

FIGURE 1

Hu5	APKGAENPCWEDEAATALEINLEEEEDDDNEDEVDEQAEOQKTHVFGQAPYSGINITKEGIQIGVESQT---
Pan-6	APKGAENSSQWEQAKTG-----NGGTMEHTHYGVA PMGSENITKDELQIGTDTVANQ
Pan-5	APKGAENTCQWTYKADG-----DTGTEKTYTYGNAFVQGISITKDGQLGTDITDD---
Pan-7	APKGAENTCQWTYKAG-----DTDTEKTYTYGNAFVQGISITKDGQLGTDITDD---
Pan-9	APKGAENTCQWTYKADG-----ETATEKTYTYGNAFVQGINITKDGQLGTDITDD---
Hu5	--PKYADKTFQPEPQIGESQWYETEIN--HAAGRVLAKKTT PMKPCYGSYAKPTNENGSGGLLVKQNN--G
Pan-6	NKPIYADKTFQPEPQVGEENWQETEN---FYGGRALKKDTNMKPCYGSYARPTNEKGGQAKLVGDDGVP
Pan-5	-QPIYADKTYQPEPQVGDAEWHIDITGDEKYGGRALKPDTMKPCYGSFAKPTNKEGGQANVKETG--G
Pan-7	-QAIYADETYQPEPQVGDAEWHIDITGDEKYGGRALKPDTMKPCYGSFAKPTNKEGGQANVKETG--G
Pan-9	-QPIYADKTYQPEPQVGDAEWHIDITGDEKYGGRALKPDTMKPCYGSFAKPTNKEGGQANVKETG--T
Hu5	KLESQVEMQOFFSTTEATAGNDNLTPKVLYSEVDIETPDTHISYMPITKEGNSRELMGQQSMENRPNY
Pan-6	TKEFDIDLAFFDTGGTVNGQDEYKADIVMYTENTYLETPDTHVVKPGKDDASSEINLVQQSMENRPNY
Pan-5	TKEYDIDMAFFDNRSAAG---LAPEIVLYTENVDIETPDTHIVYKAGTDDSSSSINLGQQSMENRPNY
Pan-7	TKEYDIDMAFFDNRSAAG---LAPEIVLYTENVDIETPDTHIVYKAGTDDSSSSINLGQQSMENRPNY
Pan-9	TKEYDIDMAFFDNRSAAG---LAPEIVLYTENVDIETPDTHIVYKAGTDDSSSSINLGQQSMENRPNY
Hu5	IAFRDNFICGLMYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDF
Pan-6	IGFRDNFICGLMYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDF
Pan-5	IGFRDNFICGLMYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDF
Pan-7	IGFRDNFICGLMYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDF
Pan-9	IGFRDNFICGLMYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDF
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Pan-6	DVRIIENHGVEDELPNYCFPLDGSSTNAAYQGVKVGQDGDVESEWENDDTVA-ARNQLCKGNIFAMEI
Pan-5	DVRIIENHGVEDELPNYCFPLDAVGRTDTYQGIKAN----GADQTTTKDDTNN-DANELGKGNFEAMEI
Pan-7	DVRIIENHGVEDELPNYCFPLDAVGRTDTYQGIKAN----GDNQTTTKDDTNN-DANELGKGNFEAMEI
Pan-9	DVRIIENHGVEDELPNYCFPLDAVGRTDTYQGIKAN----GTDQTTTKDDSVN-DANEIGKGNFEAMEI

Fig. 2

Pan-9 fiber knob	(1)	YUWTPDPSPENCQILAENNAKLECHIKKGGSOIKANVSVLVWGGSG-NENP
Pan-6 fiber knob	(1)	YUWTPDPSPENCQLLSDRAKFECHIKKGGSOIKAVAAVVGSA-NP
Ad 2 fiber knob	(1)	YUWTPDPSPENCRIHSDNCHVUANKGGSVNATAALA-SG--D-SS
Ad 5 fiber knob	(1)	YUWTPDPSPENCRLNAEKAKLEVUANKGGSOIKANVSVLA-KG--SAP
Pan-7 fiber knob	(1)	YUWTPADPSPENCKIYSEKAKLECHIKKGGSOIKETIVLA-NNG-S-NP
Pan-5 fiber knob	(1)	YUWTPADPSPENCHYSEKAKLECHIKKGGSOIKCHVSLIA-DTG-S-NP
Pan-9 fiber knob	(50)	ITGYSQAQVELREDANGVELTEHSTLKVNGYQOQDSIDGTFYINAVES
Pan-6 fiber knob	(51)	INDYKSAIVFLRPSDGVLMSSMVGDNHFFEGQITQSVAKNNAVGS
Ad 2 fiber knob	(49)	MTCHVASVSIFLRFQNGVEMENSSLKHNWFRNENSTNANPEYUNAVES
Ad 5 fiber knob	(49)	ISGYSQAHLLIRFBENGVLNNSLDPENHFNENDLTEGYAKNAVGS
Pan-7 fiber knob	(50)	ITNYSSTALVSLKFBASEVHLSSTLSDKEYWNHFKGDDVTPAEPYUNAVES
Pan-5 fiber knob	(50)	ITGYSITALVSLKETDANGVHQSSSTLSDSDNHNFFQGDVTPAFAKFNNAIG
Pan-9 fiber knob	(100)	MENLKAYFKSQSSSTTANNVGOYVANGDVSKEMIETIILNGHDDS----
Pan-6 fiber knob	(101)	MENLIGAYFKTQSKTPKNSYSQVLTETMTMTITIFENGDEK-DTTP
Ad 2 fiber knob	(99)	MENLLAYFKTQSQTAANNVSOVHLGDKTKEMIETIILNGHSESTETSE
Ad 5 fiber knob	(99)	MENLSYFKSHGKTASNNVSOVINGDKTKVETIETIILNGHGOET-GDTT
Pan-7 fiber knob	(100)	MENIKAYFKNTSAASKSHYSQVINGDEAKELMIIIFENEDAT----
Pan-5 fiber knob	(100)	MENLKAYFKNTSGAAKSHVGGKVLHDTGKELDSIIFENESDES----
Pan-9 fiber knob	(145)	NSTYSMSYSYTF-NGSYVGATFGANGYTFESVIAOF
Pan-6 fiber knob	(150)	VSTYSMTFTWQWTDGDKDKNITFATNSFSESIMAO
Ad 2 fiber knob	(149)	VSTYSMSYTSWE-SGKYTTFETATNSYTFSCIAOF
Ad 5 fiber knob	(148)	PSAYSMSYSDWS-GHNYINEIFATNSYTFVIAOF
Pan-7 fiber knob	(146)	-CTYSITQWKND-STKYTGETLATSEFTSYIAOF
Pan-5 fiber knob	(146)	-CTYKINQWQNG-ADQYKNETLAVSEFTSYIAKE

SEQUENCE LISTING

<110> The Trustees of the University of Pennsylvania

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Vectors Containing Same, and Methods of Use

<130> SP6191C

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<150> US 60/366,798

<151> 2002-03-22

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Tyr Lys Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Asn	
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Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val	
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Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val	
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Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu	
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Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser	
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Pro Phe Ile Asn Pro Pro Phe Val Ser Ser Asp Gly Phe Gln Glu
1490 1495 1500
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Lys Pro Leu Gly Val Leu Ser Leu Arg Leu Ala Asp Pro Val Thr
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Thr Lys Asn Gly Glu Ile	Thr Leu Lys Leu Gly	Asp Gly Val Asp	
1520	1525	1530	
ctc gac tcc tcg gga aaa	ctc atc tcc aac acg	gcc acc aag gcc	32292
Leu Asp Ser Ser Gly Lys	Leu Ile Ser Asn Thr	Ala Thr Lys Ala	
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Ala Ala Pro Leu Ser Phe	Ser Asn Asn Thr Ile	Ser Leu Asn Met	
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gat acc cct ttt tac aac	aac aat gga aag tta	ggc atg aaa gtc	32382
Asp Thr Pro Phe Tyr Asn	Asn Asn Gly Lys Leu	Gly Met Lys Val	
1565	1570	1575	
act gct cca ctg aag ata	cta gac aca gac ttg	cta aaa aca ctt	32427
Thr Ala Pro Leu Lys Ile	Leu Asp Thr Asp Leu	Leu Lys Thr Leu	
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gtt gta gct tat gga caa	ggt tta gga aca aac	acc act ggt gcc	32472
Val Val Ala Tyr Gly Gln	Gly Leu Gly Thr Asn	Thr Thr Gly Ala	
1595	1600	1605	
ctt gtt gcc caa cta gca	tcc cca ctt gct ttt	gat agc aat agc	32517
Leu Val Ala Gln Leu Ala	Ser Pro Leu Ala Phe	Asp Ser Asn Ser	
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aaa att gcc ctt aat tta	ggc aat gga cca ttg	aaa gtg gat gca	32562
Lys Ile Ala Leu Asn Leu	Gly Asn Gly Pro Leu	Lys Val Asp Ala	
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Asn Arg Leu Asn Ile Asn	Cys Asn Arg Gly Leu	Tyr Val Thr Thr	
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aca aaa gat gca ctg gaa	gcc aat ata agt tgg	gct aat gct atg	32652
Thr Lys Asp Ala Leu Glu	Ala Asn Ile Ser Trp	Ala Asn Ala Met	
1655	1660	1665	
aca ttt ata gga aat gcc	atg ggt gtc aat att	gat aca caa aaa	32697
Thr Phe Ile Gly Asn Ala	Met Gly Val Asn Ile	Asp Thr Gln Lys	
1670	1675	1680	
ggc ttg caa ttt ggc acc	act agt acc gtc gca	gat gtt aaa aac	32742
Gly Leu Gln Phe Gly Thr	Thr Ser Thr Val Ala	Asp Val Lys Asn	
1685	1690	1695	
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Ala Tyr Pro Ile Gln Ile	Lys Leu Gly Ala Gly	Leu Thr Phe Asp	
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Ser Thr Gly Ala Ile Val	Ala Trp Asn Lys Asp	Asp Asp Lys Leu	
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aca cta tgg acc aca gcc gac ccc tct cca aat tgt cac ata tat	32877
Thr Leu Trp Thr Thr Ala Asp Pro Ser Pro Asn Cys His Ile Tyr	
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Ser Glu Lys Asp Ala Lys Leu Thr Leu Cys Leu Thr Lys Cys Gly	
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Ser Gln Ile Leu Gly Thr Val Ser Leu Ile Ala Val Asp Thr Gly	
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agt tta aat ccc ata aca gga aca gta acc act gct ctt gtc tca	33012
Ser Leu Asn Pro Ile Thr Gly Thr Val Thr Thr Ala Leu Val Ser	
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gac tca gac tat tgg aat ttc aga cag gga gat gtt aca cct gct	33102
Asp Ser Asp Tyr Trp Asn Phe Arg Gln Gly Asp Val Thr Pro Ala	
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gaa gcc tat act aat gct ata ggt ttc atg ccc aat cta aaa gca	33147
Glu Ala Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn Leu Lys Ala	
1820 1825 1830	
tac cct aaa aac aca agt gga gct gca aaa agt cac att gtt ggg	33192
Tyr Pro Lys Asn Thr Ser Gly Ala Ala Lys Ser His Ile Val Gly	
1835 1840 1845	
aaa gtg tac cta cat ggg gat aca ggc aaa cca ctg gac ctc att	33237
Lys Val Tyr Leu His Gly Asp Thr Gly Lys Pro Leu Asp Leu Ile	
1850 1855 1860	
att act ttc aat gaa aca agt gat gaa tct tgc act tac tgt att	33282
Ile Thr Phe Asn Glu Thr Ser Asp Glu Ser Cys Thr Tyr Cys Ile	
1865 1870 1875	
aac ttt caa tgg cag tgg ggg gct gat caa tat aaa aat gaa aca	33327
Asn Phe Gln Trp Gln Trp Gly Ala Asp Gln Tyr Lys Asn Glu Thr	
1880 1885 1890	
ctt gcc gtc agt tca ttc acc ttt tcc tat att gct aaa gaa taa	33372
Leu Ala Val Ser Ser Phe Thr Phe Ser Tyr Ile Ala Lys Glu	
1895 1900 1905	
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 <212> PRT
 <213> chimpanzee adenovirus serotype Pan5

<400> 2

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		20					25						30		
Pro	Tyr	Val	Pro	Pro	Arg	Tyr	Leu	Ala	Pro	Thr	Glu	Gly	Arg	Asn	Ser
	35						40					45			
Ile	Arg	Tyr	Ser	Glu	Leu	Ala	Pro	Leu	Tyr	Asp	Thr	Thr	Arg	Leu	Tyr
	50					55					60				

Leu Val Asp Asn Lys Ser Ala Asp Ile Ala Ser Leu Asn Tyr Gln Asn
 65 70 75 80
 Asp His Ser Asn Phe Leu Thr Thr Val Val Gln Asn Asn Asp Phe Thr
 85 90 95
 Pro Thr Glu Ala Ser Thr Gln Thr Ile Asn Phe Asp Glu Arg Ser Arg
 100 105 110
 Trp Gly Gly Gln Leu Lys Thr Ile Met His Thr Asn Met Pro Asn Val
 115 120 125
 Asn Glu Phe Met Tyr Ser Asn Lys Phe Lys Ala Arg Val Met Val Ser
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 Arg Lys Thr Pro Asn Gly Val Thr Val Thr Asp Gly Ser Gln Asp Glu
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 Leu Thr Tyr Glu Trp Val Glu Phe Glu Leu Pro Glu Gly Asn Phe Ser
 165 170 175
 Val Thr Met Thr Ile Asp Leu Met Asn Asn Ala Ile Ile Asp Asn Tyr
 180 185 190
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 Leu Val Met Pro Gly Val Tyr Thr Asn Glu Ala Phe His Pro Asp Ile
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 Ile Leu Tyr Glu Asp Leu Glu Gly Gly Asn Ile Pro Ala Leu Leu Asp
 275 280 285
 Val Asp Ala Tyr Glu Lys Ser Lys Glu Asp Ser Ala Ala Ala Ala Thr
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 Ala Ala Val Ala Thr Ala Ser Thr Glu Val Arg Gly Asp Asn Phe Ala
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 Ser Ala Ala Thr Leu Ala Ala Ala Glu Ala Ala Glu Thr Glu Ser Lys
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 Ile Val Ile Gln Pro Val Glu Lys Asp Ser Lys Glu Arg Ser Tyr Asn
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Val Leu Ala Asp Lys Lys Asn Thr Ala Tyr Arg Ser Trp Tyr Leu Ala
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 Tyr Asn Tyr Gly Asp Pro Glu Lys Gly Val Arg Ser Trp Thr Leu Leu
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 Thr Thr Ser Asp Val Thr Cys Gly Val Glu Gln Val Tyr Trp Ser Leu
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 Pro Asp Met Met Gln Asp Pro Val Thr Phe Arg Ser Thr Arg Gln Val
 405 410 415
 Ser Asn Tyr Pro Val Val Gly Ala Glu Leu Leu Pro Val Tyr Ser Lys
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 Ser Phe Phe Asn Glu Gln Ala Val Tyr Ser Gln Gln Leu Arg Ala Phe
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 Thr Ser Leu Thr His Val Phe Asn Arg Phe Pro Glu Asn Gln Ile Leu
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 Val Arg Pro Pro Ala Pro Thr Ile Thr Thr Val Ser Glu Asn Val Pro
 465 470 475 480
 Ala Leu Thr Asp His Gly Thr Leu Pro Leu Arg Ser Ser Ile Arg Gly
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 Thr Phe
 530

