

SEQUENCE LISTING

<110> Freeline Therapeutics Limited

<120> POLYPEPTIDE

<130> N417179W0

<150> GB2011813.9

<151> 2020-07-29

<150> GB2100648.1

<151> 2021-01-18

<150> GB2105924.1

<151> 2021-04-26

<160> 64

<170> PatentIn version 3.5

<210> 1

<211> 536

<212> PRT

<213> Homo sapiens

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35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
50 55 60

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

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
 210 215 220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
 225 230 235 240

Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
 245 250 255

Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
 260 265 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
 275 280 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
 290 295 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
 305 310 315 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
 340 345 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
 355 360 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
 370 375 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
 405 410 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
 435 440 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

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

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
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Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
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His Thr Tyr Leu Trp Arg Arg Gln
 530 535

<210> 2
 <211> 497
 <212> PRT
 <213> Homo sapiens

<400> 2

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

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
 50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
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Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
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Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
 100 105 110

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe

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165					170					175						
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Trp	Ala	Arg	Tyr	Phe	Val	Lys	Phe	Leu	Asp	Ala	Tyr	Ala	Glu	His	Lys	
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245					250					255						
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260					265					270						
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275					280					285						
Pro	His	Trp	Ala	Lys	Val	Val	Leu	Thr	Asp	Pro	Glu	Ala	Ala	Lys	Tyr	
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305					310					315					320	

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
 325 330 335

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
 340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
 355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
 370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
 385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
 405 410 415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
 420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
 435 440 445

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
 450 455 460

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

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg
 485 490 495

Gln

<211> 497
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> VPRIV

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

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
 50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
 65 70 75 80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
 85 90 95

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

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
 115 120 125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu
 130 135 140

His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu
 145 150 155 160

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala

165

170

175

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn
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Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
 195 200 205

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
 210 215 220

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
 225 230 235 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
 245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
 260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
 275 280 285

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
 290 295 300

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala
 305 310 315 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
 325 330 335

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
 340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
 355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
 370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
 385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
 405 410 415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
 420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
 435 440 445

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
 450 455 460

Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu
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Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg
 485 490 495

Gln

<210> 4

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic GCase protein

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Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60

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

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
 85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175

Thr Pro Asp Asp Phe Gln Leu Leu Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu

210

215

220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
 225 230 235 240

Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
 245 250 255

Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
 260 265 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
 275 280 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
 290 295 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
 305 310 315 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
 340 345 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
 355 360 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
 370 375 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
 405 410 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
 435 440 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

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

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

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

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp Arg Arg Gln
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<210> 5

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic GCase protein

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Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
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Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60

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

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
 85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175

Thr Pro Asp Asp Phe Gln Leu Leu Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
 210 215 220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro

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

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
 435 440 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

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

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

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

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp Arg Arg Gln
 530 535

<210> 6
 <211> 1494
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

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<210> 7
<211> 1494
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic construct

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<211> 1494
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

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<210> 9
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 <213> Artificial Sequence

<220>
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<400> 9	
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<210> 10
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 11
<211> 1611
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic construct

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<400> 11
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aatagatcct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag	1560
acaatctcac ctggctactc catccacacc tacctgtgga ggaggcagt a	1611

<210> 12
 <211> 1611
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 12

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aggccctgca tccctaagag ctttggctac agctctgtgg tgtgtgtgtg caatgccaca	180
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<210> 13
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 13	
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aggccttgca tcccaaagtc tttcggctac agctccgtgg tgtgcgtgtg caacgccacc	180
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<210> 14
<211> 1494
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic construct

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<400> 14
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<210> 15

<211> 1494

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 15

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gagtcaacaa gatcaggaag gaggatggag ctgtcaatgg gacctatcca ggctaatac	180

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<210> 16

<211> 1494

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 16

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<210> 17
<211> 1494
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 17
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<210> 18
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 <212> DNA
 <213> Artificial Sequence

<220>
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<210> 19
<211> 1611
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic construct

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<400> 19
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tcaacaagat caggaaggag gatggagctg tcaatgggac ccatccaggc taatcacaca     300
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cccatggcca gctgtgactt ctccatcagg acctacacct atgctgacac ccctgatgat      540
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<210> 20

<211> 1611

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

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<210> 21
<211> 1611
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

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ttccagctgc acaatttttc cctgccagag gaggatacaa agctgaagat ccccctgatt 600
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<210> 22
 <211> 1494
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

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<210> 23

<211> 1494

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 23

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<210> 24

<211> 1494

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 24

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<210> 25
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 <212> DNA
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<220>
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<210> 26
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 26	
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tactgtgaca gctttgaccc cccaccttt cctgccctgg gcaccttcag cagatatgag	240
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cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat	540
ttccagctgc acaacttcag cctgcctgag gaggatacca agctgaagat cccactgatc	600
cacagggctc tgcagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc	660
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gatgaccaga ggctgctgct gccccactgg gctaagggtg tgctgactga ccctgaggct      1020
gctaaatatg tgcatggcat tgctgtgcat tgctacctgg actttctggc tcctgccaag      1080
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cacttcagca agttcatccc tgagggcagc cagagagtgg ggctgggtggc cagccagaag      1440
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aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag      1560
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<210> 27
<211> 1611
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synethtic construct

