

SEQUENCE LISTING

<110> The Trustees of the University of Pennsylvania
Janssen Biotech, Inc.

<120> Novel AAV-Mediated Influenza Vaccines

<130> 17-7987PCT

<150> 62/464753

<151> 2017-02-28

<150> 62/504293

<151> 2017-05-10

<150> 62/560834

<151> 2017-09-20

<150> 62/618443

<151> 2017-01-17

<160> 39

<170> PatentIn version 3.5

<210> 1

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the first immunoglobulin region

<400> 1

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Ile Ser Ile Phe Asp Ile Tyr
20 25 30

Ala Met Asp Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val
35 40 45

Ala Val Ser Phe Arg Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys His
85 90 95

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 2

<211> 123

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the second immunoglobulin region

<400> 2

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Tyr Ala Met Gly
20 25 30

Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Phe Val Ala Ala Ile
35 40 45

Asn Ala Leu Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg
50 55 60

Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met
65 70 75 80

Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ala Gln
85 90 95

Gly Gln Trp Arg Ala Ala Pro Val Ala Val Ala Ala Glu Tyr Glu Phe
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115

120

<210> 3

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the third immunoglobulin region

<400> 3

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
 35 40 45

Leu Cys Ile Ser Lys Ser Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Thr Thr Thr Ala Gly Gly Gly Leu Cys Trp Asp Gly Thr Thr Phe
 100 105 110

Ser Arg Leu Ala Ser Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120 125

Ser

<210> 4

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of the fourth immunoglobulin region

<400> 4

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Ser
20 25 30

Trp Met Tyr Trp Leu Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Val Ile Asn Thr Asp Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
50 55 60

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

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Lys Asp Trp Gly Gly Pro Glu Pro Thr Arg Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser
115

<210> 5

<211> 4718

<212> DNA

<213> Artificial Sequence

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<223> J210a Vector Genome with CB7 promoter and rBG polyA

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<221> repeat_region

<222> (1)..(130)

<223> 5' ITR

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<221> promoter
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 <223> CMV IE promoter

 <220>
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 <223> chicken b-actin (CB) promoter

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 <222> (956)..(1928)
 <223> chicken beta-actin intron

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 <222> (1938)..(1985)
 <223> c-myc 5'UTR

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 <222> (1986)..(1991)
 <223> kozak

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 <222> (1992)..(2051)
 <223> hmIL2 leader

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 <223> The first immunoglobulin region

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 <222> (2424)..(2453)
 <223> L1

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 <222> (2454)..(2822)
 <223> The second immunoglobulin region

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<223> L2

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<223> The third immunoglobulin region

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<223> L3

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<222> (3270)..(3617)
<223> The fourth immunoglobulin region

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<223> hinge

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<223> Fc

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<222> (4374)..(4500)
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<222> (4589)..(4718)
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aggggttcct tgtagttaat gattaacccg ccatgctact tatctaccag ggtaatgggg      180
atcctctaga actatagcta gtcgacattg attattgact agttattaat agtaatcaat      240
tacgggggtca ttagttcata gcccatatat ggagttccgc gttacataac ttacggtaaa      300
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<210> 6

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of human IL2 (hmIL2) leader

<400> 6

Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu
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Val Thr Asn Ser
20

<210> 7
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of linker 1 (L1)

<400> 7

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 8
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> hinge

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<221> CDS
<222> (1)..(15)
<223> hinge

<400> 8
gac aag acc cat acc
Asp Lys Thr His Thr
1 5

15

<210> 9
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 9

Asp Lys Thr His Thr
1 5

<210> 10
 <211> 666
 <212> DNA
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<220>
 <223> Fc

<220>
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 <222> (1)..(666)

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 Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 1 5 10 15
 ctg ttc cca cca aag cca aag gac acc ctg atg atc agc cga acc cca 96
 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 20 25 30
 gag gtg acc tgt gtg gtg gtg gac gtg agc cat gag gac cca gag gtg 144
 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 35 40 45
 aag ttc aac tgg tac gtg gac gga gtg gag gtg cat aac gca aag acc 192
 Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 50 55 60
 aag cca cga gag gag cag tac aac agc acc tac cga gtg gtg agc gtg 240
 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 65 70 75 80
 ctg acc gtg ctg cat cag gac tgg ctg aac gga aag gag tac aag tgt 288
 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 85 90 95
 aag gtg agc aac aag gca ctg cca gca cca atc gag aag acc atc agc 336
 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 100 105 110
 aag gca aag gga cag cca cga gag cca cag gtg tac acc ctg cca cca 384
 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 115 120 125
 agc cga gac gag ctg acc aag aac cag gtg agc ctg acc tgt ctg gtg 432
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 130 135 140
 aag gga ttc tac cca agc gac atc gca gtg gag tgg gag agc aac gga 480
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly

145	150	155	160	
cag cca gag aac aac tac aag acc acc cca cca gtg ctg gac agc gac				528
Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp				
	165	170	175	
gga agc ttc ttc ctg tac agc aag ctg acc gtg gac aag agc cgg tgg				576
Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp				
	180	185	190	
cag cag gga aac gtg ttc agc tgt agc gtg atg cac gag gca ctg cat				624
Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His				
	195	200	205	
aac cat tac acc cag aag agc ctg agc ctg agc cca gga aag				666
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys				
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<210> 11
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 <223> Synthetic Construct

<400> 11

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			20					25					30		

Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val
		35					40				45				

Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
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Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
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Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
				85					90					95	

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
100 105 110

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

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
130 135 140

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
145 150 155 160

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
165 170 175

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
180 185 190

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
195 200 205

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215 220

<210> 12
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<223> humanized FM1W3

<400> 12

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20 25 30

Met Asp Trp Tyr Arg Gln Ala Pro Gly Lys Gln Arg Glu Leu Val Ala
35 40 45

Val Ser Phe Arg Asp Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

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

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys His Val
85 90 95

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

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
130 135 140

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

Thr Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu
165 170 175

Phe Val Ala Ala Ile Asn Ala Leu Gly Thr Arg Thr Tyr Tyr Ala Asp
180 185 190

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

Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
210 215 220

Tyr Cys Thr Ala Gln Gly Gln Trp Arg Ala Ala Pro Val Ala Val Ala
225 230 235 240

Ala Glu Tyr Glu Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu
260 265 270

