

SEQUENCE LISTING

<110> SIGMA-ALDRICH CO. LLC

<120> HIGH FIDELITY SPCAS9 NUCLEASES FOR GENOME MODIFICATION

<130> P20-035 WO-PCT

<140>

<141>

<150> 62/988,279

<151> 2020-03-11

<160> 83

<170> PatentIn version 3.5

<210> 1

<211> 1368

<212> PRT

<213> Streptococcus pyogenes

<400> 1

Met	Asp	Lys	Lys	Tyr	Ser	Ile	Gly	Leu	Asp	Ile	Gly	Thr	Asn	Ser	Val
1				5					10					15	

Gly	Trp	Ala	Val	Ile	Thr	Asp	Glu	Tyr	Lys	Val	Pro	Ser	Lys	Lys	Phe
			20					25					30		

Lys	Val	Leu	Gly	Asn	Thr	Asp	Arg	His	Ser	Ile	Lys	Lys	Asn	Leu	Ile
		35					40					45			

Gly	Ala	Leu	Leu	Phe	Asp	Ser	Gly	Glu	Thr	Ala	Glu	Ala	Thr	Arg	Leu
	50					55					60				

Lys	Arg	Thr	Ala	Arg	Arg	Arg	Tyr	Thr	Arg	Arg	Lys	Asn	Arg	Ile	Cys
65					70					75					80

Tyr	Leu	Gln	Glu	Ile	Phe	Ser	Asn	Glu	Met	Ala	Lys	Val	Asp	Asp	Ser
				85					90					95	