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<400> 27
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ggaggagcca tgacagatgc tgctgctctc aacatcctgg ccctgtcacc ccctgccag      420
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cccatggcca gctgtgactt ctccatcagg acctacacct atgctgacac ccctgatgat      540
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cccacttggc tcaagaccaa tggagctgtg aatggaaagg gatcactcaa gggacagcct      720
ggagacatct accaccagac ctggggcaga tactttgtga agttcctgga tgcctatgct      780
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aatagatcct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag     1560
acaatctcac ctggctactc catccacacc tacctgtgga ggaggcagtg a              1611

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<210> 28

<211> 1611

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 28

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tactgtgact cctttgaccc cccacaccttt cctgccctgg gcacattctc cagatatgag	240
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cccatggcca gctgtgactt ttccatcaga acctacacct atgcagacac ccctgatgat	540
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cacttttagca agttttattcc tgagggtctc cagagagtgg ggctggttgc cagccagaag	1440
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aatagatcca gcaaggatgt gcctctgacc atcaaggatc ctgctgtggg ctttctggag	1560

acaatctcac ctggctactc cattcacacc tacctgtgga gaaggcagtg a 1611

<210> 29

<211> 1611

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 29

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aggccttgca tcccaaagtc tttcggctac agctccgtgg tgtgctgtg caacgccacc	180
tattgtgact ccttcgatcc ccctacctt cccgccctgg gcacattttc tagatacgag	240
tctacacgca gcggccggag aatggagctg agcatgggcc ctatccaggc caatcacaca	300
ggaacaggcc tgctgctgac cctgcagcca gagcagaagt tccagaaggt gaagggcttt	360
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aatcgctcta gcaaggacgt gcctctgacc atcaaggatc cagccgtggg atttctggag	1560
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<210> 30
 <211> 185
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 30	
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tacggacgag gacagggccc tgtctcctca gcttcaggca ccaccactga cctgggacag	180
tgaat	185

<210> 31
 <211> 418
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 31	
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aagtgggtact ctcccagaga ctgtctgact cacgccaccc cctccacctt ggacacagga	120
cgctgtgggt tctgagccag gtacaatgac tcctttcggt aagtgcagtg gaagctgtac	180

actgccaggg caaagcgctc gggcagcgta ggcgggcgac tcagatccca gccagtggac 240
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<210> 32
 <211> 117
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 32
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<210> 33
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 33
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 tactcatgtc cctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc 180
 cctgcctgct gaccttgag ctggggcaga ggtagagac ctctctgggc ccatgccacc 240
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 ggtttaggta gtgtgagagg g 321

<210> 34
 <211> 334
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 34

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cccctgtttg ctctccgat aactgggggtg accttggtta atattcacca gcagcctccc      240
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<210> 35

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 35

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tactcatgtc cctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc      180
cctgcctgct gaccttgag ctggggcaga ggtcagagac ctctctgggc ccatgccacc      240
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gtgaccttgg ttaatatcca ccagcagcct ccccggttgc ccctctggat cactgctta      660
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agtgaatgat cccctgatac tgcggcc

747

<210> 36
 <211> 736
 <212> PRT
 <213> adeno-associated virus 3B

<400> 36

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 37

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic capsid protein

<400> 37

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 Lys Pro
20 25 30

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 38

<211> 736

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic capsid protein

<400> 38

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 39

<211> 736

<212> PRT

<213> adeno-associated virus 9

<400> 39

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala

645	650	655
Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr		
660	665	670
Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln		
675	680	685
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn		
690	695	700
Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val		
705	710	715
Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu		
725	730	735

<210> 40
 <211> 1611
 <212> DNA
 <213> Homo sapiens

<400> 40	
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atggctggca gcctcacagg attgcttcta cttcaggcag tgtcgtgggc atcaggtgcc	120
cgcccctgca tccctaaaag cttcggctac agctcgggtg tgtgtgtctg caatgccaca	180
tactgtgact cctttgaccc cccgaccttt cctgcccttg gtaccttcag ccgctatgag	240
agtacacgca gtgggcgacg gatggagctg agtatggggc ccatccaggc taatcacacg	300
ggcacaggcc tgctactgac cctgcagcca gaacagaagt tccagaaagt gaagggattt	360
ggagggggcca tgacagatgc tgctgctctc aacatccttg ccctgtcacc ccctgcccac	420
aatttgctac ttaaatacgta cttctctgaa gaaggaatcg gatataacat catccgggta	480
cccatggcca gctgtgactt ctccatccgc acctacacct atgcagacac ccctgatgat	540
ttccagttgc acaacttcag cctcccagag gaagatacca agctcaagat acccctgatt	600
caccgagccc tgcagttggc ccagcgtccc gtttcactcc ttgccagccc ctggacatca	660