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
275 280 285

Ala Ala Ser Gly Phe Thr Leu Glu Asn Lys Ala Ile Gly Trp Phe Arg
290 295 300

Gln Ala Pro Gly Lys Glu Arg Glu Gly Val Leu Cys Ile Ser Lys Ser
305 310 315 320

Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
325 330 335

Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu Gln Met Asn Ser Leu
340 345 350

Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Thr Thr Thr Ala Gly
355 360 365

Gly Gly Leu Cys Trp Asp Gly Thr Thr Phe Ser Arg Leu Ala Ser Ser
370 375 380

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
385 390 395 400

Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu
405 410 415

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
420 425 430

Thr Phe Ser Thr Ser Trp Met Tyr Trp Leu Arg Gln Ala Pro Gly Lys
435 440 445

Gly Leu Glu Trp Val Ser Val Ile Asn Thr Asp Gly Gly Thr Tyr Tyr
450 455 460

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys

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Val Tyr Tyr Cys	Ala Lys Asp Trp Gly Gly	Pro Glu Pro Thr Arg Gly				
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Gln Gly Thr Leu Val Thr Val	Ser Ser Asp Lys Thr His Thr Cys Pro					
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Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly	Pro Ser Val Phe Leu Phe					
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Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val						
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Thr Cys Val Trp Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn						
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Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Trp Ser Val Leu Thr Val Leu						
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His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn						
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Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly						
625	630	635			640	
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu						
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Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr						
	660	665			670	
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn						
	675	680			685	

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
690 695 700

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
705 710 715 720

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
725 730 735

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
740 745

<210> 13
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<222> (17)..(146)
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<210> 16

<211> 736

<212> PRT
<213> Artificial Sequence

<220>
<223> AAV hu68 vp1

<400> 16

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

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

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

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

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

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

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

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

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

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

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

180	185	190																	
Ala	Ala	Pro	Ser	Gly	Val	Gly	Ser	Leu	Thr	Met	Ala	Ser	Gly	Gly	Gly				
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Ala	Pro	Val	Ala	Asp	Asn	Asn	Glu	Gly	Ala	Asp	Gly	Val	Gly	Ser	Ser				
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Ser	Gly	Asn	Trp	His	Cys	Asp	Ser	Gln	Trp	Leu	Gly	Asp	Arg	Val	Ile				
225					230					235					240				
Thr	Thr	Ser	Thr	Arg	Thr	Trp	Ala	Leu	Pro	Thr	Tyr	Asn	Asn	His	Leu				
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Tyr	Lys	Gln	Ile	Ser	Asn	Ser	Thr	Ser	Gly	Gly	Ser	Ser	Asn	Asp	Asn				
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Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg				
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Phe	His	Cys	His	Phe	Ser	Pro	Arg	Asp	Trp	Gln	Arg	Leu	Ile	Asn	Asn				
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Gln	Val	Lys	Glu	Val	Thr	Asp	Asn	Asn	Gly	Val	Lys	Thr	Ile	Ala	Asn				
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Pro	Tyr	Val	Leu	Gly	Ser	Ala	His	Glu	Gly	Cys	Leu	Pro	Pro	Phe	Pro				
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Gly	Ser	Gln	Ala	Val	Gly	Arg	Ser	Ser	Phe	Tyr	Cys	Leu	Glu	Tyr	Phe				
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Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

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

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

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

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

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

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

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

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

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

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

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

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

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

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

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

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

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

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

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

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

<210> 17
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> human adeno-associated virus 9 vp1

<400> 17

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
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Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
 545 550 555 560

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

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
 580 585 590

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

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

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

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

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
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Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln

675

680

685

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

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
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Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
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<210> 18

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<223> AAVhu68 vp1 coding sequence

<400> 18

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tattctgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a	2211

<210> 19

<211> 5351

<212> DNA

<213> Artificial Sequence

<220>

<223> Vector genome encoding four immunoglobulin domains with UbC

promoter and SV40 polyA

<220>

<221> repeat_region

<222> (17)..(146)

<223> AAV2-5' ITR

<220>

<221> promoter

<222> (207)..(1433)

<223> UbC promoter, including UB fow priming site

<220>

<221> Intron

<222> (1527)..(1659)

<223> chimeric intron

<220>

<221> 5'UTR

<222> (1726)..(1773)

<223> c-myc 5'UTR

<220>

<221> misc_feature

<222> (1774)..(1779)

<223> kozak

<220>

<221> misc_feature

<222> (1780)..(1839)

<223> hm IL2 leader

<220>

<221> misc_feature

<222> (1840)..(2111)

<223> coding region for the first immunoglobulin region

<220>

<221> misc_binding

<222> (2212)..(2241)

<223> linker L1

<220>

<221> misc_feature

<222> (2242)..(2610)

<223> coding sequence for the second immunoglobulin region

<220>

<221> misc_binding

<222> (2611)..(2640)

<223> linker L2

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<220>
<221> misc_feature
<222> (2641)..(3303)
<223> Fc1

<220>
<221> misc_binding
<222> (3304)..(3315)
<223> furin

<220>
<221> misc_binding
<222> (3316)..(3387)
<223> 2A

<220>
<221> misc_feature
<222> (3388)..(3447)
<223> hm1 IL2 leader

<220>
<221> misc_feature
<222> (3448)..(3834)
<223> coding sequence for the third immunoglobulin region

<220>
<221> misc_binding
<222> (3835)..(3864)
<223> linker sequence L3

<220>
<221> misc_feature
<222> (3865)..(4212)
<223> coding sequence for the fourth immunoglobulin region