<210> 3
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 <212> PRT
 <213> chimpanzee adenovirus serotype Pan5
 <400> 3

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 35 40 45
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
 50 55 60

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

Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu
 370 375 380
 Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp
 385 390 395 400
 Ala Val Gly Arg Thr Asp Thr Tyr Gln Gly Ile Lys Ala Asn Gly Ala
 405 410 415
 Asp Gln Thr Thr Trp Thr Lys Asp Asp Thr Val Asn Asp Ala Asn Glu
 420 425 430
 Leu Gly Lys Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn
 435 440 445
 Leu Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp
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 Ser Tyr Lys Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Asn
 465 470 475 480
 Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp
 485 490 495
 Ala Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn
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 Val Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser
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 Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro
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 Gln Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr
 545 550 555 560
 Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser
 565 570 575
 Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ala Phe Thr
 580 585 590
 Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala
 595 600 605
 Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe
 610 615 620
 Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn
 625 630 635 640
 Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe
 645 650 655
 Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Arg Glu Thr Pro Ser Leu
 660 665 670

Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr
 675 680 685
 Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile
 690 695 700
 Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr
 705 710 715 720
 Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn
 725 730 735
 Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu
 740 745 750
 Ala His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr
 755 760 765
 Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg
 770 775 780
 Gln Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu
 785 790 795 800
 Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr
 805 810 815
 Met Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile
 820 825 830
 Gly Lys Ser Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp
 835 840 845
 Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly
 850 855 860
 Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His
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 885 890 895
 Leu Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro
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 <213> chimpanzee adenovirus serotype Pan5

<400> 4

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Phe	Val	Ser	Ser	Asp	Gly	Phe	Gln	Glu	Lys	Pro	Leu	Gly	Val	Leu	Ser	35	40	45	
Leu	Arg	Leu	Ala	Asp	Pro	Val	Thr	Thr	Lys	Asn	Gly	Glu	Ile	Thr	Leu	50	55	60	
Lys	Leu	Gly	Asp	Gly	Val	Asp	Leu	Asp	Ser	Ser	Gly	Lys	Leu	Ile	Ser	65	70	75	80
Asn	Thr	Ala	Thr	Lys	Ala	Ala	Ala	Pro	Leu	Ser	Phe	Ser	Asn	Asn	Thr	85	90	95	
Ile	Ser	Leu	Asn	Met	Asp	Thr	Pro	Phe	Tyr	Asn	Asn	Asn	Gly	Lys	Leu	100	105	110	
Gly	Met	Lys	Val	Thr	Ala	Pro	Leu	Lys	Ile	Leu	Asp	Thr	Asp	Leu	Leu	115	120	125	
Lys	Thr	Leu	Val	Val	Ala	Tyr	Gly	Gln	Gly	Leu	Gly	Thr	Asn	Thr	Thr	130	135	140	
Gly	Ala	Leu	Val	Ala	Gln	Leu	Ala	Ser	Pro	Leu	Ala	Phe	Asp	Ser	Asn	145	150	155	160
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Lys	Asp	Ala	Leu	Glu	Ala	Asn	Ile	Ser	Trp	Ala	Asn	Ala	Met	Thr	Phe	195	200	205	
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Gln	Ile	Lys	Leu	Gly	Ala	Gly	Leu	Thr	Phe	Asp	Ser	Thr	Gly	Ala	Ile	245	250	255	
Val	Ala	Trp	Asn	Lys	Asp	Asp	Asp	Lys	Leu	Thr	Leu	Trp	Thr	Thr	Ala	260	265	270	
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tac aac gtg	gcc cag tgc aac atg	acc aag gac tgg ttc	ctg gtc	20557
Tyr Asn Val	Ala Gln Cys Asn Met	Thr Lys Asp Trp Phe	Leu Val	
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cag atg ctg	gcc cac tac aac atc	ggc tac cag ggc ttc	tac gtg	20602
Gln Met Leu	Ala His Tyr Asn Ile	Gly Tyr Gln Gly Phe	Tyr Val	
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ccc gag ggc	tac aag gac cgc atg	tac tcc ttc ttc cgc	aac ttc	20647
Pro Glu Gly	Tyr Lys Asp Arg Met	Tyr Ser Phe Phe Arg	Asn Phe	
1305	1310	1315		
cag ccc atg	agc cgc cag gtc gtg	gac gag gtc aac tac	aag gac	20692
Gln Pro Met	Ser Arg Gln Val Val	Asp Glu Val Asn Tyr	Lys Asp	
1320	1325	1330		
tac cag gcc	gtc acc ctg gcc tac	cag cac aac aac tcg	ggc ttc	20737
Tyr Gln Ala	Val Thr Leu Ala Tyr	Gln His Asn Asn Ser	Gly Phe	
1335	1340	1345		
gtc ggc tac	ctc gcg ccc acc atg	cgc cag ggc cag ccc	tac ccc	20782
Val Gly Tyr	Leu Ala Pro Thr Met	Arg Gln Gly Gln Pro	Tyr Pro	
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gcc aac tac	ccc tac ccg ctc atc	ggc aag agc gcc gtc	gcc agc	20827
Ala Asn Tyr	Pro Tyr Pro Leu Ile	Gly Lys Ser Ala Val	Ala Ser	
1365	1370	1375		
gtc acc cag	aaa aag ttc ctc tgc	gac cgg gtc atg tgg	cgc atc	20872
Val Thr Gln	Lys Lys Phe Leu Cys	Asp Arg Val Met Trp	Arg Ile	
1380	1385	1390		

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Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu	
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Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met	
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Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val	
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Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg	
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ttg act gta caa cta act Leu Thr Val Gln Leu Thr 1615	cat cct ctt aca ttc His Pro Leu Thr Phe 1620	agc tca aat agc Ser Ser Asn Ser 1625	32635
atc aca gta aaa aca gac Ile Thr Val Lys Thr Asp 1630	aaa ggg cta tat att Lys Gly Leu Tyr Ile 1635	aac tcc agt gga Asn Ser Ser Gly 1640	32680
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tat gga tct tat gat agt Tyr Gly Ser Tyr Asp Ser 1675	gat gga aaa aca aga Asp Gly Lys Thr Arg 1680	ccc gta att acc Pro Val Ile Thr 1685	32815
aaa att gga gca gga tta Lys Ile Gly Ala Gly Leu 1690	aat ttt gat gct aac Asn Phe Asp Ala Asn 1695	aaa gca ata gct Lys Ala Ile Ala 1700	32860

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aca	gct	gga	aac	aaa	cag	gat	gac	aag	cta	aca	ctt	tgg	act	acc	32950
Thr	Ala	Gly	Asn	Lys	Gln	Asp	Asp	Lys	Leu	Thr	Leu	Trp	Thr	Thr	
1720					1725					1730					
cct	gac	cca	agc	cct	aat	tgt	caa	tta	ctt	tca	gac	aga	gat	gcc	32995
Pro	Asp	Pro	Ser	Pro	Asn	Cys	Gln	Leu	Leu	Ser	Asp	Arg	Asp	Ala	
1735					1740					1745					
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Lys	Phe	Thr	Leu	Cys	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Gly	
1750					1755					1760					
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Thr	Val	Ala	Val	Ala	Ala	Val	Thr	Val	Gly	Ser	Ala	Leu	Asn	Pro	
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Ile	Asn	Asp	Thr	Val	Lys	Ser	Ala	Ile	Val	Phe	Leu	Arg	Phe	Asp	
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Ser	Asp	Gly	Val	Leu	Met	Ser	Asn	Ser	Ser	Met	Val	Gly	Asp	Tyr	
1795					1800					1805					
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Trp	Asn	Phe	Arg	Glu	Gly	Gln	Thr	Thr	Gln	Ser	Val	Ala	Tyr	Thr	
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caa	agt	aaa	aca	cct	aaa	aat	agc	ata	gtc	agt	cag	gta	tat	tta	33310
Gln	Ser	Lys	Thr	Pro	Lys	Asn	Ser	Ile	Val	Ser	Gln	Val	Tyr	Leu	
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act	gga	gaa	act	act	atg	cca	atg	aca	cta	acc	ata	act	ttc	aat	33355
Thr	Gly	Glu	Thr	Thr	Met	Pro	Met	Thr	Leu	Thr	Ile	Thr	Phe	Asn	
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ggc	act	gat	gaa	aaa	gac	aca	acc	cca	gtt	agc	acc	tac	tct	atg	33400
Gly	Thr	Asp	Glu	Lys	Asp	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Ser	Met	
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acc	ttt	gct	acc	aac	tca	ttc	tct	ttt	tcc	tac	atc	gcc	cag	gaa	33490
Thr	Phe	Ala	Thr	Asn	Ser	Phe	Ser	Phe	Ser	Tyr	Ile	Ala	Gln	Glu	
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 <213> chimpanzee adenovirus serotype Pan6

<400> 6

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

Asp Val Glu Ala Tyr Glu Lys Ser Lys Glu Asp Ser Thr Ala Ala Ala
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 Thr Ala Ala Val Ala Thr Ala Ser Thr Glu Val Arg Gly Asp Asn Phe
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 Ala Ser Ala Ala Ala Ala Ala Glu Ala Ala Glu Thr Glu Ser Lys Ile
 325 330 335
 Val Ile Gln Pro Val Glu Lys Asp Ser Lys Asp Arg Ser Tyr Asn Val
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 Asn Tyr Gly Asp Pro Glu Lys Gly Val Arg Ser Trp Thr Leu Leu Thr
 370 375 380
 Thr Ser Asp Val Thr Cys Gly Val Glu Gln Val Tyr Trp Ser Leu Pro
 385 390 395 400
 Asp Met Met Gln Asp Pro Val Thr Phe Arg Ser Thr Arg Gln Val Ser
 405 410 415
 Asn Tyr Pro Val Val Gly Ala Glu Leu Leu Pro Val Tyr Ser Lys Ser
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 Phe Phe Asn Glu Gln Ala Val Tyr Ser Gln Gln Leu Arg Ala Phe Thr
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 Ser Leu Thr His Val Phe Asn Arg Phe Pro Glu Asn Gln Ile Leu Val
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 Arg Pro Pro Ala Pro Thr Ile Thr Thr Val Ser Glu Asn Val Pro Ala
 465 470 475 480
 Leu Thr Asp His Gly Thr Leu Pro Leu Arg Ser Ser Ile Arg Gly Val
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 Tyr Lys Ala Leu Gly Val Val Ala Pro Arg Val Leu Ser Ser Arg Thr
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Phe

<210> 7
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 <213> chimpanzee adenovirus serotype Pan6
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 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
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 Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
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 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
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 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
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 Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
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 Ala Pro Asn Ser Ser Gln Trp Glu Gln Ala Lys Thr Gly Asn Gly Gly
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 Thr Met Glu Thr His Thr Tyr Gly Val Ala Pro Met Gly Gly Glu Asn
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 Ile Thr Lys Asp Gly Leu Gln Ile Gly Thr Asp Val Thr Ala Asn Gln
 165 170 175
 Asn Lys Pro Ile Tyr Ala Asp Lys Thr Phe Gln Pro Glu Pro Gln Val
 180 185 190
 Gly Glu Glu Asn Trp Gln Glu Thr Glu Asn Phe Tyr Gly Gly Arg Ala
 195 200 205
 Leu Lys Lys Asp Thr Asn Met Lys Pro Cys Tyr Gly Ser Tyr Ala Arg
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 Pro Thr Asn Glu Lys Gly Gly Gln Ala Lys Leu Lys Val Gly Asp Asp
 225 230 235 240
 Gly Val Pro Thr Lys Glu Phe Asp Ile Asp Leu Ala Phe Phe Asp Thr
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 Pro Gly Gly Thr Val Asn Gly Gln Asp Glu Tyr Lys Ala Asp Ile Val
 260 265 270
 Met Tyr Thr Glu Asn Thr Tyr Leu Glu Thr Pro Asp Thr His Val Val
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 Tyr Lys Pro Gly Lys Asp Asp Ala Ser Ser Glu Ile Asn Leu Val Gln
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 Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe
 305 310 315 320

Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala
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 Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn
 340 345 350
 Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr
 355 360 365
 Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp
 370 375 380
 Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr
 385 390 395 400
 Cys Phe Pro Leu Asp Gly Ser Gly Thr Asn Ala Ala Tyr Gln Gly Val
 405 410 415
 Lys Val Lys Asp Gly Gln Asp Gly Asp Val Glu Ser Glu Trp Glu Asn
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 Asp Asp Thr Val Ala Ala Arg Asn Gln Leu Cys Lys Gly Asn Ile Phe
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 Ala Met Glu Ile Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr
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 Ser Asn Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Thr
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 485 490 495
 Arg Val Thr Pro Pro Ser Leu Val Asp Ala Tyr Leu Asn Ile Gly Ala
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 Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys
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 Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg
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 Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg
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 Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser Ile Asn Leu Tyr Ala Thr
 595 600 605
 Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu
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Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala
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 Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser
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 660 665 670
 Leu Lys Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr
 675 680 685
 Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu
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 Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser
 705 710 715 720
 Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys
 725 730 735
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 740 745 750
 Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr
 755 760 765
 Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe
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 Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser
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 Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val
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 <400> 8