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cccacttggc tcaagaccaa tggagcgggtg aatgggaagg ggtcactcaa gggacagccc      720
ggagacatct accaccagac ctgggccaga tactttgtga agttcctgga tgcctatgct      780
gagcacaagt tacagttctg ggcagtgaca gctgaaaatg agccttctgc tgggctgttg      840
agtggatacc ccttccagtg cctgggcttc acccctgaac atcagcgaga cttcattgcc      900
cgtgacctag gtcctaccct cgccaacagt actcaccaca atgtccgcct actcatgctg      960
gatgaccaac gcttgctgct gccccactgg gcaaagggtg tactgacaga ccagaagca     1020
gctaaatatg ttcattggcat tgctgtacat tgggtacctg actttctggc tccagccaaa     1080
gccaccctag gggagacaca ccgcctgttc cccaacacca tgctctttgc ctgagaggcc     1140
tgtgtgggct ccaagttctg ggagcagagt gtgcggctag gctcctggga tcgagggatg     1200
cagtacagcc acagcatcat cacgaacctc ctgtaccatg tggtcggctg gaccgactgg     1260
aaccttgccc tgaaccccga aggaggacct aattgggtgc gtaactttgt cgacagtccc     1320
atcattgtag acatcaccaa ggacacgttt taaaacagc ccatgttcta ccaccttggc     1380
cacttcagca agttcattcc tgagggtctc cagagagtgg ggctggttgc cagtcagaag     1440
aacgacctgg acgcagtggc actgatgcat ccgatggct ctgctgttgt ggtcgtgcta     1500
aaccgctcct ctaaggatgt gcctcttacc atcaaggatc ctgctgtggg cttcctggag     1560
acaatctcac ctggctactc cattcacacc tacctgtggc gtcgccagtg a              1611

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<210> 41
<211> 536
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic GCase protein

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<400> 41

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Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
1           5           10           15

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Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
          20           25           30

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Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60

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

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
 85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
 210 215 220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
 225 230 235 240

Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
 245 250 255

Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Gln
 260 265 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
 275 280 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
 290 295 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
 305 310 315 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
 340 345 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
 355 360 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
 370 375 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
 405 410 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
 435 440 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

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

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

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

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp Arg Arg Gln
 530 535

<210> 42
 <211> 536
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic GCase protein

<400> 42

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
 1 5 10 15

Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
 20 25 30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
50 55 60

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

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
210 215 220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
225 230 235 240

Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
245 250 255

Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
260 265 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
275 280 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
290 295 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
305 310 315 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
325 330 335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Cys Tyr
340 345 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
355 360 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Cys Cys Val Gly Ser
370 375 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
385 390 395 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
405 410 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
420 425 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
435 440 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

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

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

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

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp Arg Arg Gln
 530 535

<210> 43

<211> 536

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic GCase protein

<400> 43

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
 1 5 10 15

Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
 20 25 30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60

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

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
210 215 220

Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
225 230 235 240

Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
245 250 255

Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Gln
 260 265 270

Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
 275 280 285

Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
 290 295 300

Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
 305 310 315 320

Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335

Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Cys Tyr
 340 345 350

Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
 355 360 365

Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Cys Cys Val Gly Ser
 370 375 380

Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400

Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
 405 410 415

Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430

Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp
 435 440 445

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

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

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

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

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp Arg Arg Gln
 530 535

<210> 44
 <211> 497
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic GCase protein

<400> 44

Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys
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Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
 20 25 30

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

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
 50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
 65 70 75 80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
85 90 95

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

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
115 120 125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu
130 135 140

His	Asn	Phe	Ser	Leu	Pro	Glu	Glu	Asp	Thr	Lys	Leu	Lys	Ile	Pro	Leu
145					150					155					160

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala
165 170 175

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn
180 185 190

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
195 200 205

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
210 215 220

Leu Gln Phe Trp Ala Val Thr Ala Gln Asn Glu Pro Ser Ala Gly Leu
225 230 235 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
 275 280 285

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
 290 295 300

Val His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala
 305 310 315 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
 325 330 335

Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
 340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
 355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
 370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
 385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
 405 410 415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
 420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
 435 440 445

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
 450 455 460

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

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg
 485 490 495

Gln

<210> 45
 <211> 497
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic GCase protein

<400> 45

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

Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
 50 55 60

Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
 65 70 75 80

Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
 85 90 95

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

Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe
 115 120 125

Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu
 130 135 140

His Asn Phe Ser Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu
 145 150 155 160

Ile His Arg Ala Leu Gln Leu Ala Gln Arg Pro Val Ser Leu Leu Ala
 165 170 175

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn
 180 185 190

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
 195 200 205

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
 210 215 220

Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
 225 230 235 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
 245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
 260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
 275 280 285

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
 290 295 300

Val His Gly Ile Ala Val His Cys Tyr Leu Asp Phe Leu Ala Pro Ala
 305 310 315 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
 325 330 335