<220>
<221> misc_binding
<222> (4213)..(4242)
<223> linker L4

<220>
<221> misc_feature
<222> (4243)..(4908)
<223> Fc2

<220>
<221> polyA_signal
<222> (4926)..(5157)
<223> SV40 late polyA signal

<220>
<221> repeat_region
<222> (5222)..(5351)

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<223> AAV2 - 3' ITR

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ggaagcctgc ggctgagctg cgccgccagc ggattcacc cggagaacaa ggccatcggc	1020
tggttccggc agggcccagg aaaggagcgg gagggagtgc tgtgcatcag caagagcgga	1080
agctggacct actacgccga tagcgtgaag ggacggttca ccatcagccg ggataacagc	1140
aagaacaccg tgtacctgca gatgaacagc ctgcggccag aggataccgc cgtgtactac	1200
tgcgccacca ccaccgccgg aggaggactg tgctgggacg gaaccacctt cagccggctg	1260
gccagcagct ggggacaggg aaccctggtg accgtgagca gcggaggagg aggatccgga	1320
ggaggaggat ccgaggtgca gctggtggag tcaggaggag gactggtgca gcccgaggga	1380
tcactgagac tgtcctgcgc tgcttcagga ttcaccttct caacctcctg gatgtattgg	1440

ctgagacagg ctccccgaaa aggactggag tgggtgtcag tgatcaacac cgacggagga	1500
acctattatg ctgattcagt gaaaggaaga ttcaccatct caagagataa ctcaaaaaac	1560
accctgtatc tgcagatgaa ctactgaga gctgaggata ccgctgtgta ttattgcgct	1620
aaagattggg gaggaccca gcccaccaga ggacaggga ccctggtgac cgtgtcatca	1680
gacaagaccc atacctgtcc cccctgtccc gctcccgaac tgctgggcgg cccagcgtg	1740
tttctgtttc cccccaagcc caaggacacc ctgatgatta gccggacccc cgaagtgacc	1800
tgtgtggtgg tggacgtgag ccatgaagac cccgaagtga agtttaactg gtacgtggac	1860
ggcgtggaag tgcataacgc taagaccaag ccccggaag aacagtataa cagcacctat	1920
cgggtggtga gcgtgctgac cgtgctgcat caggactggc tgaacggcaa ggaatataag	1980
tgtaaggatga gcaacaaggc tctgcccgt cccattgaaa agaccattag caaggctaag	2040
ggccagcccc gggaaccca ggtgtatacc ctgccccca gccgggacga actgaccaag	2100
aaccaggatga gcctgacctg tctggtgaag ggcttttatc ccagcgacat tgctgtggag	2160
tgggaaagca acggccagcc cgaaaacaac tataagacca cccccccgt gctggacagc	2220
gacggcagct tttttctgta tagcaagctg accgtggaca agagccggtg gcagcagggc	2280
aacgtgttta gctgtagcgt gatgcacgaa gctctgcata accattatac ccagaagagc	2340
ctgagcctga gccccggcaa g	2361

<210> 22
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker

<400> 22

Ala	Ala	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
1			5					10						15	

Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
		20						25					30		

Ser Gly Gly Gly Gly Ser

35

<210> 23
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 23

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 24
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 24

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser
35

<210> 25
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker

<400> 25

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
20 25 30

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
35 40 45

Gly Gly Gly Ser Gly Gly Gly Gly Ser
50 55

<210> 26
<211> 2307
<212> DNA
<213> Artificial Sequence

<220>
<223> J210a coding sequence

<220>
<221> CDS
<222> (1)..(2307)

<400> 26
atg tac cga atg cag ctg ctg agc tgt atc gca ctg agc ctg gca ctg 48
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15
gtg acc aac agc cag gtg cag ctg gtg gag agc gga gga gga gtg gtg 96
Val Thr Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
20 25 30
cag cca gga gga agc ctg cga ctg agc tgt gca gca agc atc agc atc 144
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Ile Ser Ile
35 40 45
ttc gac atc tac gca atg gac tgg tac cga cag gca cca gga aag cag 192
Phe Asp Ile Tyr Ala Met Asp Trp Tyr Arg Gln Ala Pro Gly Lys Gln
50 55 60
cga gag ctg gtg gca gtg agc ttc cga gac gga agc acc tac tac gca 240
Arg Glu Leu Val Ala Val Ser Phe Arg Asp Gly Ser Thr Tyr Tyr Ala
65 70 75 80
gac agc gtg aag gga cga ttc acc atc agc cga gac aac agc aag aac 288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95
acc ctg tac ctg cag atg aac agc ctg cga gca gag gac acc gca gtg 336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

tac tac tgt cat gtg agc ctg tac cgg gac cca ctg gga gtg gca gga Tyr Tyr Cys His Val Ser Leu Tyr Arg Asp Pro Leu Gly Val Ala Gly 115 120 125	384
gga atc gga gtg tac tgg gga cag gga acc ctg gtg acc gtg agc agc Gly Ile Gly Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 130 135 140	432
gga gga gga gga agc gga gga gga gga agc gaa gtg cag ctg ctg gaa Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu 145 150 155 160	480
agc ggc ggc ggc ctg gtg cag ccc ggc ggc agc ctg cgg ctg agc tgt Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys 165 170 175	528
gct gct agc ggc cgg acc tac gct atg ggc tgg ttt cgg cag gct ccc Ala Ala Ser Gly Arg Thr Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro 180 185 190	576
ggc aag gaa cgg gaa ttt gtg gct gct att aac gct ctg ggc acc cgg Gly Lys Glu Arg Glu Phe Val Ala Ala Ile Asn Ala Leu Gly Thr Arg 195 200 205	624
acc tat tat gct gac agc gtg aag ggc cgg ttt acc att agc cgg gac Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp 210 215 220	672
aac agc aag aac acc ctg tat ctg cag atg aac agc ctg cgg gct gaa Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu 225 230 235 240	720
gac acc gct gtg tat tat tgt acc gct cag ggc cag tgg cgg gct gct Asp Thr Ala Val Tyr Tyr Cys Thr Ala Gln Gly Gln Trp Arg Ala Ala 245 250 255	768
ccc gtg gct gtg gct gct gaa tac gaa ttt tgg ggc cag ggc acc ctg Pro Val Ala Val Ala Ala Glu Tyr Glu Phe Trp Gly Gln Gly Thr Leu 260 265 270	816
gtg acc gtg agc agc gga gga gga gga tct gga gga gga gga tct gag Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu 275 280 285	864
gtg cag ctg ctg gag agc gga gga gga ctg gtg cag cca gga gga agc Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser 290 295 300	912
ctg cgg ctg agc tgc gcc gcc agc gga ttc acc ctg gag aac aag gcc Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asn Lys Ala 305 310 315 320	960