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 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
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 Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
 65 70 75 80
 Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Ile Ser Asn Asn Thr
 85 90 95
 Ile Ser Leu Lys Thr Ala Ala Pro Phe Tyr Asn Asn Asn Gly Thr Leu
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 Ser Leu Asn Val Ser Thr Pro Leu Ala Val Phe Pro Thr Phe Asn Thr
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 Leu Gly Ile Ser Leu Gly Asn Gly Leu Gln Thr Ser Asn Lys Leu Leu
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 Thr Val Gln Leu Thr His Pro Leu Thr Phe Ser Ser Asn Ser Ile Thr
 145 150 155 160
 Val Lys Thr Asp Lys Gly Leu Tyr Ile Asn Ser Ser Gly Asn Arg Gly
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 Ala Ile Ala Thr Tyr Ile Gly Asn Gly Leu Asp Tyr Gly Ser Tyr Asp
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Glu Arg Ser Arg Trp Gly Gly Gln Leu Lys Thr Ile Met His Thr Asn
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Met Pro Asn Val Asn Glu Phe Met Tyr Ser Asn Lys Phe Lys Ala Arg
125 130 135 140

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Val Met Val Ser Arg Lys Thr Pro Asn Gly Val Ala Val Asp Glu Asn
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Tyr Asp Gly Ser Gln Asp Glu Leu Thr Tyr Glu Trp Val Glu Phe Glu
160 165 170

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Gln Trp Ala Tyr Met His Ile Ala Gly Gln Asp Ala Ser Glu Tyr Leu						
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Ser Pro Gly Leu Val Gln Phe Ala Arg Ala Thr Asp Thr Tyr Phe Ser						
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Leu Gly Asn Lys Phe Arg Asn Pro Thr Val Ala Pro Thr His Asp Val						
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Thr Thr Asp Arg Ser Gln Arg Leu Thr Leu Arg Phe Val Pro Val Asp						
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Arg Glu Asp Asn Thr Tyr Ser Tyr Lys Val Arg Tyr Thr Leu Ala Val						
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Gly Val Leu Asp Arg Gly Pro Ser Phe Lys Pro Tyr Ser Gly Thr Ala						
	640	645	650			
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Tyr Asn Ser Leu Ala Pro Lys Gly Ala Pro Asn Thr Cys Gln Trp Thr						
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Tyr Lys Ala Gly Asp Thr Asp Thr Glu Lys Thr Tyr Thr Tyr Gly Asn						
	670	675	680			
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Ala Pro Val Gln Gly Ile Ser Ile Thr Lys Asp Gly Ile Gln Leu Gly						
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acatctgaat gccattggtg atggacatgc ttttggtctc caggttccac acagtttcag	33675
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cctcacagct caacagctga ggattgtcct cgggtggtcgg gatcacgggtt atctggaaga	33795
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gctaccacag tggccgtcgt accagatcct caggtaaata aagtggcgct cctocagaa	34155
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ccgtggaatg ggccagaccc agccagatga tgcaattttg ttgggtttcg gtgacggcg	34935

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 gaactagttc ctgaggtaaa tccaagccag ccatagataa gagctcgcgc agagcgcctt 35295
 ccacoggcat tcttaagcac accctcataa ttccaagata ttctgctcct ggttcacctg 35355
 cagcagattg acaagoggaa tatcaaaatc tctgcgcga tccctaagct cctccctcag 35415
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 aataagatta gggcaagcca cagtacagat aaacogaagt cctccccagt gagcattgcc 35535
 aaatgcaaga ctgotataag catgctggt agaccgggtg atatottcca gataactgga 35595
 cagaaaatca ccagggcaat ttttaagaaa atcaacaaaa gaaaaatcct ccaggtgcac 35655
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 aaaattgtcg ctatgattga aaaccatcac agagagacgt tcccgggtggc cggcgtgaat 35895
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 gaggaagcaa taaggcacta caatgctcag tctcaagtcc agcaaagcga tgccatgcgg 36015
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 ctctgctcaa tatatagccc agatctacac tgacgtaaag gccaaagtct aaaaaatccc 36255
 gccaaataat cacacacgcc cagcacacgc ccagaaaccg gtgacacact caaaaaata 36315
 cgcgcacttc ctcaaacgcc caaactgcgc tcatttcggg gttccacgc taogtcatcg 36375
 gaattcgact ttcaaattcc gtgcaccgtt aaaaacgtca cccgccccgc ccttaacggg 36435
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 ttaacgcgca ccaaaagttt gaggtatatt attgatgatg 36535

<210> 10
 <211> 531
 <212> PRT
 <213> chimpanzee adenovirus serotype Pan7

<400> 10

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

Gly Phe Gln Ile Leu Tyr Glu Asp Leu Glu Gly Gly Asn Ile Pro Ala
 275 280 285
 Leu Leu Asp Val Glu Ala Tyr Glu Lys Ser Lys Glu Glu Ala Ala Ala
 290 295 300
 Ala Ala Thr Ala Ala Val Ala Thr Ala Ser Thr Glu Val Arg Gly Asp
 305 310 315 320
 Asn Phe Ala Ser Ala Ala Ala Val Ala Glu Ala Ala Glu Thr Glu Ser
 325 330 335
 Lys Ile Val Ile Gln Pro Val Glu Lys Asp Ser Lys Asp Arg Ser Tyr
 340 345 350
 Asn Val Leu Ala Asp Lys Lys Asn Thr Ala Tyr Arg Ser Trp Tyr Leu
 355 360 365
 Ala Tyr Asn Tyr Gly Asp Pro Glu Lys Gly Val Arg Ser Trp Thr Leu
 370 375 380
 Leu Thr Thr Ser Asp Val Thr Cys Gly Val Glu Gln Val Tyr Trp Ser
 385 390 395 400
 Leu Pro Asp Met Met Gln Asp Pro Val Thr Phe Arg Ser Thr Arg Gln
 405 410 415
 Val Ser Asn Tyr Pro Val Val Gly Ala Glu Leu Leu Pro Val Tyr Ser
 420 425 430
 Lys Ser Phe Phe Asn Glu Gln Ala Val Tyr Ser Gln Gln Leu Arg Ala
 435 440 445
 Phe Thr Ser Leu Thr His Val Phe Asn Arg Phe Pro Glu Asn Gln Ile
 450 455 460
 Leu Val Arg Pro Pro Ala Pro Thr Ile Thr Thr Val Ser Glu Asn Val
 465 470 475 480
 Pro Ala Leu Thr Asp His Gly Thr Leu Pro Leu Arg Ser Ser Ile Arg
 485 490 495
 Gly Val Gln Arg Val Thr Val Thr Asp Ala Arg Arg Arg Thr Cys Pro
 500 505 510
 Tyr Val Tyr Lys Ala Leu Gly Val Val Ala Pro Arg Val Leu Ser Ser
 515 520 525
 Arg Thr Phe
 530

<210> 11
 <211> 932
 <212> PRT
 <213> chimpanzee adenovirus serotype Pan7

<400> 11

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
1 5 10 15

Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
20 25 30

Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
35 40 45

Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
50 55 60

Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65 70 75 80

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

Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
100 105 110

Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
115 120 125

Ala Pro Asn Thr Cys Gln Trp Thr Tyr Lys Ala Gly Asp Thr Asp Thr
130 135 140

Glu Lys Thr Tyr Thr Tyr Gly Asn Ala Pro Val Gln Gly Ile Ser Ile
145 150 155 160

Thr Lys Asp Gly Ile Gln Leu Gly Thr Asp Ser Asp Gly Gln Ala Ile
165 170 175

Tyr Ala Asp Glu Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Ala Glu
180 185 190

Trp His Asp Ile Thr Gly Thr Asp Glu Lys Tyr Gly Gly Arg Ala Leu
195 200 205

Lys Pro Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys Pro
210 215 220

Thr Asn Lys Glu Gly Gly Gln Ala Asn Val Lys Thr Glu Thr Gly Gly
225 230 235 240

Thr Lys Glu Tyr Asp Ile Asp Met Ala Phe Phe Asp Asn Arg Ser Ala
245 250 255

Ala Ala Ala Gly Leu Ala Pro Glu Ile Val Leu Tyr Thr Glu Asn Val
260 265 270

Asp Leu Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr Asp
275 280 285

Asp Ser Ser Ser Ser Ile Asn Leu Gly Gln Gln Ser Met Pro Asn Arg
 290 295 300
 Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr
 305 310 315 320
 Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu
 325 330 335
 Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln
 340 345 350
 Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp
 355 360 365
 Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn
 370 375 380
 His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp Ala
 385 390 395 400
 Val Gly Arg Thr Asp Thr Tyr Gln Gly Ile Lys Ala Asn Gly Asp Asn
 405 410 415
 Gln Thr Thr Trp Thr Lys Asp Asp Thr Val Asn Asp Ala Asn Glu Leu
 420 425 430
 Gly Lys Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn Leu
 435 440 445
 Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp Ser
 450 455 460
 Tyr Lys Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Asn Thr
 465 470 475 480
 Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp Ala
 485 490 495
 Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn Val
 500 505 510
 Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met
 515 520 525
 Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln
 530 535 540
 Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr
 545 550 555 560
 Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser Ser
 565 570 575
 Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser
 580 585 590

Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser
 595 600 605
 Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn
 610 615 620
 Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala
 625 630 635 640
 Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg
 645 650 655
 Gly Trp Ser Phe Thr Arg Leu Lys Thr Arg Glu Thr Pro Ser Leu Gly
 660 665 670
 Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu
 675 680 685
 Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile Thr
 690 695 700
 Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro
 705 710 715 720
 Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val
 725 730 735
 Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala
 740 745 750
 His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys
 755 760 765
 Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln
 770 775 780
 Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala
 785 790 795 800
 Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met
 805 810 815
 Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly
 820 825 830
 Lys Ser Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg
 835 840 845
 Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala
 850 855 860
 Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala
 865 870 875 880
 Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu
 885 890 895

Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro His
 900 905 910
 Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly
 915 920 925
 Asn Ala Thr Thr
 930
 <210> 12
 <211> 443
 <212> PRT
 <213> chimpanzee adenovirus serotype Pan7
 <400> 12
 Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1 5 10 15
 Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
 20 25 30
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
 35 40 45
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
 50 55 60
 Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
 65 70 75 80
 Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
 85 90 95
 Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Thr Lys Asp Gly Lys Leu
 100 105 110
 Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Lys Ser Thr Ile Leu
 115 120 125
 Asn Thr Leu Ala Val Ala Tyr Gly Ser Gly Leu Gly Leu Ser Gly Gly
 130 135 140
 Thr Ala Leu Ala Val Gln Leu Ala Ser Pro Leu Thr Phe Asp Glu Lys
 145 150 155 160
 Gly Asn Ile Lys Ile Asn Leu Ala Ser Gly Pro Leu Thr Val Asp Ala
 165 170 175
 Ser Arg Leu Ser Ile Asn Cys Lys Arg Gly Val Thr Val Thr Thr Ser
 180 185 190
 Gly Asp Ala Ile Glu Ser Asn Ile Ser Trp Pro Lys Gly Ile Arg Phe
 195 200 205

Glu Gly Asn Gly Ile Ala Ala Asn Ile Gly Arg Gly Leu Glu Phe Gly
 210 215 220
 Thr Thr Ser Thr Glu Thr Asp Val Thr Asp Ala Tyr Pro Ile Gln Val
 225 230 235 240
 Lys Leu Gly Thr Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile Val Ala
 245 250 255
 Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala Asp Pro
 260 265 270
 Ser Pro Asn Cys Lys Ile Tyr Ser Glu Lys Asp Ala Lys Leu Thr Leu
 275 280 285
 Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Thr Val Leu
 290 295 300
 Ala Val Asn Asn Gly Ser Leu Asn Pro Ile Thr Asn Thr Val Ser Thr
 305 310 315 320
 Ala Leu Val Ser Leu Lys Phe Asp Ala Ser Gly Val Leu Leu Ser Ser
 325 330 335
 Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp Val Thr
 340 345 350
 Pro Ala Glu Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn Ile Lys
 355 360 365
 Ala Tyr Pro Lys Asn Thr Ser Ala Ala Ser Lys Ser His Ile Val Ser
 370 375 380
 Gln Val Tyr Leu Asn Gly Asp Glu Ala Lys Pro Leu Met Leu Ile Ile
 385 390 395 400
 Thr Phe Asn Glu Thr Glu Asp Ala Thr Cys Thr Tyr Ser Ile Thr Phe
 405 410 415
 Gln Trp Lys Trp Asp Ser Thr Lys Tyr Thr Gly Glu Thr Leu Ala Thr
 420 425 430
 Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
 435 440

<210> 13
 <211> 338
 <212> PRT
 <213> simian serotype C1
 <400> 13

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

Trp Lys Asp Leu Asp Pro Asn Gly Ile Ser Glu Leu Ala Lys Gly Asn
 325 330 335

Pro Phe

<210> 14
 <211> 315
 <212> PRT
 <213> chimpanzee adenovirus Pan-9

<400> 14

Ala Pro Lys Gly Ala Pro Asn Thr Cys Gln Trp Thr Tyr Lys Ala Asp
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 Gly Glu Thr Ala Thr Glu Lys Thr Tyr Thr Tyr Gly Asn Ala Pro Val
 20 25 30
 Gln Gly Ile Asn Ile Thr Lys Asp Gly Ile Gln Leu Gly Thr Asp Thr
 35 40 45
 Asp Asp Gln Pro Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro Gln
 50 55 60
 Val Gly Asp Ala Glu Trp His Asp Ile Thr Gly Thr Asp Glu Lys Tyr
 65 70 75 80
 Gly Gly Arg Ala Leu Lys Pro Asp Thr Lys Met Lys Pro Cys Tyr Gly
 85 90 95
 Ser Phe Ala Lys Pro Thr Asn Lys Glu Gly Gly Gln Ala Asn Val Lys
 100 105 110
 Thr Gly Thr Gly Thr Thr Lys Glu Tyr Asp Ile Asp Met Ala Phe Phe
 115 120 125
 Asp Asn Arg Ser Ala Ala Ala Ala Gly Leu Ala Pro Glu Ile Val Leu
 130 135 140
 Tyr Thr Glu Asn Val Asp Leu Glu Thr Pro Asp Thr His Ile Val Tyr
 145 150 155 160
 Lys Ala Gly Thr Asp Asp Ser Ser Ser Ser Ile Asn Leu Gly Gln Gln
 165 170 175
 Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile
 180 185 190
 Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly
 195 200 205
 Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr
 210 215 220

Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg
 225 230 235 240
 Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val
 245 250 255
 Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys
 260 265 270
 Phe Pro Leu Asp Ala Val Gly Arg Thr Asp Thr Tyr Gln Gly Ile Lys
 275 280 285
 Ala Asn Gly Thr Asp Gln Thr Thr Trp Thr Lys Asp Asp Ser Val Asn
 290 295 300
 Asp Ala Asn Glu Ile Gly Lys Gly Asn Pro Phe
 305 310 315