Phe Ala Ser Glu Cys Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
 340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
 355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
 370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
 385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
 405 410 415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
 420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
 435 440 445

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
 450 455 460

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

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg
 485 490 495

Gln

<210> 46

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic GCase protein

<400> 46

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Val	Cys	Asn	Ala	Thr	Tyr	Cys	Asp	Ser	Phe	Asp	Pro	Pro	Thr	Phe	Pro
			20					25					30		

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

Met	Glu	Leu	Ser	Met	Gly	Pro	Ile	Gln	Ala	Asn	His	Thr	Gly	Thr	Gly
	50					55					60				

Leu	Leu	Leu	Thr	Leu	Gln	Pro	Glu	Gln	Lys	Phe	Gln	Lys	Val	Lys	Gly
65					70					75					80

Phe	Gly	Gly	Ala	Met	Thr	Asp	Ala	Ala	Ala	Leu	Asn	Ile	Leu	Ala	Leu
				85					90					95	

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

Gly	Ile	Gly	Tyr	Asn	Ile	Ile	Arg	Val	Pro	Met	Ala	Ser	Cys	Asp	Phe
		115					120					125			

Ser	Ile	Arg	Thr	Tyr	Thr	Tyr	Ala	Asp	Thr	Pro	Asp	Asp	Phe	Gln	Leu
	130					135					140				

His	Asn	Phe	Ser	Leu	Pro	Glu	Glu	Asp	Thr	Lys	Leu	Lys	Ile	Pro	Leu
145					150					155					160

Ile	His	Arg	Ala	Leu	Gln	Leu	Ala	Gln	Arg	Pro	Val	Ser	Leu	Leu	Ala
				165				170						175	

Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys Thr Asn Gly Ala Val Asn
 180 185 190

Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile Tyr His Gln Thr
 195 200 205

Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu His Lys
 210 215 220

Leu Gln Phe Trp Ala Val Thr Ala Gln Asn Glu Pro Ser Ala Gly Leu
 225 230 235 240

Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
 245 250 255

Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
 260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu
 275 280 285

Pro His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr
 290 295 300

Val His Gly Ile Ala Val His Cys Tyr Leu Asp Phe Leu Ala Pro Ala
 305 310 315 320

Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu
 325 330 335

Phe Ala Ser Glu Cys Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val
 340 345 350

Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile
 355 360 365

Thr Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala
 370 375 380

Leu Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser
 385 390 395 400

Pro Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met
 405 410 415

Phe Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln
 420 425 430

Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala
 435 440 445

Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser
 450 455 460

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

Glu Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp Arg Arg
 485 490 495

Gln

<210> 47
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 47
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 aggccctgca tccctaagag ctttggttac agctctgtgg tgtgtgtgtg caatgccacc 180

tactgtgaca gctttgaccc cccaccttt cctgccctgg gcaccttcag cagatatgag	240
agcaccaggt ctgggaggag gatggagctg agcatggggc ccatccaggc taatcacact	300
ggcactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaagggcttt	360
ggagggggcca tgactgatgc tgctgctctg aacatcctgg ccctgagccc ccctgcccag	420
aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg	480
cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat	540
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cacagggctc tgcagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc	660
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gagaacaagc tgcagttctg ggctgtgact gctgagaatg agccttctgc tgggctgctg	840
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cacttcagca agttcatccc tgagggcagc cagagagtgg ggctgggtggc cagccagaag	1440
aatgacctgg atgctgtggc tctgatgcat cctgatggct ctgctgtggt ggtgggtgctg	1500
aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag	1560
accatcagcc ctggctacag catccacacc tacctgtgga ggaggcagtg a	1611

<210> 48
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 48
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 tactgtgaca gctttgaccc cccaccttt cctgccctgg gcaccttcag cagatatgag 240
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 ggcactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaaggccttt 360
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 aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg 480
 cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat 540
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 cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct 720
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 gccaccctgg gggagaccca caggctgttc cccaacacca tgctgtttgc ctctgaggcc 1140
 tgtgtgggca gcaagttctg ggagcagtct gtgaggctgg gcagctggga taggggggatg 1200
 cagtacagcc acagcatcat caccaacctg ctgtaccatg tgggtgggctg gactgactgg 1260

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cacttcagca agttcatccc tgagggcagc cagagagtgg ggctgggtggc cagccagaag	1440
aatgacctgg atgctgtggc tctgatgcat cctgatggct ctgctgtggt ggtggtgctg	1500
aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag	1560
accatcagcc ctggctacag catccacacc tacctgtgga ggaggcagtg a	1611

<210> 49

<211> 1611

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 49

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aggccctgca tccctaagag ctttggctac agctctgtgg tgtgtgtgtg caatgccacc	180
tactgtgaca gctttgacct cccacacctt cctgccctgg gcaccttcag cagatatgag	240
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aatctgtctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg	480
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cacagggtc tgcagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc	660
cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct	720
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gagcacaagc tgcagttctg ggctgtgact gctgagaatg agccttctgc tgggctgctg	840