atc ggc tgg ttc cgg cag gcc cca gga aag gag cgg gag gga gtg ctg	1008
Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val Leu	
325 330 335	
tgc atc agc aag agc gga agc tgg acc tac tac gcc gat agc gtg aag	1056
Cys Ile Ser Lys Ser Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val Lys	
340 345 350	
gga cgg ttc acc atc agc cgg gat aac agc aag aac acc gtg tac ctg	1104
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu	
355 360 365	
cag atg aac agc ctg cgg cca gag gat acc gcc gtg tac tac tgc gcc	1152
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
370 375 380	
acc acc acc gcc gga gga gga ctg tgc tgg gac gga acc acc ttc agc	1200
Thr Thr Thr Ala Gly Gly Gly Leu Cys Trp Asp Gly Thr Thr Phe Ser	
385 390 395 400	
cgg ctg gcc agc agc tgg gga cag gga acc ctg gtg acc gtg agc agc	1248
Arg Leu Ala Ser Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	
405 410 415	
gga gga gga gga tcc gga gga gga gga tcc gag gtg cag ctg gtg gag	1296
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu	
420 425 430	
tca gga gga gga ctg gtg cag ccc gga gga tca ctg aga ctg tcc tgc	1344
Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys	
435 440 445	
gct gct tca gga ttc acc ttc tca acc tcc tgg atg tat tgg ctg aga	1392
Ala Ala Ser Gly Phe Thr Phe Ser Thr Ser Trp Met Tyr Trp Leu Arg	
450 455 460	
cag gct ccc gga aaa gga ctg gag tgg gtg tca gtg atc aac acc gac	1440
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val Ile Asn Thr Asp	
465 470 475 480	
gga gga acc tat tat gct gat tca gtg aaa gga aga ttc acc atc tca	1488
Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser	
485 490 495	
aga gat aac tca aaa aac acc ctg tat ctg cag atg aac tca ctg aga	1536
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg	
500 505 510	
gct gag gat acc gct gtg tat tat tgc gct aaa gat tgg gga gga ccc	1584
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Trp Gly Gly Pro	
515 520 525	
gag ccc acc aga gga cag gga acc ctg gtg acc gtg tca tca gac aag	1632

Glu	Pro	Thr	Arg	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Asp	Lys		
530						535					540						
acc	cat	acc	tgt	cca	cct	tgt	cca	gca	cca	gag	ctg	ctg	gga	gga	cca	1680	
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro		
545					550					555					560		
agc	gtg	ttc	ctg	ttc	cca	cca	aag	cca	aag	gac	acc	ctg	atg	atc	agc	1728	
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser		
				565						570				575			
cga	acc	cca	gag	gtg	acc	tgt	gtg	gtg	gtg	gac	gtg	agc	cat	gag	gac	1776	
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp		
			580					585					590				
cca	gag	gtg	aag	ttc	aac	tgg	tac	gtg	gac	gga	gtg	gag	gtg	cat	aac	1824	
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn		
			595				600					605					
gca	aag	acc	aag	cca	cga	gag	gag	cag	tac	aac	agc	acc	tac	cga	gtg	1872	
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val		
	610					615					620						
gtg	agc	gtg	ctg	acc	gtg	ctg	cat	cag	gac	tgg	ctg	aac	gga	aag	gag	1920	
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu		
625					630					635					640		
tac	aag	tgt	aag	gtg	agc	aac	aag	gca	ctg	cca	gca	cca	atc	gag	aag	1968	
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys		
				645					650					655			
acc	atc	agc	aag	gca	aag	gga	cag	cca	cga	gag	cca	cag	gtg	tac	acc	2016	
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr		
			660					665					670				
ctg	cca	cca	agc	cga	gac	gag	ctg	acc	aag	aac	cag	gtg	agc	ctg	acc	2064	
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr		
			675				680					685					
tgt	ctg	gtg	aag	gga	ttc	tac	cca	agc	gac	atc	gca	gtg	gag	tgg	gag	2112	
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu		
	690					695					700						
agc	aac	gga	cag	cca	gag	aac	aac	tac	aag	acc	acc	cca	cca	gtg	ctg	2160	
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu		
705					710				715						720		
gac	agc	gac	gga	agc	ttc	ttc	ctg	tac	agc	aag	ctg	acc	gtg	gac	aag	2208	
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys		
				725					730					735			
agc	cgg	tgg	cag	cag	gga	aac	gtg	ttc	agc	tgt	agc	gtg	atg	cac	gag	2256	
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu		

740	745	750	
gca ctg cat aac cat tac acc cag aag agc ctg agc ctg agc cca gga			2304
Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly			
755	760	765	

aag	2307
Lys	

<210> 27
 <211> 769
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 27

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val
20 25 30

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Ile Ser Ile
35 40 45

Phe Asp Ile Tyr Ala Met Asp Trp Tyr Arg Gln Ala Pro Gly Lys Gln
50 55 60

Arg Glu Leu Val Ala Val Ser Phe Arg Asp Gly Ser Thr Tyr Tyr Ala
65 70 75 80

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
85 90 95

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys His Val Ser Leu Tyr Arg Asp Pro Leu Gly Val Ala Gly
115 120 125