<210> 15
 <211> 315
 <212> PRT
 <213> chimpanzee adenovirus Pan-5

<400> 15

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

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

<210> 16
 <211> 324
 <212> PRT
 <213> chimpanzee adenovirus Pan-6
 <400> 16

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

Ser Tyr Ala Arg Pro Thr Asn Glu Lys Gly Gly Gln Ala Lys Leu Lys
 100 105 110
 Val Gly Asp Asp Gly Val Pro Thr Lys Glu Phe Asp Ile Asp Leu Ala
 115 120 125
 Phe Phe Asp Thr Pro Gly Gly Thr Val Asn Gly Gln Asp Glu Tyr Lys
 130 135 140
 Ala Asp Ile Val Met Tyr Thr Glu Asn Thr Tyr Leu Glu Thr Pro Asp
 145 150 155 160
 Thr His Val Val Tyr Lys Pro Gly Lys Asp Asp Ala Ser Ser Glu Ile
 165 170 175
 Asn Leu Val Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe
 180 185 190
 Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met
 195 200 205
 Gly Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu
 210 215 220
 Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu
 225 230 235 240
 Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser
 245 250 255
 Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu
 260 265 270
 Leu Pro Asn Tyr Cys Phe Pro Leu Asp Gly Ser Gly Thr Asn Ala Ala
 275 280 285
 Tyr Gln Gly Val Lys Val Lys Asp Gly Gln Asp Gly Asp Val Glu Ser
 290 295 300
 Glu Trp Glu Asn Asp Asp Thr Val Ala Ala Arg Asn Gln Leu Cys Lys
 305 310 315 320
 Gly Asn Ile Phe

<210> 17
 <211> 314
 <212> PRT
 <213> chimpanzee adenovirus Pan-7

<400> 17

Ala Pro Lys Gly Ala Pro Asn Thr Cys Gln Trp Thr Tyr Lys Ala Gly
 1 5 10 15
 Asp Thr Asp Thr Glu Lys Thr Tyr Thr Tyr Gly Asn Ala Pro Val Gln
 20 25 30

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

<210> 18
 <211> 179
 <212> PRT
 <213> chimpanzee adenovirus Pan9

<400> 18

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Ile	Leu	Ala	Thr	Val	Ser	Val	Leu	Val	Val	Gly	Ser	Gly	Asn	Leu	Asn
		35					40					45			
Pro	Ile	Thr	Gly	Thr	Val	Ser	Ser	Ala	Gln	Val	Phe	Leu	Arg	Phe	Asp
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Ala	Asn	Gly	Val	Leu	Leu	Thr	Glu	His	Ser	Thr	Leu	Lys	Lys	Tyr	Trp
65					70					75					80
Gly	Tyr	Arg	Gln	Gly	Asp	Ser	Ile	Asp	Gly	Thr	Pro	Tyr	Thr	Asn	Ala
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Val	Gly	Phe	Met	Pro	Asn	Leu	Lys	Ala	Tyr	Pro	Lys	Ser	Gln	Ser	Ser
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Thr	Thr	Lys	Asn	Asn	Ile	Val	Gly	Gln	Val	Tyr	Met	Asn	Gly	Asp	Val
		115					120						125		
Ser	Lys	Pro	Met	Leu	Leu	Thr	Ile	Thr	Leu	Asn	Gly	Thr	Asp	Asp	Ser
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Tyr	Val	Gly	Ala	Thr	Phe	Gly	Ala	Asn	Ser	Tyr	Thr	Phe	Ser	Tyr	Ile
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Ala Gln Glu

<210> 19
 <211> 185
 <212> PRT
 <213> chimpanzee adenovirus Pan6

<400> 19

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			20					25					30		

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

<210> 20
 <211> 179
 <212> PRT
 <213> chimpanzee adenovirus Pan7
 <400> 20

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

Ile Gly Phe Met Pro Asn Ile Lys Ala Tyr Pro Lys Asn Thr Ser Ala
 100 105 110
 Ala Ser Lys Ser His Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Glu
 115 120 125
 Ala Lys Pro Leu Met Leu Ile Ile Thr Phe Asn Glu Thr Glu Asp Ala
 130 135 140
 Thr Cys Thr Tyr Ser Ile Thr Phe Gln Trp Lys Trp Asp Ser Thr Lys
 145 150 155 160
 Tyr Thr Gly Glu Thr Leu Ala Thr Ser Ser Phe Thr Phe Ser Tyr Ile
 165 170 175
 Ala Gln Glu

<210> 21
 <211> 179
 <212> PRT
 <213> chimpanzee adenovirus Pan5

<400> 21

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

Ala Lys Glu

<210> 22
<211> 183
<212> PRT
<213> human adenovirus Ad 2

<400> 22

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

<210> 23
<211> 182
<212> PRT
<213> human adenovirus Ad 5

<400> 23

Thr Leu Trp Thr Thr Pro Ala Pro Ser Pro Asn Cys Arg Leu Asn Ala
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Glu Lys Asp Ala Lys Leu Thr Leu Val Leu Thr Lys Cys Gly Ser Gln
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 Ile Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro
 35 40 45
 Ile Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu
 50 55 60
 Asn Gly Val Leu Ile Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn
 65 70 75 80
 Phe Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val
 85 90 95
 Gly Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr
 100 105 110
 Ala Lys Ser Asn Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Thr
 115 120 125
 Lys Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly
 130 135 140
 Asp Thr Thr Pro Ser Ala Tyr Ser Met Ser Phe Ser Trp Asp Trp Ser
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 Gly His Asn Tyr Ile Asn Glu Ile Phe Ala Thr Ser Ser Tyr Thr Glu
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 Ser Tyr Ile Ala Gln Glu
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 <222> (16841)..(19636)
 <223> L3 Hexon

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 <222> (28059)..(29150)
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 <222> (29183)..(30865)
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<400> 24

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Thr Pro Ala Ala	Tyr Glu Gly Pro Pro	Pro Ser Tyr Glu	Ser Val Met			
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Gly Ser Ala Asn	Val Pro Ala Thr	Leu Glu Ala Pro	Tyr Val Pro Pro			
	25	30	35			
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Arg Tyr Leu Gly	Pro Thr Glu Gly	Arg Asn Ser Ile	Arg Tyr Ser Glu			
	40	45	50	55		
ctg gca ccc ctg	tac gat acc acc	aag gtg tac ctg	gtg gac aac aag			12666
Leu Ala Pro Leu	Tyr Asp Thr Thr	Lys Val Tyr Leu	Val Asp Asn Lys			
	60	65	70			
tcg gcg gac atc	gcc tcc ctg aat	tat caa aac gat	cac agc aat ttt			12714
Ser Ala Asp Ile	Ala Ser Leu Asn	Tyr Gln Asn Asp	His Ser Asn Phe			
	75	80	85			
ctg act acc gtg	gtg cag aac aat	gac ttc acc ccg	acg gag gcg ggc			12762
Leu Thr Thr Val	Val Gln Asn Asn	Asp Phe Thr Pro	Thr Glu Ala Gly			
	90	95	100			
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Thr Gln Thr Ile	Asn Phe Asp Glu	Arg Ser Arg Trp	Gly Gly Gln Leu			
	105	110	115			
aaa acc atc ctg	cac acc aac atg	ccc aac atc aac	gag ttc atg tcc			12858
Lys Thr Ile Leu	His Thr Asn Met	Pro Asn Ile Asn	Glu Phe Met Ser			
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Ser Thr Gly Asn	Cys Thr Val Tyr Ser	Glu Gly Asp Ser Leu Leu	
1640	1645	1650	
agt ctc tgt tta	acc aaa tgc gga gct	cac gtc tta gga agt gta	28754
Ser Leu Cys Leu	Thr Lys Cys Gly Ala	His Val Leu Gly Ser Val	
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agt tta acc ggt	tta aca gga acc ata	acc caa atg act gat att	28799
Ser Leu Thr Gly	Leu Thr Gly Thr Ile	Thr Gln Met Thr Asp Ile	
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tct gtc acc att	caa ttt aca ttt gac	aac aat ggt aag cta cta	28844
Ser Val Thr Ile	Gln Phe Thr Phe Asp	Asn Asn Gly Lys Leu Leu	
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agc tct cca ctt	ata aac aac gcc ttt	agt att cga cag aat gac	28889
Ser Ser Pro Leu	Ile Asn Asn Ala Phe	Ser Ile Arg Gln Asn Asp	
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agt acg gcc tca	aac cct acc tac aac	gcc ctg gcg ttt atg cct	28934
Ser Thr Ala Ser	Asn Pro Thr Tyr Asn	Ala Leu Ala Phe Met Pro	
1715	1720	1725	
aac agt acc ata	tat gca aga ggg gga	ggt ggt gaa cca cga aac	28979
Asn Ser Thr Ile	Tyr Ala Arg Gly Gly	Gly Gly Glu Pro Arg Asn	
1730	1735	1740	

aac tac tac gtc	caa acg tat ctt agg	gga aat gtt caa aaa cca	29024
Asn Tyr Tyr Val	Gln Thr Tyr Leu Arg	Gly Asn Val Gln Lys Pro	
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atc att ctt act	gta acc tac aac tca	gtc gcc aca gga tat tcc	29069
Ile Ile Leu Thr	Val Thr Tyr Asn Ser	Val Ala Thr Gly Tyr Ser	
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tta tot ttt aag	tgg act gct ctt gca	cgt gaa aag ttt gca acc	29114
Leu Ser Phe Lys	Trp Thr Ala Leu Ala	Arg Glu Lys Phe Ala Thr	
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Pro Thr Thr Ser	Phe Cys Tyr Ile Thr	Glu Gln	
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		gcg aga gtt gat gaa gac	
		Ala Arg Val Asp Glu Asp	
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ttc aac cca gtg	tac cct tat gac ccc	cca cat gct cct gtt atg	29254
Phe Asn Pro Val	Tyr Pro Tyr Asp Pro	Pro His Ala Pro Val Met	
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ccc ttc att act	cca cct ttt acc tcc	tcg gat ggg ttg cag gaa	29299
Pro Phe Ile Thr	Pro Pro Phe Thr Ser	Ser Asp Gly Leu Gln Glu	
1825	1830	1835	
aaa cca ctt gga	gtg tta agt tta aac	tac aga gat ccc att act	29344
Lys Pro Leu Gly	Val Leu Ser Leu Asn	Tyr Arg Asp Pro Ile Thr	
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acg caa aat gag	tot ctt aca att aaa	cta gga aac ggc ctc act	29389
Thr Gln Asn Glu	Ser Leu Thr Ile Lys	Leu Gly Asn Gly Leu Thr	
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cta gac aac cag	gga caa cta aca tca	acc gct ggc gaa gta gaa	29434
Leu Asp Asn Gln	Gly Gln Leu Thr Ser	Thr Ala Gly Glu Val Glu	
1870	1875	1880	
cct cca ctc act	aac gct aac aac aaa	ctt gca ctg gtc tat agc	29479
Pro Pro Leu Thr	Asn Ala Asn Asn Lys	Leu Ala Leu Val Tyr Ser	
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gat cct tta gca	gta aag cgc aac agc	cta acc tta tcg cac acc	29524
Asp Pro Leu Ala	Val Lys Arg Asn Ser	Leu Thr Leu Ser His Thr	
1900	1905	1910	
gct ccc ctt gtt	att gct gat aac tct	tta gca ttg caa gtt tca	29569
Ala Pro Leu Val	Ile Ala Asp Asn Ser	Leu Ala Leu Gln Val Ser	
1915	1920	1925	
gag cct att ttt	ata aat gac aag gac	aaa cta gcc ctg caa aca	29614
Glu Pro Ile Phe	Ile Asn Asp Lys Asp	Lys Leu Ala Leu Gln Thr	
1930	1935	1940	