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gatgaccaga ggctgctgct gccccactgg gctaagggtg tgctgactga ccctgaggct	1020
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cacttcagca agttcatccc tgagggcagc cagagagtgg ggctggtggc cagccagaag	1440
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aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag	1560
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<210> 50
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 50	
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aggccctgca tccctaagag ctttggctac agctctgtgg tgtgtgtgtg caatgccacc	180
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agcaccaggt ctgggaggag gatggagctg agcatggggc ccatccaggc taatcacact	300
ggcactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaagggcttt	360
ggagggggcca tgactgatgc tgctgctctg aacatcctgg ccctgagccc ccctgcccag	420

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aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg      480
cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat      540
ttccagctgc acaacttcag cctgcctgag gaggatacca agctgaagat cccactgatc      600
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cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct      720
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aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag     1560
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<210> 51

<211> 1611

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 51

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aggccctgca tccctaagag ctttggctac agctctgttg tgtgtgtgtg caatgccacc	180
tactgtgaca gctttgaccc cccaccttt cctgccctgg gcaccttcag cagatatgag	240
agcaccaggt ctgggaggag gatggagctg agcatggggc ccatccaggc taatcacact	300
ggcactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaagggcttt	360
ggagggggcca tgactgatgc tgctgctctg aacatcctgg ccctgagccc ccctgcccag	420
aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg	480
cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat	540
ttccagctgc acaacttcag cctgcctgag gaggatacca agctgaagat cccactgatc	600
cacagggctc tgcagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc	660
cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct	720
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aacctggccc tgaacctga gggaggacct aactgggtca gaaactttgt ggacagcccc	1320
atcattgtgg acatcaccaa ggacaccttt tacaagcagc ccatgttcta ccacctgggc	1380
cacttcagca agttcatccc tgagggcagc cagagagtgg ggctgggtggc cagccagaag	1440
aatgacctgg atgctgtggc tctgatgcat cctgatggct ctgctgtggt ggtggtgctg	1500

aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag 1560
 accatcagcc ctggctacag catccacacc tacctgtgga acaggcagtg a 1611

<210> 52
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 52
 atggagtttt caagtccttc cagagaggaa tgtcccaagc ctttgagtag ggtaagcatc 60
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 aggccctgca tccctaagag ctttggctac agctctgttg tgtgtgtgtg caatgccacc 180
 tactgtgaca gctttgaccc cccaccttt cctgccctgg gcaccttcag cagatatgag 240
 agcaccaggt ctgggaggag gatggagctg agcatggggc ccatccaggc taatcacact 300
 ggcaactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaagggcttt 360
 ggagggggcca tgactgatgc tgctgctctg aacatcctgg ccctgagccc ccctgcccag 420
 aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg 480
 cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat 540
 ttccagctgc tgaacttcag cctgcctgag gaggatacca agctgaagat cccactgatc 600
 cacagggctc tgcagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc 660
 cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct 720
 ggagacatct accaccagac ctgggccaga tactttgtga agttcctgga tgcctatgct 780
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 gatgaccaga ggctgctgct gccccactgg gctaagggtg tgctgactga ccctgaggct 1020
 gctaaatatg tgcatggcat tgctgtgcat tgggtacctg acttttctggc tcctgccaag 1080

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gccaccctgg gggagacca caggctgttc cccaacacca tgctgtttgc ctctgaggcc 1140
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cagtacagcc acagcatcat caccaacctg ctgtaccatg tggtagggctg gactgactgg 1260
aacctggccc tgaaccctga gggaggacct aactgggtca gaaactttgt ggacagcccc 1320
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cacttcagca agttcatccc tgagggcagc cagagagtgg ggctgggtggc cagccagaag 1440
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aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag 1560
accatcagcc ctggctacag catccacacc tacctgtgga ggaggcagtg a 1611

```

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<210> 53
<211> 1611
<212> DNA
<213> Artificial Sequence

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```

<220>
<223> Synthetic construct

```

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<400> 53
atggagtttt caagtccttc cagagaggaa tgtcccaagc ctttgagtag ggtaagcatc 60
atggctggca gcctcacagg attgcttcta cttcaggcag tgtcgtgggc atcaggtgcc 120
aggccctgca tccctaagag ctttggctac agctctgttg tgtgtgtgtg caatgccacc 180
tactgtgaca gctttgacct cccaccttt cctgccctgg gcaccttcag cagatatgag 240
agcaccaggt ctgggaggag gatggagctg agcatggggc ccatccaggc taatcacact 300
ggcactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaagggcttt 360
ggagggggcca tgactgatgc tgctgctctg aacatcctgg ccctgagccc ccctgcccag 420
aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg 480
cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat 540
ttccagctgc tgaacttcag cctgcctgag gaggatacca agctgaagat cccactgatc 600
cacagggctc tgcagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc 660

```