Gly Ile Gly Val Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu
 145 150 155 160

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
 165 170 175

Ala Ala Ser Gly Arg Thr Tyr Ala Met Gly Trp Phe Arg Gln Ala Pro
 180 185 190

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

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 210 215 220

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
 225 230 235 240

Asp Thr Ala Val Tyr Tyr Cys Thr Ala Gln Gly Gln Trp Arg Ala Ala
 245 250 255

Pro Val Ala Val Ala Ala Glu Tyr Glu Phe Trp Gly Gln Gly Thr Leu
 260 265 270

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
 275 280 285

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 290 295 300

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu Asn Lys Ala
 305 310 315 320

Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val Leu
 325 330 335

Cys Ile Ser Lys Ser Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val Lys

340

345

350

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Tyr Leu
 355 360 365

Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 370 375 380

Thr Thr Thr Ala Gly Gly Gly Leu Cys Trp Asp Gly Thr Thr Phe Ser
 385 390 395 400

Arg Leu Ala Ser Ser Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 405 410 415

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu
 420 425 430

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
 435 440 445

Ala Ala Ser Gly Phe Thr Phe Ser Thr Ser Trp Met Tyr Trp Leu Arg
 450 455 460

Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val Ile Asn Thr Asp
 465 470 475 480

Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 485 490 495

Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
 500 505 510

Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Trp Gly Gly Pro
 515 520 525

Glu Pro Thr Arg Gly Gln Gly Thr Leu Val Thr Val Ser Ser Asp Lys
 530 535 540

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 545 550 555 560

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
565 570 575

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
580 585 590

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
595 600 605

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
610 615 620

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
625 630 635 640

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
645 650 655

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
660 665 670

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
675 680 685

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
690 695 700

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
725 730 735

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
740 745 750

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
755 760 765

Lys

<210> 28
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer prm504

<400> 28
gctgcgycaa ctggaccaat gagaac 26

<210> 29
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> primer prm505

<400> 29
cgcagagacc aaagttcaac tgaaacga 28

<210> 30
<211> 772
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of MD3606

<220>
<221> MISC_FEATURE
<222> (24)..(147)
<223> The first immunoglobulin region with I110M

<220>
<221> MISC_FEATURE
<222> (158)..(280)
<223> The second immunoglobulin region

<220>
<221> MISC_FEATURE
<222> (291)..(419)
<223> The third immunoglobulin region

<220>
 <221> MISC_FEATURE
 <222> (430)..(485)
 <223> The fourth immunoglobulin region

<220>
 <221> MISC_FEATURE
 <222> (551)..(772)
 <223> Fc

<400> 30

Glu Phe Ala Thr Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala
 1 5 10 15

Ala Ala Gln Ser Ile Gln Ala Gln Val Gln Leu Val Glu Ser Gly Gly
 20 25 30

Gly Val Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 35 40 45

Ile Ser Ile Phe Asp Ile Tyr Ala Met Asp Trp Tyr Arg Gln Ala Pro
 50 55 60

Gly Lys Gln Arg Glu Leu Val Ala Val Ser Phe Arg Asp Gly Ser Thr
 65 70 75 80

Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 85 90 95

Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
 100 105 110

Thr Ala Val Tyr Tyr Cys His Val Ser Leu Tyr Arg Asp Pro Leu Gly
 115 120 125

Val Ala Gly Gly Met Gly Val Tyr Trp Gly Gln Gly Thr Leu Val Thr
 130 135 140

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

Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg

165

170

175

Leu Ser Cys Ala Ala Ser Gly Arg Thr Tyr Ala Met Gly Trp Phe Arg
 180 185 190

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

Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
 210 215 220

Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
 225 230 235 240

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Ala Gln Gly Gln Trp
 245 250 255

Arg Ala Ala Pro Val Ala Val Ala Ala Glu Tyr Glu Phe Trp Gly Gln
 260 265 270

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 275 280 285

Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
 290 295 300

Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Glu
 305 310 315 320

Asn Lys Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu
 325 330 335

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

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
 355 360 365

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

Tyr Cys Ala Thr Thr Thr Ala Gly Gly Gly Leu Cys Trp Asp Gly Thr
 385 390 395 400

Thr Phe Ser Arg Leu Ala Ser Ser Trp Gly Gln Gly Thr Leu Val Thr
 405 410 415

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
 420 425 430

Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
 435 440 445

Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Ser Trp Met Tyr
 450 455 460

Trp Leu Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val Ile
 465 470 475 480

Asn Thr Asp Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe
 485 490 495

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
 500 505 510

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Trp
 515 520 525

Gly Gly Pro Glu Pro Thr Arg Gly Gln Gly Thr Leu Val Thr Val Ser
 530 535 540

Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 545 550 555 560

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 565 570 575

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 580 585 590

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
595 600 605

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
610 615 620

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
625 630 635 640

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
645 650 655

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
660 665 670

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
675 680 685

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
690 695 700

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
705 710 715 720

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
725 730 735

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
740 745 750

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
755 760 765

Ser Pro Gly Lys
770

<210> 31
<211> 4690
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV vector genome AAV.CB7.hJAB Fc

<220>
<221> repeat_region
<222> (1)..(130)
<223> 5' IRT

<220>
<221> promoter
<222> (198)..(579)
<223> CMV IE promoter

<220>
<221> enhancer
<222> (279)..(538)
<223> C4 enhancer with 2 mismatches

<220>
<221> promoter
<222> (582)..(862)
<223> CB promoter

<220>
<221> TATA_signal
<222> (836)..(839)
<223> TATA

<220>
<221> Intron
<222> (956)..(1928)
<223> chicken beta-actin intron

<220>
<221> misc_feature
<222> (1941)..(4259)
<223> coding sequence for MD3606

<220>
<221> polyA_signal
<222> (4346)..(4472)
<223> Rabbit globin poly A

<220>
<221> repeat_region
<222> (4561)..(4690)
<223> 3' ITR

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caccataat acccattacc ctggtagata agtagcatgg cgggttaatc attaactaca	4560
aggaaccct agtgatggag ttggccactc cctctctgcg cgctcgctcg ctactgagg	4620
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gagcgcgcag	4690

