaaccaccag acctatcgga	1740
acccgatacc ttacccgacc cctttaa	1767

<210> 17

<211> 1599

<212> DNA

<213> Artificial sequence

<223> The isolated nucleic acid encoding altered VP3 protein of the
 adeno-associated virus serotype 5 (AAV5) capsid with amino acid T519S
 substitution

<400> 17

atgtctgcgg gaggtggcgg ccattgggc gacaataacc aaggtgccga tggagtgggc	60
aatgcctcgg gagattggca ttgcgattcc acgtggatgg gggacagagt cgtcaccaag	120
tccaccgaa cctgggtgct gcccagctac aacaaccacc agtaccgaga gatcaaaagc	180
ggctccgtcg acggaagcaa cgccaacgcc tactttggat acagcacccc ctgggggtac	240
tttgacttta accgcttcca cagccactgg agccccgag actggcaaag actcatcaac	300
aactactggg gcttcagacc ccggtccctc agagtcaaaa tcttcaacat tcaagtcaaa	360
gaggtcacgg tgcaggactc caccaccacc atcgccaaca acctcacctc caccgtccaa	420
gtgttttacgg acgacgacta ccagctgccc tacgtcgtcg gcaacgggac cgagggatgc	480
ctgccggcct tccctccgca ggtctttacg ctgccgcagt acggttacgc gacgctgaac	540
cgcgacaaca cagaaaatcc caccgagagg agcagcttct tctgcctaga gtactttccc	600
agcaagatgc tgagaacggg caacaacttt gagtttacct acaactttga ggaggtgccc	660
ttccactcca gcttcgctcc cagtcagaac ctcttcaagc tggccaaccc gctggtggac	720

cagtacttgt accgcttcgt gagcacaat aacactggcg gagtccagtt caacaagaac	780
ctggccggga gatacgcaa cacctacaaa aactggttcc cggggcccat gggccgaacc	840
cagggtctga acctgggctc cggggtcaac cgcgccagtg tcagcgcctt cgccacgacc	900
aataggatgg agctcgaggg cgcgagttac caggtgcccc cgcagccgaa cggcatgacc	960
aacaacctcc agggcagcaa cacctatgcc ctggagaaca ctatgatctt caacagccag	1020
ccggcgaacc cgggcaccac cgccacgtac ctcgagggca acatgctcat caccagcgag	1080
agcgagacgc agccggtgaa ccgcgtggcg tacaacgtcg gcgggcagat ggccaccaac	1140
aaccagagct ccaccactgc ccccgcgacc ggcacgtaca acctccagga aatcgtgccc	1200
ggcagcgtgt ggatggagag ggacgtgtac ctccaaggac ccatctgggc caagatccca	1260
gagacggggg cgcactttca cccctctccg gccatgggcg gattcggact caaacacca	1320
ccgcccata tgctcatcaa gaacacgcct gtgcccggaa atatcaccag cttctcggac	1380
gtgcccgtca gcagcttcat caccagctac agcaccgggc aggtcaccgt ggagatggag	1440
tgggagctca agaaggaaaa ctccaagagg tggaaccag agatccagta cacaacaac	1500
tacaacgacc ccagtttgt ggactttgcc ccggacagca ccggggaata cagaagcacc	1560
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<210> 18

<211> 1599

<212> DNA

<213> Artificial sequence

<223> The isolated nucleic acid encoding altered aforementioned VP3 of the adeno-associated virus serotype 5 (AAV5) capsid of the wild-type

<400> 18

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