```

cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct      720
ggagacatct accaccagac ctgggccaga tactttgtga agttcctgga tgcctatgct      780
gagcacaagc tgcagttctg ggctgtgact gctgagaatg agccttctgc tgggctgctg      840
tctggctacc ctttccaatg cctgggcttc acccctgagc atcagaggga cttcattgcc      900
agggacctgg gccctaccct ggccaacagc actcaccata atgttaggct gctgatgctg      960
gatgaccaga ggctgctgct gccccactgg gctaagggtg tgctgactga ccctgaggct     1020
gctaaatatg tgcattggcat tgctgtgcat tggtagctgg actttctggc tcctgccaac     1080
gccaccctgg gggagaccca caggctgttc cccaacacca tgctgtttgc ctctgaggcc     1140
tgtgtgggca gcaagttctg ggagcagtct gtgaggctgg gcagctggga tagggggatg     1200
cagtacagcc acagcatcat caccaacctg ctgtaccatg tggtaggctg gactgactgg     1260
aacctggccc tgaaccctga gggaggacct aactgggtca gaaactttgt ggacagcccc     1320
atcattgtgg acatcaccaa ggacaccttt tacaagcagc ccatgttcta ccacctgggc     1380
cacttcagca agttcatccc tgagggcagc cagagagtgg ggctgggtggc cagccagaag     1440
aatgacctgg atgctgtggc tctgatgcat cctgatggct ctgctgtggt ggtggtgctg     1500
aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag     1560
accatcagcc ctggctacag catccacacc tacctgtgga ggaggcagtg a              1611

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```

<210> 54
<211> 1611
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Synthetic construct

```

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<400> 54
atggagtttt caagtccttc cagagaggaa tgtcccaagc ctttgagtag ggtaagcatc      60
atggctggca gcctcacagg attgcttcta cttcaggcag tgtcgtgggc atcaggtgcc     120
aggccctgca tccctaagag ctttggctac agctctgtgg tgtgtgtgtg caatgccacc     180
tactgtgaca gctttgaccc cccaccttt cctgccctgg gcaccttcag cagatatgag     240