gcc gcg ccc ctt	gta act aac gct	ggc acc ctt cgc tta caa agc	29659
Ala Ala Pro Leu	Val Thr Asn Ala Gly	Thr Leu Arg Leu Gln Ser	
1945	1950	1955	
gcc gcc cct tta	ggc att gca gac caa	acc cta aaa ctc ctg ttt	29704
Ala Ala Pro Leu	Gly Ile Ala Asp Gln	Thr Leu Lys Leu Leu Phe	
1960	1965	1970	
acc aac cct ttg	tac ttg cag aat aac	ttt ctc acg tta gcc att	29749
Thr Asn Pro Leu	Tyr Leu Gln Asn Asn	Phe Leu Thr Leu Ala Ile	
1975	1980	1985	
gaa cga ccc ctt	gcc att acc aat act	gga aag ctg gct cta cag	29794
Glu Arg Pro Leu	Ala Ile Thr Asn Thr	Gly Lys Leu Ala Leu Gln	
1990	1995	2000	
ctc tcc cca ccg	cta caa aca gca gac	aca ggc ttg act ttg caa	29839
Leu Ser Pro Pro	Leu Gln Thr Ala Asp	Thr Gly Leu Thr Leu Gln	
2005	2010	2015	
acc aac gtg cca	tta act gta agc aac	ggg acc cta ggc tta gcc	29884
Thr Asn Val Pro	Leu Thr Val Ser Asn	Gly Thr Leu Gly Leu Ala	
2020	2025	2030	
ata aag cgc cca	ctt att att cag gac	aac aac ttg ttt ttg gac	29929
Ile Lys Arg Pro	Leu Ile Ile Gln Asp	Asn Asn Leu Phe Leu Asp	
2035	2040	2045	
ttc aga gct ccc	ctg cgt ctt ttc aac	agc gac cca gta cta ggg	29974
Phe Arg Ala Pro	Leu Arg Leu Phe Asn	Ser Asp Pro Val Leu Gly	
2050	2055	2060	
ctt aac ttt tac	acc cct ctt gcg gta	cgc gat gag gcg ctc act	30019
Leu Asn Phe Tyr	Thr Pro Leu Ala Val	Arg Asp Glu Ala Leu Thr	
2065	2070	2075	
gtt aac aca ggc	cgc ggc ctc aca gtg	agt tac gat ggt tta att	30064
Val Asn Thr Gly	Arg Gly Leu Thr Val	Ser Tyr Asp Gly Leu Ile	
2080	2085	2090	
tta aat ctt ggt	aag gat ctt cgc ttt	gac aac aac acc gtt tct	30109
Leu Asn Leu Gly	Lys Asp Leu Arg Phe	Asp Asn Asn Thr Val Ser	
2095	2100	2105	
gtc gct ctt agt	gct gct ttg cct tta	caa tac act gat cag ctt	30154
Val Ala Leu Ser	Ala Ala Leu Pro Leu	Gln Tyr Thr Asp Gln Leu	
2110	2115	2120	
cgc ctt aac gtg	ggc gct ggg ctg cgt	tac aat cca gtg agt aag	30199
Arg Leu Asn Val	Gly Ala Gly Leu Arg	Tyr Asn Pro Val Ser Lys	
2125	2130	2135	
aaa ttg gac gtg	aac ccc aat caa aac	aag ggt tta acc tgg gaa	30244
Lys Leu Asp Val	Asn Pro Asn Gln Asn	Lys Gly Leu Thr Trp Glu	
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aat gac tac ctc	att gta aag cta gga	aat gga tta ggt ttt gat	30289
Asn Asp Tyr Leu	Ile Val Lys Leu Gly	Asn Gly Leu Gly Phe Asp	
2155	2160	2165	
ggc gat gga aac	ata gct gtt tct cct	caa gtt aca tcg cct gac	30334
Gly Asp Gly Asn	Ile Ala Val Ser Pro	Gln Val Thr Ser Pro Asp	
2170	2175	2180	
acc tta tgg acc	act gcc gac cca tcc	ccc aat tgt tcc atc tac	30379
Thr Leu Trp Thr	Thr Ala Asp Pro Ser	Pro Asn Cys Ser Ile Tyr	
2185	2190	2195	
act gat tta gat	gcc aaa atg tgg ctc	tcg ttg gta aaa caa ggg	30424
Thr Asp Leu Asp	Ala Lys Met Trp Leu	Ser Leu Val Lys Gln Gly	
2200	2205	2210	
ggg gtg gtt cac	ggg tct gtt gct tta	aaa gca ttg aaa gga acc	30469
Gly Val Val His	Gly Ser Val Ala Leu	Lys Ala Leu Lys Gly Thr	
2215	2220	2225	
cta ttg agt cct	acg gaa agc gcc att	gtt att ata cta cat ttt	30514
Leu Leu Ser Pro	Thr Glu Ser Ala Ile	Val Ile Ile Leu His Phe	
2230	2235	2240	
gac aat tat gga	gtg cga att ctc aat	tat ccc act ttg ggc act	30559
Asp Asn Tyr Gly	Val Arg Ile Leu Asn	Tyr Pro Thr Leu Gly Thr	
2245	2250	2255	
caa ggc acg ttg	gga aat aat gca act	tggt ggt tat agg cag gga	30604
Gln Gly Thr Leu	Gly Asn Asn Ala Thr	Trp Gly Tyr Arg Gln Gly	
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gaa tct gca gac	act aat gta ctc aat	gca cta gca ttt atg ccc	30649
Glu Ser Ala Asp	Thr Asn Val Leu Asn	Ala Leu Ala Phe Met Pro	
2275	2280	2285	
agt tca aaa agg	tac cca aga ggg cgt	gga agc gaa gtt cag aat	30694
Ser Ser Lys Arg	Tyr Pro Arg Gly Arg	Gly Ser Glu Val Gln Asn	
2290	2295	2300	
caa act gtg ggc	tac act tgt ata cag	ggg gac ttt tct atg ccc	30739
Gln Thr Val Gly	Tyr Thr Cys Ile Gln	Gly Asp Phe Ser Met Pro	
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gta ccg tac caa	ata cag tac aac tat	gga cca act ggc tac tcc	30784
Val Pro Tyr Gln	Ile Gln Tyr Asn Tyr	Gly Pro Thr Gly Tyr Ser	
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ttt aaa ttt att	tggt aga act gtt tca	aga caa cca ttt gac atc	30829
Phe Lys Phe Ile	Trp Arg Thr Val Ser	Arg Gln Pro Phe Asp Ile	
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Pro Cys Cys Phe	Phe Ser Tyr Ile Thr	Glu Glu	
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<400> 25

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Glu	Ala	Pro	Tyr	Val	Pro	Pro	Arg	Tyr	Leu	Gly	Pro	Thr	Glu	Gly	Arg	35	40	45	
Asn	Ser	Ile	Arg	Tyr	Ser	Glu	Leu	Ala	Pro	Leu	Tyr	Asp	Thr	Thr	Lys	50	55	60	
Val	Tyr	Leu	Val	Asp	Asn	Lys	Ser	Ala	Asp	Ile	Ala	Ser	Leu	Asn	Tyr	65	70	75	80
Gln	Asn	Asp	His	Ser	Asn	Phe	Leu	Thr	Thr	Val	Val	Gln	Asn	Asn	Asp	85	90	95	
Phe	Thr	Pro	Thr	Glu	Ala	Gly	Thr	Gln	Thr	Ile	Asn	Phe	Asp	Glu	Arg	100	105	110	
Ser	Arg	Trp	Gly	Gly	Gln	Leu	Lys	Thr	Ile	Leu	His	Thr	Asn	Met	Pro	115	120	125	
Asn	Ile	Asn	Glu	Phe	Met	Ser	Thr	Asn	Lys	Phe	Arg	Ala	Arg	Leu	Met	130	135	140	
Val	Lys	Lys	Ala	Glu	Asn	Gln	Pro	Pro	Glu	Tyr	Glu	Trp	Phe	Glu	Phe	145	150	155	160
Thr	Ile	Pro	Glu	Gly	Asn	Tyr	Ser	Glu	Thr	Met	Thr	Ile	Asp	Leu	Met	165	170	175	
Asn	Asn	Ala	Ile	Val	Asp	Asn	Tyr	Leu	Gln	Val	Gly	Arg	Gln	Asn	Gly	180	185	190	
Val	Leu	Glu	Ser	Asp	Ile	Gly	Val	Lys	Phe	Asp	Thr	Arg	Asn	Phe	Arg	195	200	205	
Leu	Gly	Trp	Asp	Pro	Val	Thr	Lys	Leu	Val	Met	Pro	Gly	Val	Tyr	Thr	210	215	220	
Asn	Glu	Ala	Phe	His	Pro	Asp	Ile	Val	Leu	Leu	Pro	Gly	Cys	Gly	Val	225	230	235	240
Asp	Phe	Thr	Gln	Ser	Arg	Leu	Ser	Asn	Leu	Leu	Gly	Ile	Arg	Lys	Arg	245	250	255	
Arg	Pro	Phe	Gln	Glu	Gly	Phe	Gln	Ile	Met	Tyr	Glu	Asp	Leu	Glu	Gly	260	265	270	

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 Thr Glu Pro His Glu Leu Val Ile Lys Pro Leu Glu Gln Asp Ser Lys
 305 310 315 320
 Lys Arg Ser Tyr Asn Ile Ile Ser Gly Thr Met Asn Thr Leu Tyr Arg
 325 330 335
 Ser Trp Phe Leu Ala Tyr Asn Tyr Gly Asp Pro Glu Lys Gly Val Arg
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 Ser Trp Thr Ile Leu Thr Thr Thr Asp Val Thr Cys Gly Ser Gln Gln
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 Val Tyr Trp Ser Leu Pro Asp Met Met Gln Asp Pro Val Thr Phe Arg
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<400> 26

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 65 70 75 80
 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
 85 90 95
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 Pro Gln Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro Gln Ile Gly Glu
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 Asn Thr Pro Lys Ala Val Leu Tyr Ala Glu Asp Val Ser Ile Glu Ala
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 Pro Asp Thr His Leu Val Phe Lys Pro Thr Val Thr Glu Gly Ile Thr
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 Tyr Ile Ala Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser
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Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala
 325 330 335
 Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Met
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 Ser Gly Asn Met Phe Ala Met Glu Ile Asn Leu Gln Ala Asn Leu Trp
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 Arg Ser Phe Leu Tyr Ser Asn Ile Gly Leu Tyr Leu Pro Asp Ser Leu
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 Lys Ile Thr Pro Asp Asn Ile Thr Leu Pro Glu Asn Lys Asn Thr Tyr
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 Gln Tyr Met Asn Gly Arg Val Thr Pro Pro Gly Leu Val Asp Thr Tyr
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 580 585 590
 Asn Leu Tyr Ala Asn Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr
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Tyr Leu Cys Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr
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Gln Ser Asn Met Thr Lys Asp Trp Phe Leu Ile Gln Met Leu Ser His
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Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Asn Tyr Lys Asp
755 760 765
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Gln His Asn Asn Ser Gly Phe Val Gly Tyr Met Gly Pro Thr Met Arg
805 810 815
Glu Gly Gln Ala Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Ala
820 825 830
Thr Ala Val Pro Ser Leu Thr Gln Lys Lys Phe Leu Cys Asp Arg Val
835 840 845
Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ser Leu
850 855 860
Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu
865 870 875 880
Asp Met Thr Phe Glu Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr
885 890 895
Val Leu Phe Glu Val Phe Asp Val Val Arg Ile His Gln Pro His Arg
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Ala Thr Thr
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Ile Ala Lys Pro Leu Tyr Phe Asp Met Glu Arg Lys Leu Ala Leu Ser
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Leu Gly Arg Gly Leu Thr Ile Thr Ala Ala Gly Gln Leu Glu Ser Thr
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Gln Ser Val Gln Thr Asn Pro Pro Leu Ile Ile Thr Asn Asn Asn Thr
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Leu Thr Leu Arg His Ser Pro Pro Leu Asn Leu Thr Asp Asn Ser Leu
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Val Leu Gly Tyr Ser Ser Pro Leu Arg Val Thr Asp Asn Lys Leu Thr
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Phe Asn Phe Thr Ser Pro Leu Arg Tyr Glu Asn Glu Asn Leu Thr Phe
 130 135 140

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

Ile Asn Ser Ser Lys Gly Leu Ser Ser Val Gly Gly Ser Leu Ala Val
 165 170 175

Asn Leu Ser Ser Asp Leu Lys Phe Asp Ser Asn Gly Ser Ile Ala Phe
 180 185 190

Gly Ile Gln Thr Leu Trp Thr Ala Pro Thr Ser Thr Gly Asn Cys Thr
 195 200 205

Val Tyr Ser Glu Gly Asp Ser Leu Leu Ser Leu Cys Leu Thr Lys Cys
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Gly Ala His Val Leu Gly Ser Val Ser Leu Thr Gly Leu Thr Gly Thr
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Ile Thr Gln Met Thr Asp Ile Ser Val Thr Ile Gln Phe Thr Phe Asp
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Asn Asn Gly Lys Leu Leu Ser Ser Pro Leu Ile Asn Asn Ala Phe Ser
 260 265 270

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

Ala Phe Met Pro Asn Ser Thr Ile Tyr Ala Arg Gly Gly Gly Gly Glu
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Pro Arg Asn Asn Tyr Tyr Val Gln Thr Tyr Leu Arg Gly Asn Val Gln
 305 310 315 320

Lys Pro Ile Ile Leu Thr Val Thr Tyr Asn Ser Val Ala Thr Gly Tyr
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Pro Thr Thr Ser Phe Cys Tyr Ile Thr Glu Gln
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Ser Ser Asp Gly Leu Gln Glu Lys Pro Leu Gly Val Leu Ser Leu Asn
 35 40 45

Tyr Arg Asp Pro Ile Thr Thr Gln Asn Glu Ser Leu Thr Ile Lys Leu
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Gly Asn Gly Leu Thr Leu Asp Asn Gln Gly Gln Leu Thr Ser Thr Ala
 65 70 75 80

Gly Glu Val Glu Pro Pro Leu Thr Asn Ala Asn Asn Lys Leu Ala Leu
 85 90 95

Val Tyr Ser Asp Pro Leu Ala Val Lys Arg Asn Ser Leu Thr Leu Ser
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His Thr Ala Pro Leu Val Ile Ala Asp Asn Ser Leu Ala Leu Gln Val
 115 120 125
 Ser Glu Pro Ile Phe Ile Asn Asp Lys Asp Lys Leu Ala Leu Gln Thr
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 Ala Ala Pro Leu Val Thr Asn Ala Gly Thr Leu Arg Leu Gln Ser Ala
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 Ala Pro Leu Gly Ile Ala Asp Gln Thr Leu Lys Leu Leu Phe Thr Asn
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 Pro Leu Tyr Leu Gln Asn Asn Phe Leu Thr Leu Ala Ile Glu Arg Pro
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 Thr Val Ser Asn Gly Thr Leu Gly Leu Ala Ile Lys Arg Pro Leu Ile
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 Ile Gln Asp Asn Asn Leu Phe Leu Asp Phe Arg Ala Pro Leu Arg Leu
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 Ser Tyr Asp Gly Leu Ile Leu Asn Leu Gly Lys Asp Leu Arg Phe Asp
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 Val Ser Lys Lys Leu Asp Val Asn Pro Asn Gln Asn Lys Gly Leu Thr
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Val His Gly Ser Val Ala Leu Lys Ala Leu Lys Gly Thr Leu Leu Ser
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Tyr	Ser	Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe	Tyr	Leu	Asn	
1175					1180					1185					
cac	act	ttc	aaa	aag	gtg	tct	att	atg	ttt	gac	tcc	tgc	gtt	agc	18777
His	Thr	Phe	Lys	Lys	Val	Ser	Ile	Met	Phe	Asp	Ser	Ser	Val	Ser	
1190					1195					1200					
tgg	ccc	ggc	aac	gac	cgc	ctg	cta	acg	ccc	aac	gag	ttc	gaa	att	18822
Trp	Pro	Gly	Asn	Asp	Arg	Leu	Leu	Thr	Pro	Asn	Glu	Phe	Glu	Ile	
1205					1210					1215					
aag	cgt	tcc	gtg	gac	ggt	gaa	ggg	tac	aac	gtg	gcc	cag	agc	aac	18867
Lys	Arg	Ser	Val	Asp	Gly	Glu	Gly	Tyr	Asn	Val	Ala	Gln	Ser	Asn	
1220					1225					1230					
atg	acc	aag	gac	tgg	ttt	cta	att	caa	atg	ctc	agt	cac	tat	aat	18912
Met	Thr	Lys	Asp	Trp	Phe	Leu	Ile	Gln	Met	Leu	Ser	His	Tyr	Asn	
1235					1240					1245					
ata	ggt	tac	cag	ggc	ttc	tat	gtg	ccc	gag	aac	tac	aag	gac	cgc	18957
Ile	Gly	Tyr	Gln	Gly	Phe	Tyr	Val	Pro	Glu	Asn	Tyr	Lys	Asp	Arg	
1250					1255					1260					
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Met	Tyr	Ser	Phe	Phe	Arg	Asn	Phe	Gln	Pro	Met	Ser	Arg	Gln	Val	
1265					1270					1275					
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Val	Asp	Thr	Val	Thr	Tyr	Thr	Asp	Tyr	Lys	Asp	Val	Lys	Leu	Pro	
1280					1285					1290					
tac	caa	cac	aac	aac	tca	ggg	ttc	gtg	ggc	tac	atg	gga	ccc	acc	19092
Tyr	Gln	His	Asn	Asn	Ser	Gly	Phe	Val	Gly	Tyr	Met	Gly	Pro	Thr	
1295					1300					1305					
atg	cga	gag	gga	cag	gcc	tac	cgg	gcc	aac	tat	ccc	tac	ccc	ctg	19137
Met	Arg	Glu	Gly	Gln	Ala	Tyr	Pro	Ala	Asn	Tyr	Pro	Tyr	Pro	Leu	
1310					1315					1320					
atc	gga	gag	act	gcc	gta	ccc	agc	ctc	acg	cag	aaa	aag	ttc	ctc	19182
Ile	Gly	Glu	Thr	Ala	Val	Pro	Ser	Leu	Thr	Gln	Lys	Lys	Phe	Leu	
1325					1330					1335					