<210> 32
<211> 2319

<212> DNA
 <213> Artificial Sequence

<220>
 <223> coding sequence of MD3606

<400> 32
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 atacaggccc aggtgcagct ggtggagagc ggcggcggcg tggatgcagcc cggcggcagc 120
 ctgcgctga gctgcgccgc cagcatcagc atcttcgaca tctacgccat ggactggtac 180
 cgccaggccc ccggcaagca gcgcgagctg gtggccgtga gcttccgcga cggcagcacc 240
 tactagccg acagcgtgaa gggccgcttc accatcagcc gcgacaacag caagaacacc 300
 ctgtacctgc agatgaacag cctgcgcgcc gaggacaccg ccgtgtacta ctgccacgtg 360
 agcctgtacc gcgaccccct gggcgtggcc ggcggcattg gcgtgtactg gggccagggc 420
 accctggtga ccgtgagcag cggcggcggc ggacgcggcg gcggcggcag cgaggtgcag 480
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 gccagcggcc gcacctacgc catgggctgg ttccgccagg ccccggaagg gagcgcgag 600
 ttcgtggccg ccatcaacgc cctgggcacc cgcacctact acgccgacag cgtgaagggc 660
 cgcttcacca tcagccgcga caacagcaag aacaccctgt acctgcagat gaacagcctg 720
 cgcgccgagg acaccgccgt gtactactgc accgcccagg gccagtggcg cgccgcccc 780
 gtggccgtgg ccgccgagta cgagttctgg ggccagggca ccctggtgac cgtgagcagc 840
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agctggatgt actggctgcg ccaggccccc ggcaagggcc tggagtgggt gagcgtgac	1440
aacaccgacg gcggcaccta ctacgccgac agcgtgaagg gccgcttcac catcagccgc	1500
gacaacagca agaacaccct gtacctgcag atgaacagcc tgcgcgccga ggacaccgcc	1560
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agggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	2280
tacacgcaga agagcctctc cctgtctccg ggtaaata	2319

<210> 33
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Spacer

<400> 33	
atgacttaaa ccaggt	16

<210> 34
 <211> 736
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human AAVhu31 vp1

<400> 34

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

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

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

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

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

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met

625 630 635 640

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

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

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

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

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

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

<210> 35
 <211> 736
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human AAVhu32 vp1

<400> 35

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg

275

280

285

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

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

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

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

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

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

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

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

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

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

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

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

<210> 36
<211> 2211
<212> DNA
<213> Artificial Sequence

<220>
<223> AAV9 capsid vp1 coding sequence

<400> 36
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gagtgggtggg ctttgaaacc tggagcccct caaccaagg caaatcaaca acatcaagac 120
aacgctcgag gtcttgtgct tccgggttac aaataccttg gaccggaac cggactcgac 180
aagggggagc cgggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac 240
cagcagctca aggccggaga caaccggtac ctcaagtaca accacgccga cgccgagttc 300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag 360
gccaaaaaga ggcttcttga acctcttggt ctggttgagg aagcggctaa gacggctcct 420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc ggggtattggc 480
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tcagtcccag accctcaacc aatcggagaa cctcccgag cccctcagg tgtgggatct 600
cttacaatgg cttcaggtgg tggcgacca gtggcagaca ataacgaagg tgccgatgga 660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcac 720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaatac 780
tccaacagca catctggagg atcttcaaata gacaacgcct acttcggcta cagcaccacc 840
tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga 900
ctcatcaaca acaactgggg attccggcct aagcgactca acttcaagct cttcaacatt 960
cagggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc 1020
acgggtccagg tcttcacgga ctcagactat cagctcccggt acgtgctcgg gtcggctcac 1080

gagggctgcc tcccgccgtt cccagcggac gttttcatga ttcctcagta cgggtatctg	1140
acgcttaatg atggaagcca ggccgtgggt cgttcgtcct ttactgcct ggaatatttc	1200
ccgtcgcaaa tgctaagaac gggtaacaac ttccagttca gctacgagtt tgagaacgta	1260
cctttccata gcagctacgc tcacagccaa agcctggacc gactaatgaa tccactcatc	1320
gaccaatact tgtactatct ctcaaagact attaacggtt ctggacagaa tcaacaaacg	1380
ctaaaattca gtgtggccgg acccagcaac atggctgtcc aggaagaaa ctacatacct	1440
ggaccagct accgacaaca acgtgtctca accactgtga ctcaaaacaa caacagcgaa	1500
tttgcttggc ctggagcttc ttcttgggct ctcaatggac gtaatagctt gatgaatcct	1560
ggacctgcta tggccagcca caaagaagga gaggaccgtt tctttccttt gtctggatct	1620
ttaatTTTTg gcaacaagg aactggaaga gacaacgtgg atgcggacaa agtcatgata	1680
accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg	1740
gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga	1800
atacttccgg gtatggtttg gcaggacaga gatgtgtacc tgcaaggacc catttgggcc	1860
aaaattcctc acacggacgg caactttcac ctttctccgc tgatgggagg gtttggaatg	1920
aagcaccgc ctcctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg	1980
gccttcaaca aggacaagct gaactctttc atcaccagt attctactgg ccaagtcagc	2040
gtggagatcg agtgggagct gcagaaggaa aacagcaagc gctggaacc ggagatccag	2100
tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta	2160
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<210> 37