```

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agcaccaggt ctgggaggag gatggagctg agcatggggc ccatccaggc taatcacact      300
ggcactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaagggcttt      360
ggagggggcca tgactgatgc tgctgctctg aacatcctgg ccctgagccc ccctgcccag      420
aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg      480
cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat      540
ttccagctgc acaacttcag cctgcctgag gaggatacca agctgaagat cccactgatc      600
cacagggttc tgcagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc      660
cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct      720
ggagacatct accaccagac ctggggcaga tactttgtga agttcctgga tgcctatgct      780
gagcacaagc tgcagttctg ggctgtgact gctgagaatg agccttctgc tgggctgctg      840
tctggctacc ctttccaatg cctgggcttc acccctgagc atcagaggga cttcattgcc      900
agggacctgg gccctaccct ggccaacagc actcaccata atgttaggct gctgatgctg      960
gatgaccaga ggctgctgct gccccactgg gctaagggtg tgctgactga ccctgaggct     1020
gctaaatatg tgcatggcat tgctgtgcat tgggtacctg actttctggc tcctgccaag     1080
gccaccctgg gggagaccca caggctgttc cccaacacca tgctgtttgc ctctgaggcc     1140
tgtgtgggca gcaagttctg ggagcagtct gtgaggctgg gcagctggga taggggggatg     1200
cagtacagcc acagcatcat caccaacctg ctgtaccatg tgggtgggctg gactgactgg     1260
aacctggccc tgaaccctga gggaggacct aactgggtca gaaactttgt ggacagcccc     1320
atcattgtgg acatcaccaa ggacaccttt tacaagcagc ccatgttcta ccacctgggc     1380
cacttcagca agttcatccc tgagggcagc cagagagtgg ggctggtggc cagccagaag     1440
aattgcctgg atgctgtggc tctgatgcat cctgatggct ctgctgtggt ggtggtgctg     1500
aacagggtgct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag     1560
accatcagcc ctggctacag catccacacc tacctgtgga ggaggcagtg a              1611

```

<210> 55

<211> 1611

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic construct

<400> 55

atggagtttt caagtccttc cagagaggaa tgtcccaagc ctttgagtag ggtaagcatc	60
atggctggca gcctcacagg attgcttcta cttcaggcag tgtcgtgggc atcaggtgcc	120
aggccctgca tccctaagag ctttggctac agctctgttg tgtgtgtgtg caatgccacc	180
tactgtgaca gctttgaccc cccaccttt cctgccctgg gcaccttcag cagatatgag	240
agcaccaggt ctgggaggag gatggagctg agcatggggc ccatccaggc taatcacact	300
ggcactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaagggcttt	360
ggagggggcca tgactgatgc tgctgctctg aacatcctgg ccctgagccc ccctgcccag	420
aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg	480
cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat	540
ttccagctgc acaacttcag cctgcctgag gaggatacca agctgaagat ccactgatc	600
cacagggttc tgcagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc	660
cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct	720
ggagacatct accaccagac ctggggcaga tactttgtga agttcctgga tgcctatgct	780
gagcacaagc tgcagttctg ggctgtgact gctgagaatg agccttctgc tgggctgctg	840
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agggacctgg gccctaccct ggccaacagc actcaccata atgttaggct gctgatgctg	960
gatgaccaga ggctgctgct gccccactgg gctaagggtg tgctgactga ccctgaggct	1020
gctaaatatg tgcatggcat tgctgtgcat tggtacctgg actttctggc tcctgccaag	1080
gccaccctgg gggagacca caggctgttc cccaacacca tgctgtttgc ctctgaggcc	1140
tgtgtgggca gcaagttctg ggagcagtct gtgaggctgg gcagctggga taggggggatg	1200
cagtacagcc acagcatcat caccaacctg ctgtaccatg tggtgggctg gactgactgg	1260
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atcattgtgg acatcaccaa ggacaccttt tacaagcagc ccatgttcta ccacctgggc	1380
cacttcagca agttcatccc tgagggcagc cagagagtgg ggctgggtggc cagccagaag	1440
aatgacctgg atgctgtggc tctgatgcat cctgatggct gcgctgtggt ggtgggtgctg	1500
aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag	1560
accatcagcc ctggctacag catccacacc tacctgtggt gcaggcagtg a	1611

<210> 56
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 56	
atggagtttt caagtccttc cagagaggaa tgtcccaagc ctttgagtag ggtaagcatc	60
atggctggca gcctcacagg attgcttcta cttcaggcag tgtcgtgggc atcaggtgcc	120
aggccctgca tccctaagag ctttggctac agctctgtgg tgtgtgtgtg caatgccacc	180
tactgtgaca gctttgaccc cccacacctt cctgccctgg gcaccttcag cagatatgag	240
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ggcactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaagggcttt	360
ggagggggcca tgactgatgc tgctgctctg aacatcctgg ccctgagccc ccctgcccag	420
aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg	480
cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat	540
ttccagctgc acaacttcag cctgcctgag gaggatacca agctgaagat ccactgatc	600
cacagggctc tgcagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc	660
cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct	720
ggagacatct accaccagac ctgggccaga tactttgtga agttcctgga tgcctatgct	780
gagcacaagc tgcagttctg ggctgtgact gctgagaatg agccttctgc tgggctgctg	840
tctggctacc ctttccaatg cctgggcttc acccctgagc atcagaggga cttcattgcc	900

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agggacctgg gccctaccct ggccaacagc actcaccata atgttaggct gctgatgctg      960
gatgaccaga ggctgctgct gcccactgg gctaagggtg tgctgactga ccctgaggct      1020
gctaaatatg tgcatggcat tgctgtgcat tgggtacctg actttctggc tcctgccaag      1080
gccaccctgg gggagacca caggctgttc cccaacacca tgctgtttgc ctctgaggcc      1140
tgtgtgggca gcaagtctg ggagcagtct gtgaggctgg gcagctggga tagggggatg      1200
cagtacagcc acagcatctg caccaacctg ctgtaccatg tgggtgggctg gactgactgg      1260
aacctggccc tgaaccctga gggaggacct aactgggtca gaaactttgt ggacagcccc      1320
atcattgtgg acatcaccaa ggacaccttt tacaagcagc ccatgttcta ccacctgggc      1380
cacttcagca agttcatccc tgagggcagc cagagagtgg ggctgggtggc cagccagaag      1440
aatgacctgt gcgctgtggc tctgatgcat cctgatggct ctgctgtggt ggtggtgctg      1500
aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag      1560
accatcagcc ctggctacag catccacacc tacctgtgga ggaggcagtg a              1611

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<210> 57
<211> 66
<212> DNA
<213> Simian virus 40

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<400> 57
gtaaatataa aatttttaag tgtataatgt gttaaactac tgattctaatt tgtttctctc      60
tttttag                                           66