tgc gac cgg gtg atg tgg agg ata ccc ttc tct agc aac ttt atg	19227
Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met	
1340 1345 1350	
tog atg ggc tcc ctc acc gac ctg ggg cag aac atg ctg tac gcc	19272
Ser Met Gly Ser Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala	
1355 1360 1365	
aac tcc gct cac gcc ttg gac atg act ttt gag gtg gat ccc atg	19317
Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu Val Asp Pro Met	
1370 1375 1380	
gat gag ccc acg ctt ctc tat gtt ctg ttt gaa gtc ttc gac gtg	19362
Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe Glu Val Phe Asp Val	
1385 1390 1395	
gtg cgc atc cac cag ccg cac cgc ggc gtc atc gag gcc gtc tac	19407
Val Arg Ile His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr	
1400 1405 1410	
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Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr	
1415 1420 1425	
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 actaccatca cctgtttctg catctgcccc acgccggat tac atg aag atc tgt 25391
 Met Lys Ile Cys
 1430
 gtt gtc atc ttt gcg ctc agt tta ata aaa act gaa ctt ttt gcc 25436
 Val Val Ile Phe Ala Leu Ser Leu Ile Lys Thr Glu Leu Phe Ala
 1435 1440 1445

gta cct tca acg cca	cgc gtt gtt tct cct	tgt gaa aaa acc cca	25481
Val Pro Ser Thr Pro	Arg Val Val Ser Pro	Cys Glu Lys Thr Pro	
1450	1455	1460	
gga gtc ctt aac tta	cac ata gca aaa ccc	ttg tat ttt acc ata	25526
Gly Val Leu Asn Leu	His Ile Ala Lys Pro	Leu Tyr Phe Thr Ile	
1465	1470	1475	
gaa aaa caa cta gcc	ctt tca att gga aaa	ggg tta aca att tct	25571
Glu Lys Gln Leu Ala	Leu Ser Ile Gly Lys	Gly Leu Thr Ile Ser	
1480	1485	1490	
gct aca gga cag ttg	gaa agc aca gca agc	gta cag gac agc gct	25616
Ala Thr Gly Gln Leu	Glu Ser Thr Ala Ser	Val Gln Asp Ser Ala	
1495	1500	1505	
aca cca ccc cta cgt	ggt att tcc cct tta	aag ctg aca gac aac	25661
Thr Pro Pro Leu Arg	Gly Ile Ser Pro Leu	Lys Leu Thr Asp Asn	
1510	1515	1520	
ggt tta aca tta agc	tat tca gat ccc ctg	cgt gtg gta ggt gac	25706
Gly Leu Thr Leu Ser	Tyr Ser Asp Pro Leu	Arg Val Val Gly Asp	
1525	1530	1535	
caa ctt acg ttt aat	ttt act tct cca cta	cgt tac gaa aat ggc	25751
Gln Leu Thr Phe Asn	Phe Thr Ser Pro Leu	Arg Tyr Glu Asn Gly	
1540	1545	1550	
agt ctt aca ttc aac	tac act tct ccc atg	aca cta ata aac aac	25796
Ser Leu Thr Phe Asn	Tyr Thr Ser Pro Met	Thr Leu Ile Asn Asn	
1555	1560	1565	
agt ctt gct att aac	gtc aat acc tcc aaa	ggc ctc agt agt gac	25841
Ser Leu Ala Ile Asn	Val Asn Thr Ser Lys	Gly Leu Ser Ser Asp	
1570	1575	1580	
aac ggc aca ctc gct	gta aat gtt act cca	gat ttt aga ttt aac	25886
Asn Gly Thr Leu Ala	Val Asn Val Thr Pro	Asp Phe Arg Phe Asn	
1585	1590	1595	
agc tct ggt gcc tta	act ttt ggc ata caa	agt cta tgg act ttt	25931
Ser Ser Gly Ala Leu	Thr Phe Gly Ile Gln	Ser Leu Trp Thr Phe	
1600	1605	1610	
cca acc aaa act cct	aac tgt acc gtg ttt	acc gaa agt gac tcc	25976
Pro Thr Lys Thr Pro	Asn Cys Thr Val Phe	Thr Glu Ser Asp Ser	
1615	1620	1625	
ctg ctg agt ctt tgc	ttg act aaa tgc gga	gct cac gta ctt gga	26021
Leu Leu Ser Leu Cys	Leu Thr Lys Cys Gly	Ala His Val Leu Gly	
1630	1635	1640	
agc gtg agt tta agc	gga gtg gca gga acc	atg cta aaa atg acc	26066
Ser Val Ser Leu Ser	Gly Val Ala Gly Thr	Met Leu Lys Met Thr	
1645	1650	1655	

cac act tct gtt acc gtt cag ttt tog ttt gat gac agt ggt aaa His Thr Ser Val Thr Val Gln Phe Ser Phe Asp Asp Ser Gly Lys 1660 1665 1670	26111
cta ata ttc tct cca ctt gcg aac aac act tgg ggt gtt cga caa Leu Ile Phe Ser Pro Leu Ala Asn Asn Thr Trp Gly Val Arg Gln 1675 1680 1685	26156
agc gag agt ccg ttg ccc aac cca tcc ttc aac gct ctc acg ttt Ser Glu Ser Pro Leu Pro Asn Pro Ser Phe Asn Ala Leu Thr Phe 1690 1695 1700	26201
atg cca aac agt acc att tat tct aga gga gca agt aac gaa cct Met Pro Asn Ser Thr Ile Tyr Ser Arg Gly Ala Ser Asn Glu Pro 1705 1710 1715	26246
caa aac aat tat tat gtc cag acg tat ctt aga ggc aac gtg cga Gln Asn Asn Tyr Tyr Val Gln Thr Tyr Leu Arg Gly Asn Val Arg 1720 1725 1730	26291
aag cca att cta cta act gtt acc tac aac tca gtt aat tca gga Lys Pro Ile Leu Leu Thr Val Thr Tyr Asn Ser Val Asn Ser Gly 1735 1740 1745	26336
tat tcc tta act ttt aaa tgg gat gct gtc gcc aat gaa aaa ttt Tyr Ser Leu Thr Phe Lys Trp Asp Ala Val Ala Asn Glu Lys Phe 1750 1755 1760	26381
gcc act cct aca tct tog ttt tgc tat gtt gca gag caa taa Ala Thr Pro Thr Ser Ser Phe Cys Tyr Val Ala Glu Gln 1765 1770	26423
aaccctgtta cccacccgtc tcgttttttt cag atg aaa cga gcg aga gtt Met Lys Arg Ala Arg Val 1775	26474
gat gaa gac ttc aac cca gtg tac cct tat gac ccc cca tac gct Asp Glu Asp Phe Asn Pro Val Tyr Pro Tyr Asp Pro Pro Tyr Ala 1780 1785 1790	26519
ccc gtc atg ccc ttc att act ccg cct ttt acc tcc tog gat ggg Pro Val Met Pro Phe Ile Thr Pro Pro Phe Thr Ser Ser Asp Gly 1795 1800 1805	26564
ttg cag gaa aaa cca ctt gga gtg tta agt tta aac tac agg gat Leu Gln Glu Lys Pro Leu Gly Val Leu Ser Leu Asn Tyr Arg Asp 1810 1815 1820	26609
ccc att act aca caa aat ggg tct ctc acg tta aaa cta gga aac Pro Ile Thr Thr Gln Asn Gly Ser Leu Thr Leu Lys Leu Gly Asn 1825 1830 1835	26654
ggc ctc act cta aac aac cag gga cag tta aca tca act gct ggc Gly Leu Thr Leu Asn Asn Gln Gly Gln Leu Thr Ser Thr Ala Gly 1840 1845 1850	26699

gaa	gtg	gag	cct	ccg	ctc	act	aat	gct	aac	aac	aaa	ctt	gca	cta	26744
Glu	Val	Glu	Pro	Pro	Leu	Thr	Asn	Ala	Asn	Asn	Lys	Leu	Ala	Leu	
1855					1860					1865					
gcc	tat	agc	gaa	cca	tta	gca	gta	aaa	agc	aac	cgc	cta	act	cta	26789
Ala	Tyr	Ser	Glu	Pro	Leu	Ala	Val	Lys	Ser	Asn	Arg	Leu	Thr	Leu	
1870					1875					1880					
tca	cac	acc	gct	ccc	ctt	gtc	atc	gct	aat	aat	tct	tta	gcg	ttg	26834
Ser	His	Thr	Ala	Pro	Leu	Val	Ile	Ala	Asn	Asn	Ser	Leu	Ala	Leu	
1885					1890					1895					
caa	gtt	tca	gag	cct	att	ttt	gta	aat	gac	gat	gac	aag	cta	gcc	26879
Gln	Val	Ser	Glu	Pro	Ile	Phe	Val	Asn	Asp	Asp	Asp	Lys	Leu	Ala	
1900					1905					1910					
ctg	cag	aca	gcc	gcc	ccc	ctt	gta	acc	aac	gct	ggc	acc	ctt	cgc	26924
Leu	Gln	Thr	Ala	Ala	Pro	Leu	Val	Thr	Asn	Ala	Gly	Thr	Leu	Arg	
1915					1920					1925					
tta	cag	agc	gct	gcc	cct	tta	gga	ttg	gtt	gaa	aat	act	ctt	aaa	26969
Leu	Gln	Ser	Ala	Ala	Pro	Leu	Gly	Leu	Val	Glu	Asn	Thr	Leu	Lys	
1930					1935					1940					
ctg	ctg	ttt	tct	aaa	ccc	ttg	tat	ttg	caa	aat	gat	ttt	ctt	gca	27014
Leu	Leu	Phe	Ser	Lys	Pro	Leu	Tyr	Leu	Gln	Asn	Asp	Phe	Leu	Ala	
1945					1950					1955					
tta	gcc	att	gaa	cgc	ccc	ctg	gct	gta	gca	gcc	gca	ggg	act	ctg	27059
Leu	Ala	Ile	Glu	Arg	Pro	Leu	Ala	Val	Ala	Ala	Ala	Gly	Thr	Leu	
1960					1965					1970					
acc	cta	caa	ctt	act	cct	cca	tta	aag	act	aac	gat	gac	ggg	cta	27104
Thr	Leu	Gln	Leu	Thr	Pro	Pro	Leu	Lys	Thr	Asn	Asp	Asp	Gly	Leu	
1975					1980					1985					
aca	cta	tcc	aca	gtc	gag	cca	tta	act	gta	aaa	aac	gga	aac	cta	27149
Thr	Leu	Ser	Thr	Val	Glu	Pro	Leu	Thr	Val	Lys	Asn	Gly	Asn	Leu	
1990					1995					2000					
ggc	ttg	caa	ata	tcg	cgc	cct	tta	gtt	gtt	caa	aac	aac	ggc	ctt	27194
Gly	Leu	Gln	Ile	Ser	Arg	Pro	Leu	Val	Val	Gln	Asn	Asn	Gly	Leu	
2005					2010					2015					
tcg	ctt	gct	att	acc	ccc	ccg	ctg	cgt	ttg	ttt	aac	agc	gac	ccc	27239
Ser	Leu	Ala	Ile	Thr	Pro	Pro	Leu	Arg	Leu	Phe	Asn	Ser	Asp	Pro	
2020					2025					2030					
gtt	ctt	ggg	ttg	ggc	ttc	act	ttt	ccc	cta	gct	gtc	aca	aac	aac	27284
Val	Leu	Gly	Leu	Gly	Phe	Thr	Phe	Pro	Leu	Ala	Val	Thr	Asn	Asn	
2035					2040					2045					
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gog att gcc gta acg ctt act gcc gaa tta cct ttg caa tac act Ala Ile Ala Val Thr Leu Thr Ala Glu Leu Pro Leu Gln Tyr Thr 2080 2085 2090	27419
aac aaa ctt caa ctg aat att gga gct ggc ctt cgt tac aat gga Asn Lys Leu Gln Leu Asn Ile Gly Ala Gly Leu Arg Tyr Asn Gly 2095 2100 2105	27464
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caa ttt gac cct aat ggc aac atc gct gtt atc cct gaa acc gtg Gln Phe Asp Pro Asn Gly Asn Ile Ala Val Ile Pro Glu Thr Val 2140 2145 2150	27599
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tca gtg tac cag gac ttg gat gcc agg ctg tgg ctc gct ctt gtt Ser Val Tyr Gln Asp Leu Asp Ala Arg Leu Trp Leu Ala Leu Val 2170 2175 2180	27689
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aaa ggg acg ttg cta aat cct aca gcc agc tac att tcc att gtg Lys Gly Thr Leu Leu Asn Pro Thr Ala Ser Tyr Ile Ser Ile Val 2200 2205 2210	27779
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cga cag ggg caa tct gct aac act aat gtg acc aat gcc act gaa Arg Gln Gly Gln Ser Ala Asn Thr Asn Val Thr Asn Ala Thr Glu 2245 2250 2255	27914
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gct	atg	cct	gtc	ccg	ttc	cgt	gta	aca	tat	aat	cac	gcc	ctg	gaa	28049
Ala	Met	Pro	Val	Pro	Phe	Arg	Val	Thr	Tyr	Asn	His	Ala	Leu	Glu	
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ggg	tat	tcc	ctt	aag	ttc	acc	tgg	cgc	gtt	gta	gcc	aat	cag	gcc	28094
Gly	Tyr	Ser	Leu	Lys	Phe	Thr	Trp	Arg	Val	Val	Ala	Asn	Gln	Ala	
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Phe	Asp	Ile	Pro	Cys	Cys	Ser	Phe	Ser	Tyr	Ile	Thr	Glu			
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<210> 30
 <211> 505
 <212> PRT
 <213> simian adenovirus SV-25

<400> 30

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Glu Ala Pro Tyr Val Pro Pro Arg Tyr Leu Gly Pro Thr Glu Gly Arg
          35           40           45