<211> 2211

<212> DNA

<213> Artificial sequence

<220>

<223> AAVhu31 coding sequence

<400> 37

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gagtgggtggg ctttgaaacc tggagcccct caaccaagg caaatcaaca acatcaagac	120
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aacgctcgag gtcttgtgct tccgggttac aaataccttg gacccggcaa cggactcgac	180
aaggggggagc cgggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aggccggaga caacccttac ctcaagtaca accacgccga cgccgagttc	300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaaaaaga ggcttcttga acctcttggg ctggttgagg aagcggctaa gacggctcct	420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggatttggc	480
aaatcgggtg cacagccgc taaaaagaga ctcaatttcg gtcagactgg cgacacagag	540
tcagtcccag accctcaacc aatcggagaa cctcccgag cccctcagg tgtgggatct	600
cttacaatgg cttcaggtgg tggcgcacca gtggcagaca ataacgaagg tgccgatgga	660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcac	720
accaccagca cccgaacctg ggccctgccc acctacaaca atcacctcta caagcaaadc	780
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tgggggtatt ttgacttcaa cagattccac tgccacttct caccacgtga ctggcagcga	900
ctcatcaaca acaactgggg attccggcct aagcgcactca acttcaagct cttcaacatt	960
caggtcaaag aggttacgga caacaatgga gtcaagacca tcgccaataa ccttaccagc	1020
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accaacgaag aagaaattaa aactactaac ccggtagcaa cggagtccta tggacaagtg	1740

gccacaaacc accagagtgc ccaagcacag gcgcagaccg gctgggttca aaaccaagga	1800
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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta	2160
tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a	2211

<210> 38

<211> 2211

<212> DNA

<213> Artificial sequence

<220>

<223> AAVhu32 VP1 coding sequence

<400> 38

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gacagcaggg gtcttgtgct tcctgggtac aagtacctcg gaccggaac cggactcgac	180
aagggggagc cgggtcaacgc agcagacgcg gcggccctcg agcacgacaa ggcctacgac	240
cagcagctca aggccggaga caaccgtac ctcaagtaca accacgccga cgccgagttc	300
caggagcggc tcaaagaaga tacgtctttt gggggcaacc tcgggcgagc agtcttccag	360
gccaaaaaga ggcttcttga acctcttggg ctggttgagg aagcggctaa gacggctcct	420
ggaaagaaga ggcctgtaga gcagtctcct caggaaccgg actcctccgc gggatttggc	480
aaatcgggtt cacagcccg ctaaaaagaaa ctcaatttcg gtcagactgg cgacacagag	540
tcagtccccg acctcaacc aatcggagaa cctccgcag cccctcagg tgtgggatct	600
cttacaatgg cttcaggtgg tggcgacca gtggcagaca ataacgaagg tgccgatgga	660
gtgggtagtt cctcgggaaa ttggcattgc gattcccaat ggctggggga cagagtcac	720
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tccaacagca catctggagg atcttcaa at gacaacgcct acttcggcta cagcaccccc	840
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acggtccagg tcttcacgga ctgagactat cagctcccggt acgtgctcgg gtcggctcac	1080
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aagcaccgc ctctcagat cctcatcaaa aacacacctg tacctgcgga tcctccaacg	1980
gctttcaata aggacaagct gaactctttc atcaccagct attctactgg ccaagtcagc	2040
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tacacttcca actattacaa gtctaataat gttgaatttg ctgttaatac tgaaggtgta	2160
tatagtgaac cccgccccat tggcaccaga tacctgactc gtaatctgta a	2211

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 <212> PRT
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<220>
 <223> modified hu68vp1

<220>
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 <222> (23)..(23)
 <223> Xaa may be W (Trp, tryptophan), or oxidated W.

<220>
 <221> MISC_FEATURE
 <222> (35)..(35)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
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 <222> (57)..(57)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
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 <222> (66)..(66)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
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 <222> (94)..(94)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
 <221> MISC_FEATURE
 <222> (97)..(97)
 <223> Xaa may be D (asp, aspartic acid), or isomerized D.

<220>
 <221> MISC_FEATURE
 <222> (107)..(107)
 <223> Xaa may be D (asp, aspartic acid), or isomerized D.

<220>
 <221> misc_feature
 <222> (113)..(113)
 <223> Xaa can be any naturally occurring amino acid

<220>
 <221> MISC_FEATURE
 <222> (149)..(149)
 <223> Xaa may be S (Ser, serine), or Phosphorilated S

<220>
 <221> MISC_FEATURE
 <222> (149)..(149)

<223> Xaa may be S (Ser, serine), or Phosphorylated S

<220>
 <221> MISC_FEATURE
 <222> (247)..(247)
 <223> Xaa may be W (Trp, tryptophan), or oxidated W (e.g., kynurenine).

<220>
 <221> MISC_FEATURE
 <222> (253)..(253)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
 <221> MISC_FEATURE
 <222> (259)..(259)
 <223> Xaa represents Q, or Q deamidated to glutamic acid (alpha-glutamic acid), gamma-glutamic acid (Glu), or a blend of alpha- and gamma-glutamic acid

<220>
 <221> MISC_FEATURE
 <222> (270)..(270)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
 <221> MISC_FEATURE
 <222> (297)..(297)
 <223> Xaa represents D (Asp, aspartic acid) or amidated D to N (Asn, asparagine)

<220>
 <221> MISC_FEATURE
 <222> (304)..(304)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
 <221> MISC_FEATURE
 <222> (306)..(306)
 <223> Xaa may be W (Trp, tryptophan), or oxidated W (e.g., kynurenine).

<220>
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 <222> (314)..(314)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
 <221> MISC_FEATURE
 <222> (319)..(319)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
 <221> MISC_FEATURE
 <222> (329)..(329)

<223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp
 <220>
 <221> MISC_FEATURE
 <222> (332)..(332)
 <223> Xaa may be K (lys, lysine), or acetylated K
 <220>
 <221> MISC_FEATURE
 <222> (336)..(336)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp
 <220>
 <221> MISC_FEATURE
 <222> (384)..(384)
 <223> Xaa may be D (asp, aspartic acid), or isomerized D.
 <220>
 <221> MISC_FEATURE
 <222> (404)..(404)
 <223> Xaa may be M (Met, Methionine), or oxidated M.
 <220>
 <221> MISC_FEATURE
 <222> (409)..(409)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp
 <220>
 <221> MISC_FEATURE
 <222> (436)..(436)
 <223> Xaa may be M (Met, Methionine), or oxidated M.
 <220>
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 <222> (452)..(452)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp
 <220>
 <221> MISC_FEATURE
 <222> (477)..(477)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp
 <220>
 <221> MISC_FEATURE
 <222> (499)..(499)
 <223> Xaa may be S (Ser, serine), or Phosphorylated S
 <220>
 <221> MISC_FEATURE
 <222> (512)..(512)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp
 <220>

<221> MISC_FEATURE
 <222> (515)..(515)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
 <221> MISC_FEATURE
 <222> (518)..(518)
 <223> Xaa may be M (Met, Methionine), or oxidated M.