```

```

<210> 58
<211> 208
<212> DNA
<213> Bos taurus

```

```

<400> 58
ctgtgccttc tagttgccag ccatctgttg ttgcccctc ccccgtcct tccttgacct      60
tggaagggtgc cactcccact gtcctttcct aataaaatga ggaaattgca tcgcattgtc      120
tgagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag ggggaggatt      180
gggaagacaa tagcaggcat gctgggga                                           208

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<210> 59
 <211> 1494
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 59
 gccaggccct gcatccctaa gagctttggc tacagctctg tgggtgtgtgt gtgcaatgcc 60
 acctactgtg acagctttga cccccccacc tttcctgccc tgggcacctt cagcagatat 120
 gagagcacca ggtctgggag gaggatggag ctgagcatgg ggcccatcca ggctaatacac 180
 actggcactg gcctgctgct gaccctgcag cctgagcaga agttccagaa agtaaagggc 240
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 cagaatctgc tgctgaagag ctactttctt gaggagggca ttggctataa catcatcagg 360
 gtgcccattg ccagctgtga cttcagcatc aggacctaca cctatgctga caccctgat 420
 gatttccagc tgcacaactt cagcctgcct gaggaggata ccaagctgaa gatccactg 480
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 agccccactt ggctgaagac caatggggct gtgaatggga aggggagcct gaagggacag 600
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 gctgagcaca agctgcagtt ctgggctgtg actgctgaga atgagccttc tgctgggctg 720
 ctgtctggct accccttcca atgcctgggc ttcaccctg agcatcagag ggacttcatt 780
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 gctgctaaat atgtgcatgg cattgctgtg cattggtacc tggactttct ggctcctgcc 960
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 atgcagtaca gccacagcat catcaccaac ctgctgtacc atgtgggtggg ctggactgac 1140
 tggaacctgg ccctgaaccc tgaggaggga cctaactggg tcagaaactt tgtggacagc 1200

cccatcattg tggacatcac caaggacacc ttttacaagc agcccatggt ctaccacctg	1260
ggccacttca gcaagttcat ccctgagggc agccagagag tggggctggt ggccagccag	1320
aagaatgacc tggatgctgt ggctctgatg catcctgatg gctctgctgt ggtggtggtg	1380
ctgaacagga gctctaagga tgtgcctctg accatcaagg atcctgctgt gggcttcctg	1440
gagacatca gccctggcta cagcatccac acctacctgt ggaggaggca gtga	1494

<210> 60
 <211> 1611
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic construct

<400> 60	
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atggctggca gcctcacagg attgcttcta cttcaggcag tgtcgtgggc atcaggtgcc	120
aggccctgca tccctaagag ctttggctac agctctgttg tgtgtgtgtg caatgccacc	180
tactgtgaca gctttgaccc cccaccttt cctgccctgg gcaccttcag cagatatgag	240
agcaccaggt ctgggaggag gatggagctg agcatggggc ccatccaggc taatcacact	300
ggcactggcc tgctgctgac cctgcagcct gagcagaagt tccagaaagt aaagggcttt	360
ggagggggcca tgactgatgc tgctgctctg aacatcctgg ccctgagccc ccctgcccag	420
aatctgctgc tgaagagcta cttctctgag gagggcattg gctataacat catcagggtg	480
cccatggcca gctgtgactt cagcatcagg acctacacct atgctgacac ccctgatgat	540
ttccagctgc acaacttcag cctgcctgag gaggatacca agctgaagat cccactgac	600
cacagggtc tgcaagctggc ccagaggcct gtgagcctgc tggccagccc ctggaccagc	660
cccacttggc tgaagaccaa tggggctgtg aatgggaagg ggagcctgaa gggacagcct	720
ggagacatct accaccagac ctgggccaga tactttgtga agttcctgga tgcctatgct	780
gagcacaagc tgcagttctg ggctgtgact gctgagaatg agccttctgc tgggctgctg	840
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agggacctgg gccctaccct ggccaacagc actcaccata atgttaggct gctgatgctg      960
gatgaccaga ggctgctgct gcccactgg gctaagggtg tgctgactga ccctgaggct      1020
gctaaatatg tgcatggcat tgctgtgcat tgggtacctg acttttctggc tcctgccaag      1080
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aacctggccc tgaaccctga gggaggacct aactgggtca gaaactttgt ggacagcccc      1320
atcattgtgg acatcaccaa ggacaccttt tacaagcagc ccatgttcta ccacctgggc      1380
cacttcagca agttcatccc tgagggcagc cagagagtgg ggctgggtggc cagccagaag      1440
aatgacctgg atgctgtggc tctgatgcat cctgatggct ctgctgtggt ggtggtgctg      1500
aacaggagct ctaaggatgt gcctctgacc atcaaggatc ctgctgtggg cttcctggag      1560
accatcagcc ctggctacag catccacacc tacctgtgga ggaggcagtg a              1611

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<210> 61
<211> 588
<212> DNA
<213> Woodchuck hepatitis virus

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<400> 61
atcaacctct ggattacaaa atttgtgaaa gattgactgg tattcttaac tatgttgctc      60
cttttacgct atgtggatac gctgctttaa tgcctttgta tcatgctatt gcttcccgta      120
tggttttcat tttctcctcc ttgtataaat cctggttgct gtctctttat gaggagtgtg      180
ggcccgttgt caggcaacgt ggcgtggtgt gcactgtgtt tgctgacgca acccccactg      240
gttggggcat tgccaccacc tgtcagctcc tttccgggac tttcgctttc cccctcccta      300
ttgccacggc ggaactcatc gccgcctgcc ttgcccgctg ctggacaggg gctcggctgt      360
tgggcactga caattccgtg gtgttgctcg ggaaatcatc gtcctttcct tggctgctcg      420
cctgtgttgc cacctggatt ctgcgcggga cgtccttctg ctacgtccct tcggccctca      480
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