Asn Ser Ile Arg Tyr Ser Glu Leu Ala Pro Leu Tyr Asp Thr Thr Lys
          50           55           60

Val Tyr Leu Val Asp Asn Lys Ser Ala Asp Ile Ala Ser Leu Asn Tyr
          65           70           75           80

Gln Asn Asp His Ser Asn Phe Leu Thr Thr Val Val Gln Asn Asn Asp
          85           90           95

Phe Thr Pro Thr Glu Ala Gly Thr Gln Thr Ile Asn Phe Asp Glu Arg
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Ser Arg Trp Gly Gly Gln Leu Lys Thr Ile Leu His Thr Asn Met Pro
          115          120          125

Asn Ile Asn Glu Phe Met Ser Thr Asn Lys Phe Arg Ala Lys Leu Met
          130          135          140

Val Glu Lys Ser Asn Ala Glu Thr Arg Gln Pro Arg Tyr Glu Trp Phe
          145          150          155          160

Glu Phe Thr Ile Pro Glu Gly Asn Tyr Ser Glu Thr Met Thr Ile Asp
          165          170          175

Leu Met Asn Asn Ala Ile Val Asp Asn Tyr Leu Gln Val Gly Arg Gln
          180          185          190

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

Phe Arg Leu Gly Trp Asp Pro Val Thr Lys Leu Val Met Pro Gly Val
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Tyr Thr Asn Glu Ala Phe His Pro Asp Ile Val Leu Leu Pro Gly Cys
          225          230          235          240

Gly Val Asp Phe Thr Gln Ser Arg Leu Ser Asn Leu Leu Gly Ile Arg
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Lys Arg Arg Pro Phe Gln Glu Gly Phe Gln Ile Met Tyr Glu Asp Leu
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 Glu Gly Gly Asn Ile Pro Ala Leu Leu Asp Val Ser Lys Tyr Glu Ala
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 Ser Ile Gln Arg Ala Lys Ala Glu Gly Arg Glu Ile Arg Gly Asp Thr
 290 295 300
 Phe Ala Val Ala Pro Gln Asp Leu Glu Ile Val Pro Leu Thr Lys Asp
 305 310 315 320
 Ser Lys Asp Arg Ser Tyr Asn Ile Ile Asn Asn Thr Thr Asp Thr Leu
 325 330 335
 Tyr Arg Ser Trp Phe Leu Ala Tyr Asn Tyr Gly Asp Pro Glu Lys Gly
 340 345 350
 Val Arg Ser Trp Thr Ile Leu Thr Thr Thr Asp Val Thr Cys Gly Ser
 355 360 365
 Gln Gln Val Tyr Trp Ser Leu Pro Asp Met Met Gln Asp Pro Val Thr
 370 375 380
 Phe Arg Pro Ser Thr Gln Val Ser Asn Phe Pro Val Val Gly Thr Glu
 385 390 395 400
 Leu Leu Pro Val His Ala Lys Ser Phe Tyr Asn Glu Gln Ala Val Tyr
 405 410 415
 Ser Gln Leu Ile Arg Gln Ser Thr Ala Leu Thr His Val Phe Asn Arg
 420 425 430
 Phe Pro Glu Asn Gln Ile Leu Val Arg Pro Pro Ala Pro Thr Ile Thr
 435 440 445
 Thr Val Ser Glu Asn Val Pro Ala Leu Thr Asp His Gly Thr Leu Pro
 450 455 460
 Leu Arg Ser Ser Ile Ser Gly Val Gln Arg Val Thr Ile Thr Asp Ala
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 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
 50 55 60
 Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
 65 70 75 80
 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
 85 90 95
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
 100 105 110
 Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
 115 120 125
 Ala Pro Asn Pro Ser Glu Trp Thr Asp Thr Ser Asp Asn Lys Leu Lys
 130 135 140
 Ala Tyr Ala Gln Ala Pro Tyr Gln Ser Gln Gly Leu Thr Lys Asp Gly
 145 150 155 160
 Ile Gln Val Gly Leu Val Val Thr Glu Ser Gly Gln Thr Pro Gln Tyr
 165 170 175
 Ala Asn Lys Val Tyr Gln Pro Glu Pro Gln Ile Gly Glu Asn Gln Trp
 180 185 190
 Asn Leu Glu Gln Glu Asp Lys Ala Ala Gly Arg Val Leu Lys Lys Asp
 195 200 205
 Thr Pro Met Phe Pro Cys Tyr Gly Ser Tyr Ala Arg Pro Thr Asn Glu
 210 215 220
 Gln Gly Gly Gln Ala Lys Asn Gln Glu Val Asp Leu Gln Phe Phe Ala
 225 230 235 240
 Thr Pro Gly Asp Thr Gln Asn Thr Ala Lys Val Val Leu Tyr Ala Glu
 245 250 255
 Asn Val Asn Leu Glu Thr Pro Asp Thr His Leu Val Phe Lys Pro Asp
 260 265 270
 Asp Asp Ser Thr Ser Ser Lys Leu Leu Leu Gly Gln Gln Ala Ala Pro
 275 280 285
 Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met
 290 295 300

Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser
 305 310 315 320
 Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser
 325 330 335
 Tyr Gln Leu Met Leu Asp Ala Leu Gly Asp Arg Ser Arg Tyr Phe Ser
 340 345 350
 Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile
 355 360 365
 Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu
 370 375 380
 Gly Gly Met Val Val Thr Asp Asn Tyr Asn Ser Val Thr Pro Gln Asn
 385 390 395 400
 Gly Gly Ser Gly Asn Thr Trp Gln Ala Asp Asn Thr Thr Phe Ser Gln
 405 410 415
 Arg Gly Ala Gln Ile Gly Ser Gly Asn Met Phe Ala Leu Glu Ile Asn
 420 425 430
 Leu Gln Ala Asn Leu Trp Arg Gly Phe Leu Tyr Ser Asn Ile Gly Leu
 435 440 445
 Tyr Leu Pro Asp Ser Leu Lys Ile Thr Pro Asp Asn Ile Thr Leu Pro
 450 455 460
 Glu Asn Lys Asn Thr Tyr Gln Tyr Met Asn Gly Arg Val Thr Pro Pro
 465 470 475 480
 Gly Leu Ile Asp Thr Tyr Val Asn Val Gly Ala Arg Trp Ser Pro Asp
 485 490 495
 Val Met Asp Ser Ile Asn Pro Phe Asn His His Arg Asn Ala Gly Leu
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 Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His
 515 520 525
 Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Asn Leu Leu Leu Leu
 530 535 540
 Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met
 545 550 555 560
 Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Val Asp Gly Ala Ser
 565 570 575
 Ile Arg Phe Asp Ser Ile Asn Leu Tyr Ala Asn Phe Phe Pro Met Ala
 580 585 590
 His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn
 595 600 605

Asp Gln Ser Phe Asn Asp Tyr Leu Cys Ala Ala Asn Met Leu Tyr Pro
 610 615 620
 Ile Pro Ala Asn Ala Thr Ser Val Pro Ile Ser Ile Pro Ser Arg Asn
 625 630 635 640
 Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Lys Glu
 645 650 655
 Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly
 660 665 670
 Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys
 675 680 685
 Lys Val Ser Ile Met Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp
 690 695 700
 Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Ser Val Asp Gly
 705 710 715 720
 Glu Gly Tyr Asn Val Ala Gln Ser Asn Met Thr Lys Asp Trp Phe Leu
 725 730 735
 Ile Gln Met Leu Ser His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val
 740 745 750
 Pro Glu Asn Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln
 755 760 765
 Pro Met Ser Arg Gln Val Val Asp Thr Val Thr Tyr Thr Asp Tyr Lys
 770 775 780
 Asp Val Lys Leu Pro Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr
 785 790 795 800
 Met Gly Pro Thr Met Arg Glu Gly Gln Ala Tyr Pro Ala Asn Tyr Pro
 805 810 815
 Tyr Pro Leu Ile Gly Glu Thr Ala Val Pro Ser Leu Thr Gln Lys Lys
 820 825 830
 Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe
 835 840 845
 Met Ser Met Gly Ser Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala
 850 855 860
 Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu Val Asp Pro Met Asp
 865 870 875 880
 Glu Pro Thr Leu Leu Tyr Val Leu Phe Glu Val Phe Asp Val Val Arg
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Pro Phe Ser Ala Gly Asn Ala Thr Thr
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 <212> PRT
 <213> simian adenovirus SV-25

<400> 32

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 35 40 45
 Ile Glu Lys Gln Leu Ala Leu Ser Ile Gly Lys Gly Leu Thr Ile Ser
 50 55 60
 Ala Thr Gly Gln Leu Glu Ser Thr Ala Ser Val Gln Asp Ser Ala Thr
 65 70 75 80
 Pro Pro Leu Arg Gly Ile Ser Pro Leu Lys Leu Thr Asp Asn Gly Leu
 85 90 95
 Thr Leu Ser Tyr Ser Asp Pro Leu Arg Val Val Gly Asp Gln Leu Thr
 100 105 110
 Phe Asn Phe Thr Ser Pro Leu Arg Tyr Glu Asn Gly Ser Leu Thr Phe
 115 120 125
 Asn Tyr Thr Ser Pro Met Thr Leu Ile Asn Asn Ser Leu Ala Ile Asn
 130 135 140
 Val Asn Thr Ser Lys Gly Leu Ser Ser Asp Asn Gly Thr Leu Ala Val
 145 150 155 160
 Asn Val Thr Pro Asp Phe Arg Phe Asn Ser Ser Gly Ala Leu Thr Phe
 165 170 175
 Gly Ile Gln Ser Leu Trp Thr Phe Pro Thr Lys Thr Pro Asn Cys Thr
 180 185 190
 Val Phe Thr Glu Ser Asp Ser Leu Leu Ser Leu Cys Leu Thr Lys Cys
 195 200 205
 Gly Ala His Val Leu Gly Ser Val Ser Leu Ser Gly Val Ala Gly Thr
 210 215 220
 Met Leu Lys Met Thr His Thr Ser Val Thr Val Gln Phe Ser Phe Asp
 225 230 235 240

Asp Ser Gly Lys Leu Ile Phe Ser Pro Leu Ala Asn Asn Thr Trp Gly
 245 250 255
 Val Arg Gln Ser Glu Ser Pro Leu Pro Asn Pro Ser Phe Asn Ala Leu
 260 265 270
 Thr Phe Met Pro Asn Ser Thr Ile Tyr Ser Arg Gly Ala Ser Asn Glu
 275 280 285
 Pro Gln Asn Asn Tyr Tyr Val Gln Thr Tyr Leu Arg Gly Asn Val Arg
 290 295 300
 Lys Pro Ile Leu Leu Thr Val Thr Tyr Asn Ser Val Asn Ser Gly Tyr
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 Ser Leu Thr Phe Lys Trp Asp Ala Val Ala Asn Glu Lys Phe Ala Thr
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 Pro Thr Ser Ser Phe Cys Tyr Val Ala Glu Gln
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<210> 33
 <211> 559
 <212> PRT
 <213> simian adenovirus SV-25

<400> 33

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 35 40 45
 Tyr Arg Asp Pro Ile Thr Thr Gln Asn Gly Ser Leu Thr Leu Lys Leu
 50 55 60
 Gly Asn Gly Leu Thr Leu Asn Asn Gln Gly Gln Leu Thr Ser Thr Ala
 65 70 75 80
 Gly Glu Val Glu Pro Pro Leu Thr Asn Ala Asn Asn Lys Leu Ala Leu
 85 90 95
 Ala Tyr Ser Glu Pro Leu Ala Val Lys Ser Asn Arg Leu Thr Leu Ser
 100 105 110
 His Thr Ala Pro Leu Val Ile Ala Asn Asn Ser Leu Ala Leu Gln Val
 115 120 125
 Ser Glu Pro Ile Phe Val Asn Asp Asp Asp Lys Leu Ala Leu Gln Thr
 130 135 140

Ala Ala Pro Leu Val Thr Asn Ala Gly Thr Leu Arg Leu Gln Ser Ala
 145 150 155 160
 Ala Pro Leu Gly Leu Val Glu Asn Thr Leu Lys Leu Leu Phe Ser Lys
 165 170 175
 Pro Leu Tyr Leu Gln Asn Asp Phe Leu Ala Leu Ala Ile Glu Arg Pro
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 Leu Ala Val Ala Ala Ala Gly Thr Leu Thr Leu Gln Leu Thr Pro Pro
 195 200 205
 Leu Lys Thr Asn Asp Asp Gly Leu Thr Leu Ser Thr Val Glu Pro Leu
 210 215 220
 Thr Val Lys Asn Gly Asn Leu Gly Leu Gln Ile Ser Arg Pro Leu Val
 225 230 235 240
 Val Gln Asn Asn Gly Leu Ser Leu Ala Ile Thr Pro Pro Leu Arg Leu
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 260 265 270
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 290 295 300
 Asn Gly Ala Ile Ala Val Thr Leu Thr Ala Glu Leu Pro Leu Gln Tyr
 305 310 315 320
 Thr Asn Lys Leu Gln Leu Asn Ile Gly Ala Gly Leu Arg Tyr Asn Gly
 325 330 335
 Ala Ser Arg Lys Leu Asp Val Asn Ile Asn Gln Asn Lys Gly Leu Thr
 340 345 350
 Trp Asp Asn Asp Ala Val Ile Pro Lys Leu Gly Ser Gly Leu Gln Phe
 355 360 365
 Asp Pro Asn Gly Asn Ile Ala Val Ile Pro Glu Thr Val Lys Pro Gln
 370 375 380
 Thr Leu Trp Thr Thr Ala Asp Pro Ser Pro Asn Cys Ser Val Tyr Gln
 385 390 395 400
 Asp Leu Asp Ala Arg Leu Trp Leu Ala Leu Val Lys Ser Gly Asp Met
 405 410 415
 Val His Gly Ser Ile Ala Leu Lys Ala Leu Lys Gly Thr Leu Leu Asn
 420 425 430
 Pro Thr Ala Ser Tyr Ile Ser Ile Val Ile Tyr Phe Tyr Ser Asn Gly
 435 440 445

Val Arg Arg Thr Asn Tyr Pro Thr Phe Asp Asn Glu Gly Thr Leu Ala
450 455 460

Asn Ser Ala Thr Trp Gly Tyr Arg Gln Gly Gln Ser Ala Asn Thr Asn
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Val Thr Asn Ala Thr Glu Phe Met Pro Ser Ser Ser Arg Tyr Pro Val
485 490 495