<220>
 <221> MISC_FEATURE
 <222> (524)..(524)
 <223> Xaa may be M (Met, Methionine), or oxidated M.

<220>
 <221> MISC_FEATURE
 <222> (559)..(559)
 <223> Xaa may be M (Met, Methionine), or oxidated M.

<220>
 <221> MISC_FEATURE
 <222> (569)..(569)
 <223> Xaa may be T (Thr, threonine), or Phosphorylated T

<220>
 <221> MISC_FEATURE
 <222> (586)..(586)
 <223> Xaa may be S (Ser, serine), or Phosphorylated S

<220>
 <221> MISC_FEATURE
 <222> (599)..(599)
 <223> Xaa represents Q, or Q deamidated to glutamic acid
 (alpha-glutamic acid), gamma-glutamic acid (Glu), or a blend of
 alpha- and gamma-glutamic acid

<220>
 <221> MISC_FEATURE
 <222> (605)..(605)
 <223> Xaa may be M (Met, Methionine), or oxidated M.

<220>
 <221> MISC_FEATURE
 <222> (619)..(619)
 <223> Xaa may be W (Trp, tryptophan), or oxidated W (e.g., kynurenine).

<220>
 <221> MISC_FEATURE
 <222> (628)..(628)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

<220>
 <221> MISC_FEATURE

<222> (640)..(640)
 <223> Xaa may be M (Met, Methionine), or oxidated M.

 <220>
 <221> MISC_FEATURE
 <222> (651)..(651)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

 <220>
 <221> MISC_FEATURE
 <222> (663)..(663)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

 <220>
 <221> MISC_FEATURE
 <222> (666)..(666)
 <223> Xaa may be K (lys, lysine), or acetylated K

 <220>
 <221> MISC_FEATURE
 <222> (689)..(689)
 <223> Xaa may be K (lys, lysine), or acetylated K

 <220>
 <221> MISC_FEATURE
 <222> (693)..(693)
 <223> Xaa may be K (lys, lysine), or acetylated K

 <220>
 <221> MISC_FEATURE
 <222> (695)..(695)
 <223> Xaa may be W (Trp, tryptophan), or oxidated W.

 <220>
 <221> MISC_FEATURE
 <222> (709)..(709)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

 <220>
 <221> MISC_FEATURE
 <222> (735)..(735)
 <223> Xaa may be Asn, or deamidated to Asp, isoAsp, or Asp/isoAsp

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 1 5 10 15

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Thr Ser Thr Arg Thr Xaa Ala Leu Pro Thr Tyr Xaa Asn His Leu

	245		250		255										
Tyr	Lys	Xaa	Ile	Ser	Asn	Ser	Thr	Ser	Gly	Gly	Ser	Ser	Xaa	Asp	Asn
			260					265					270		
Ala	Tyr	Phe	Gly	Tyr	Ser	Thr	Pro	Trp	Gly	Tyr	Phe	Asp	Phe	Asn	Arg
		275					280					285			
Phe	His	Cys	His	Phe	Ser	Pro	Arg	Xaa	Trp	Gln	Arg	Leu	Ile	Asn	Xaa
	290					295					300				
Asn	Xaa	Gly	Phe	Arg	Pro	Lys	Arg	Leu	Xaa	Phe	Lys	Leu	Phe	Xaa	Ile
305					310					315					320
Gln	Val	Lys	Glu	Val	Thr	Asp	Asn	Xaa	Gly	Val	Xaa	Thr	Ile	Ala	Xaa
				325					330					335	
Asn	Leu	Thr	Ser	Thr	Val	Gln	Val	Phe	Thr	Asp	Ser	Asp	Tyr	Gln	Leu
			340					345					350		
Pro	Tyr	Val	Leu	Gly	Ser	Ala	His	Glu	Gly	Cys	Leu	Pro	Pro	Phe	Pro
		355					360					365			
Ala	Asp	Val	Phe	Met	Ile	Pro	Gln	Tyr	Gly	Tyr	Leu	Thr	Leu	Asn	Xaa
	370					375					380				
Gly	Ser	Gln	Ala	Val	Gly	Arg	Ser	Ser	Phe	Tyr	Cys	Leu	Glu	Tyr	Phe
385					390					395					400
Pro	Ser	Gln	Xaa	Leu	Arg	Thr	Gly	Xaa	Asn	Phe	Gln	Phe	Ser	Tyr	Glu
				405					410					415	
Phe	Glu	Asn	Val	Pro	Phe	His	Ser	Ser	Tyr	Ala	His	Ser	Gln	Ser	Leu
			420					425					430		
Asp	Arg	Leu	Xaa	Asn	Pro	Leu	Ile	Asp	Gln	Tyr	Leu	Tyr	Tyr	Leu	Ser
		435					440					445			
Lys	Thr	Ile	Xaa	Gly	Ser	Gly	Gln	Asn	Gln	Gln	Thr	Leu	Lys	Phe	Ser
	450					455					460				

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

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

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

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

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

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Xaa Ile
 545 550 555 560

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

Tyr Gly Gln Val Ala Thr Asn His Gln Xaa Ala Gln Ala Gln Ala Gln
 580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Xaa Val Trp Gln
 595 600 605

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

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

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

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

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

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

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

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