Asn Lys Gly Asp Asn Ile Gln Asn Gln Ser Phe Ser Tyr Thr Cys Ile
500 505 510

Lys Gly Asp Phe Ala Met Pro Val Pro Phe Arg Val Thr Tyr Asn His
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Gln Ala Phe Asp Ile Pro Cys Cys Ser Phe Ser Tyr Ile Thr Glu
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<212> DNA
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<223> L2 Penton

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<400> 34

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Lys Leu Met Val Ala His Glu Ala Asp Lys Asp Pro Val Tyr Glu Trp	
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Val Gln Leu Thr Leu Pro Glu Gly Asn Phe Ser Glu Ile Met Thr Ile	
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Cys Gly Val Asp Phe Thr Tyr Ser Arg Leu Asn Asn Leu Leu Gly Ile	
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Glu Ser Ile Ala Asn Ala Arg Glu Ala Ala Ile Arg Gly Asp Asn Phe	
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Val Pro Val Asp Lys Glu Asp Thr Ala Tyr Ser Tyr Lys Thr Arg Phe	
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Ser Thr Leu Gly Asn Asp Leu	Arg Val Asp Gly Ala	Ser Val Arg	
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Ile Asp Ser Val Asn Leu Tyr	Ala Asn Phe Phe Pro	Met Ala His	
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Val Tyr Ser Gly Thr Ile Pro	Tyr Leu Asp Gly Ser	Phe Tyr Leu	
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Asn Ile Gly Tyr Gln Gly Phe	Tyr Val Pro Glu Gly	Tyr Lys Asp	
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cgggaggaca aggaagcaga ggcagaggca taggcaaagc aacagaattt ttattccaac 32616
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<210> 35
 <211> 503
 <212> PRT
 <213> simian adenovirus SV-39

<400> 35

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

Leu Thr Leu Pro Glu Gly Asn Phe Ser Glu Ile Met Thr Ile Asp Leu
 165 170 175
 Met Asn Asn Ala Ile Ile Asp His Tyr Leu Ala Val Ala Arg Gln Gln
 180 185 190
 Gly Val Lys Glu Ser Glu Ile Gly Val Lys Phe Asp Thr Arg Asn Phe
 195 200 205
 Arg Leu Gly Trp Asp Pro Glu Thr Gly Leu Val Met Pro Gly Val Tyr
 210 215 220
 Thr Asn Glu Ala Phe His Pro Asp Val Val Leu Leu Pro Gly Cys Gly
 225 230 235 240
 Val Asp Phe Thr Tyr Ser Arg Leu Asn Asn Leu Leu Gly Ile Arg Lys
 245 250 255
 Arg Met Pro Phe Gln Glu Gly Phe Gln Ile Leu Tyr Glu Asp Leu Glu
 260 265 270
 Gly Gly Asn Ile Pro Ala Leu Leu Asp Val Pro Ala Tyr Glu Glu Ser
 275 280 285
 Ile Ala Asn Ala Arg Glu Ala Ala Ile Arg Gly Asp Asn Phe Ala Ala
 290 295 300
 Gln Pro Gln Ala Ala Pro Thr Ile Lys Pro Val Leu Glu Asp Ser Lys
 305 310 315 320
 Gly Arg Ser Tyr Asn Val Ile Ala Asn Thr Asn Asn Thr Ala Tyr Arg
 325 330 335
 Ser Trp Tyr Leu Ala Tyr Asn Tyr Gly Asp Pro Glu Lys Gly Val Arg
 340 345 350
 Ala Trp Thr Leu Leu Thr Thr Pro Asp Val Thr Cys Gly Ser Glu Gln
 355 360 365
 Val Tyr Trp Ser Leu Pro Asp Met Tyr Val Asp Pro Val Thr Phe Arg
 370 375 380
 Ser Thr Gln Gln Val Ser Asn Tyr Pro Val Val Gly Ala Glu Leu Met
 385 390 395 400
 Pro Ile His Ser Lys Ser Phe Tyr Asn Glu Gln Ala Val Tyr Ser Gln
 405 410 415
 Leu Ile Arg Gln Thr Thr Ala Leu Thr His Val Phe Asn Arg Phe Pro
 420 425 430
 Glu Asn Gln Ile Leu Val Arg Pro Pro Ala Pro Thr Ile Thr Thr Val
 435 440 445
 Ser Glu Asn Val Pro Ala Leu Thr Asp His Gly Thr Leu Pro Leu Gln
 450 455 460

Asn Ser Ile Arg Gly Val Gln Arg Val Thr Ile Thr Asp Ala Arg Arg
 465 470 475 480

Arg Thr Cys Pro Tyr Val Tyr Lys Ala Leu Gly Ile Val Ala Pro Arg
 485 490 495

Val Leu Ser Ser Arg Thr Phe
 500

<210> 36
 <211> 917
 <212> PRT
 <213> simian adenovirus SV-39

<400> 36

Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ala
 1 5 10 15

Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
 20 25 30

Arg Ala Thr Glu Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
 35 40 45

Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
 50 55 60

Thr Ile Arg Phe Val Pro Val Asp Lys Glu Asp Thr Ala Tyr Ser Tyr
 65 70 75 80

Lys Thr Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
 85 90 95

Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Ile Asp Arg Gly Pro Ser
 100 105 110

Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
 115 120 125

Ala Pro Asn Asn Ser Gln Trp Asn Ala Thr Asp Asn Gly Asn Lys Pro
 130 135 140

Val Cys Phe Ala Gln Ala Ala Phe Ile Gly Gln Ser Ile Thr Lys Asp
 145 150 155 160

Gly Val Gln Ile Gln Asn Ser Glu Asn Gln Gln Ala Ala Ala Asp Lys
 165 170 175

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

Val Thr Ser Asn Ala Ala Gly Arg Val Leu Lys Ala Thr Thr Pro Met
 195 200 205

Leu Pro Cys Tyr Gly Ser Tyr Ala Asn Pro Thr Asn Pro Asn Gly Gly
 210 215 220
 Gln Ala Lys Thr Glu Gly Asp Ile Ser Leu Asn Phe Phe Thr Thr Thr
 225 230 235 240
 Ala Ala Ala Asp Asn Asn Pro Lys Val Val Leu Tyr Ser Glu Asp Val
 245 250 255
 Asn Leu Gln Ala Pro Asp Thr His Leu Val Tyr Lys Pro Thr Val Gly
 260 265 270
 Glu Asn Val Ile Ala Ala Glu Ala Leu Leu Thr Gln Gln Ala Cys Pro
 275 280 285
 Asn Arg Ala Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met
 290 295 300
 Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser
 305 310 315 320
 Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser
 325 330 335
 Tyr Gln Leu Met Leu Asp Ala Leu Gly Asp Arg Thr Arg Tyr Phe Ser
 340 345 350
 Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile
 355 360 365
 Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu
 370 375 380
 Pro Gly Met Gly Ile Phe Asn Ser Tyr Lys Gly Val Lys Pro Gln Asn
 385 390 395 400
 Gly Gly Asn Gly Asn Trp Glu Ala Asn Gly Asp Leu Ser Asn Ala Asn
 405 410 415
 Glu Ile Ala Leu Gly Asn Ile Phe Ala Met Glu Ile Asn Leu His Ala
 420 425 430
 Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn Val Ala Leu Tyr Leu Pro
 435 440 445
 Asp Ser Tyr Lys Phe Thr Pro Ala Asn Ile Thr Leu Pro Ala Asn Gln
 450 455 460
 Asn Thr Tyr Glu Tyr Ile Asn Gly Arg Val Thr Ser Pro Thr Leu Val
 465 470 475 480
 Asp Thr Phe Val Asn Ile Gly Ala Arg Trp Ser Pro Asp Pro Met Asp
 485 490 495
 Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg
 500 505 510

Ser Met Leu Leu Gly Asn Gly Arg Val Val Pro Phe His Ile Gln Val
 515 520 525
 Pro Gln Lys Phe Phe Ala Ile Lys Asn Leu Leu Leu Leu Pro Gly Ser
 530 535 540
 Tyr Thr Tyr Glu Trp Ser Phe Arg Lys Asp Val Asn Met Ile Leu Gln
 545 550 555 560
 Ser Thr Leu Gly Asn Asp Leu Arg Val Asp Gly Ala Ser Val Arg Ile
 565 570 575
 Asp Ser Val Asn Leu Tyr Ala Asn Phe Phe Pro Met Ala His Asn Thr
 580 585 590
 Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser
 595 600 605
 Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala
 610 615 620
 Asn Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala
 625 630 635 640
 Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Ala Lys Glu Thr Pro Ser
 645 650 655
 Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Thr Ile Pro
 660 665 670
 Tyr Leu Asp Gly Ser Phe Tyr Leu Asn His Thr Phe Lys Arg Leu Ser
 675 680 685
 Ile Met Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu
 690 695 700
 Thr Pro Asn Glu Phe Glu Ile Lys Arg Ile Val Asp Gly Glu Gly Tyr
 705 710 715 720
 Asn Val Ala Gln Ser Asn Met Thr Lys Asp Trp Phe Leu Ile Gln Met
 725 730 735
 Leu Ser His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly
 740 745 750
 Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser
 755 760 765
 Arg Gln Val Pro Asp Pro Thr Ala Ala Gly Tyr Gln Ala Val Pro Leu
 770 775 780
 Pro Arg Gln His Asn Asn Ser Gly Phe Val Gly Tyr Met Gly Pro Thr
 785 790 795 800
 Met Arg Glu Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile
 805 810 815

Gly Ala Thr Ala Val Pro Ala Ile Thr Gln Lys Lys Phe Leu Cys Asp
 820 825 830

Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly
 835 840 845

Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His
 850 855 860

Ala Leu Asp Met Thr Phe Glu Val Asp Pro Met Asn Glu Pro Thr Leu
 865 870 875 880

Leu Tyr Met Leu Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro
 885 890 895

His Arg Gly Ile Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala
 900 905 910

Gly Asn Ala Thr Thr
 915

<210> 37
 <211> 533
 <212> PRT
 <213> simian adenovirus SV-39

<400> 37

Met Lys Arg Ala Lys Val Glu Glu Gly Phe Asn Pro Val Tyr Pro Tyr
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Gly Tyr Ser Thr Pro Thr Asp Val Ala Pro Pro Phe Val Ala Ser Asp
 20 25 30

Gly Leu Gln Glu Asn Pro Pro Gly Val Leu Ser Leu Lys Ile Ser Lys
 35 40 45

Pro Leu Thr Phe Asn Ala Ser Lys Ala Leu Ser Leu Ala Ile Gly Pro
 50 55 60

Gly Leu Lys Ile Gln Asp Gly Lys Leu Val Gly Glu Gly Gln Ala Ile
 65 70 75 80

Leu Ala Asn Leu Pro Leu Gln Ile Thr Asn Asn Thr Ile Ser Leu Arg
 85 90 95

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

Leu Lys Ser Ser Ser Pro Leu Lys Ile Thr Asp Gln Thr Leu Ser Leu
 115 120 125

Asn Ile Gly Asp Ser Leu Ala Ile Lys Asp Asp Lys Leu Glu Ser Ala
 130 135 140

Leu Gln Ala Thr Leu Pro Leu Ser Ile Ser Asn Asn Thr Ile Ser Leu
 145 150 155 160
 Asn Val Gly Thr Gly Leu Thr Ile Asn Gly Asn Val Leu Gln Ala Val
 165 170 175
 Pro Leu Asn Ala Leu Ser Pro Leu Thr Ile Ser Asn Asn Asn Ile Ser
 180 185 190
 Leu Arg Tyr Gly Ser Ser Leu Thr Val Leu Asn Asn Glu Leu Gln Ser
 195 200 205
 Asn Leu Thr Val His Ser Pro Leu Lys Leu Asn Ser Asn Asn Ser Ile
 210 215 220
 Ser Leu Asn Thr Leu Ser Pro Phe Arg Ile Glu Asn Gly Phe Leu Thr
 225 230 235 240
 Leu Tyr Leu Gly Thr Lys Ser Gly Leu Leu Val Gln Asn Ser Gly Leu
 245 250 255
 Lys Val Gln Ala Gly Tyr Gly Leu Gln Val Thr Asp Thr Asn Ala Leu
 260 265 270
 Thr Leu Arg Tyr Leu Ala Pro Leu Thr Ile Pro Asp Ser Gly Ser Glu
 275 280 285
 Gln Gly Ile Leu Lys Val Asn Thr Gly Gln Gly Leu Ser Val Asn Gln
 290 295 300
 Ala Gly Ala Leu Glu Thr Ser Leu Gly Gly Gly Leu Lys Tyr Ala Asp
 305 310 315 320
 Asn Lys Ile Thr Phe Asp Thr Gly Asn Gly Leu Thr Leu Ser Glu Asn
 325 330 335
 Lys Leu Ala Val Ala Ala Gly Ser Gly Leu Thr Phe Arg Asp Gly Ala
 340 345 350
 Leu Val Ala Thr Gly Thr Ala Phe Thr Gln Thr Leu Trp Thr Thr Ala
 355 360 365
 Asp Pro Ser Pro Asn Cys Thr Ile Ile Gln Asp Arg Asp Thr Lys Phe
 370 375 380
 Thr Leu Ala Leu Thr Ile Ser Gly Ser Gln Val Leu Gly Thr Val Ser
 385 390 395 400
 Ile Ile Gly Val Lys Gly Pro Leu Ser Ser Ser Ile Pro Ser Ala Thr
 405 410 415
 Val Thr Val Gln Leu Asn Phe Asp Ser Asn Gly Ala Leu Leu Ser Ser
 420 425 430
 Ser Ser Leu Lys Gly Tyr Trp Gly Tyr Arg Gln Gly Pro Ser Ile Asp
 435 440 445

Pro Tyr Pro Ile Ile Asn Ala Leu Asn Phe Met Pro Asn Ser Leu Ala
450 455 460

Tyr Pro Pro Gly Gln Glu Ile Gln Ala Lys Cys Asn Met Tyr Val Ser
465 470 475 480

Thr Phe Leu Arg Gly Asn Pro Gln Arg Pro Ile Val Leu Asn Ile Thr
485 490 495

Phe Asn Asn Gln Thr Ser Gly Phe Ser Ile Arg Phe Thr Trp Thr Asn
500 505 510

Leu Thr Thr Gly Glu Ala Phe Ala Met Pro Pro Cys Thr Phe Ser Tyr
515 520 525

Ile Ala Glu Gln Gln
530

<210> 38
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> oligomer SV25T

<400> 38
aattttaata cgtagcgcac tagtcgcgct aagcgcggat atcattttaa

50

<210> 39
<211> 49
<212> DNA
<213> Artificial sequence

<220>
<223> oligomer SV25B

<400> 39
tattttaaatg atatccgcgc ttaagcgcga ctagtcgcgct acgtattta

49