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

His Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr
 115 120 125

His Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp
 130 135 140

Ser Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His
 145 150 155 160

Met Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro
 165 170 175

Asp Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr
 180 185 190

Asn Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala
 195 200 205

Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn
 210 215 220

Leu Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn
 225 230 235 240

Leu Ile Ala Leu Ser Leu Gly Leu Thr Pro Asn Phe Lys Ser Asn Phe
 245 250 255

Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp
 260 265 270

Asp Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp
 275 280 285

Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp
 290 295 300

Ile Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser
 305 310 315 320

Met Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys
 325 330 335

Ala Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe
 340 345 350

Asp Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser
 355 360 365

Gln Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp
 370 375 380

Gly Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg
 385 390 395 400

Lys Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu
 405 410 415

Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe
 420 425 430

Leu Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile
 435 440 445

Pro Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp
 450 455 460

Met Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu
 465 470 475 480

Val Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr
 485 490 495

Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser
 500 505 510

Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys

515

520

525

Tyr Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln
 530 535 540

Lys Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr
 545 550 555 560

Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp
 565 570 575

Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly
 580 585 590

Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp
 595 600 605

Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr
 610 615 620

Leu Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala
 625 630 635 640

His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr
 645 650 655

Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp
 660 665 670

Lys Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe
 675 680 685

Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe
 690 695 700

Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu
 705 710 715 720

His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly
 725 730 735

Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly
 740 745 750

Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln
 755 760 765

Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile
 770 775 780

Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro
 785 790 795 800

Val Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu
 805 810 815

Gln Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg
 820 825 830

Leu Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys
 835 840 845

Asp Asp Ser Ile Asp Asn Lys Val Leu Thr Arg Ser Asp Lys Asn Arg
 850 855 860

Gly Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys
 865 870 875 880

Asn Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys
 885 890 895

Phe Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp
 900 905 910

Lys Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr
 915 920 925

Lys His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp
 930 935 940

Glu Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser
 945 950 955 960

Lys Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg
 965 970 975

Glu Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val
 980 985 990

Val Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
 995 1000 1005

Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
 1010 1015 1020

Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
 1025 1030 1035

Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
 1040 1045 1050

Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
 1055 1060 1065

Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
 1070 1075 1080

Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
 1085 1090 1095

Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
 1100 1105 1110

Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
 1115 1120 1125

Lys	Lys	Tyr	Gly	Gly	Phe	Asp	Ser	Pro	Thr	Val	Ala	Tyr	Ser	Val
1130						1135					1140			
Leu	Val	Val	Ala	Lys	Val	Glu	Lys	Gly	Lys	Ser	Lys	Lys	Leu	Lys
1145						1150					1155			
Ser	Val	Lys	Glu	Leu	Leu	Gly	Ile	Thr	Ile	Met	Glu	Arg	Ser	Ser
1160						1165					1170			
Phe	Glu	Lys	Asn	Pro	Ile	Asp	Phe	Leu	Glu	Ala	Lys	Gly	Tyr	Lys
1175						1180					1185			
Glu	Val	Lys	Lys	Asp	Leu	Ile	Ile	Lys	Leu	Pro	Lys	Tyr	Ser	Leu
1190						1195					1200			
Phe	Glu	Leu	Glu	Asn	Gly	Arg	Lys	Arg	Met	Leu	Ala	Ser	Ala	Gly
1205						1210					1215			
Glu	Leu	Gln	Lys	Gly	Asn	Glu	Leu	Ala	Leu	Pro	Ser	Lys	Tyr	Val
1220						1225					1230			
Asn	Phe	Leu	Tyr	Leu	Ala	Ser	His	Tyr	Glu	Lys	Leu	Lys	Gly	Ser
1235						1240					1245			
Pro	Glu	Asp	Asn	Glu	Gln	Lys	Gln	Leu	Phe	Val	Glu	Gln	His	Lys
1250						1255					1260			
His	Tyr	Leu	Asp	Glu	Ile	Ile	Glu	Gln	Ile	Ser	Glu	Phe	Ser	Lys
1265						1270					1275			
Arg	Val	Ile	Leu	Ala	Asp	Ala	Asn	Leu	Asp	Lys	Val	Leu	Ser	Ala
1280						1285					1290			
Tyr	Asn	Lys	His	Arg	Asp	Lys	Pro	Ile	Arg	Glu	Gln	Ala	Glu	Asn
1295						1300					1305			
Ile	Ile	His	Leu	Phe	Thr	Leu	Thr	Asn	Leu	Gly	Ala	Pro	Ala	Ala

1310

1315

1320

Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser
 1325 1330 1335

Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr
 1340 1345 1350

Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp
 1355 1360 1365

<210> 2

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 2

Pro Lys Lys Lys Arg Lys Val
 1 5

<210> 3

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 3

Pro Lys Lys Lys Arg Arg Val
 1 5

<210> 4

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

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

<400> 4
 Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys
 1 5 10 15

<210> 5
 <211> 11
 <212> PRT
 <213> Artificial Sequence

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

<400> 5
 Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1 5 10

<210> 6
 <211> 9
 <212> PRT
 <213> Artificial Sequence

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

<400> 6
 Arg Lys Lys Arg Arg Gln Arg Arg Arg
 1 5

<210> 7
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 7
 Pro Ala Ala Lys Arg Val Lys Leu Asp

1

5

<210> 8

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 8

Arg Gln Arg Arg Asn Glu Leu Lys Arg Ser Pro

1

5

10

<210> 9

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 9

Val Ser Arg Lys Arg Pro Arg Pro

1

5

<210> 10

<211> 8

<212> PRT

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

<400> 10

Pro Pro Lys Lys Ala Arg Glu Asp

1

5

<210> 11

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 11

Pro Gln Pro Lys Lys Lys Pro Leu
1 5

<210> 12

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 12

Ser Ala Leu Ile Lys Lys Lys Lys Lys Met Ala Pro
1 5 10

<210> 13

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 13

Pro Lys Gln Lys Lys Arg Lys
1 5

<210> 14

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 14

Arg Lys Leu Lys Lys Lys Ile Lys Lys Leu
1 5 10

<210> 15

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 15

Arg Glu Lys Lys Lys Phe Leu Lys Arg Arg
1 5 10

<210> 16

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 16

Lys Arg Lys Gly Asp Glu Val Asp Gly Val Asp Glu Val Ala Lys Lys
1 5 10 15

Lys Ser Lys Lys
20

<210> 17

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 17

Arg Lys Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys
 1 5 10 15

Lys

<210> 18
 <211> 38
 <212> PRT
 <213> Artificial Sequence

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

<400> 18
 Asn Gln Ser Ser Asn Phe Gly Pro Met Lys Gly Gly Asn Phe Gly Gly
 1 5 10 15

Arg Ser Ser Gly Pro Tyr Gly Gly Gly Gly Gln Tyr Phe Ala Lys Pro
 20 25 30

Arg Asn Gln Gly Gly Tyr
 35

<210> 19
 <211> 42
 <212> PRT
 <213> Artificial Sequence

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

<400> 19
 Arg Met Arg Ile Glx Phe Lys Asn Lys Gly Lys Asp Thr Ala Glu Leu
 1 5 10 15

Arg Arg Arg Arg Val Glu Val Ser Val Glu Leu Arg Lys Ala Lys Lys
 20 25 30

Asp Glu Gln Ile Leu Lys Arg Arg Asn Val

35

40

<210> 20
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic
 peptide"

<400> 20
 Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Pro Lys Lys
 1 5 10 15

Lys Arg Lys Val
 20

<210> 21
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic
 peptide"

<400> 21
 Pro Leu Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro Pro Lys Lys Lys
 1 5 10 15

Arg Lys Val

<210> 22
 <211> 24
 <212> PRT
 <213> Artificial Sequence

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

<400> 22

Gly Ala Leu Phe Leu Gly Trp Leu Gly Ala Ala Gly Ser Thr Met Gly
1 5 10 15

Ala Pro Lys Lys Lys Arg Lys Val
20

<210> 23

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 23

Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly
1 5 10 15

Ala Trp Ser Gln Pro Lys Lys Lys Arg Lys Val
20 25

<210> 24

<211> 21

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 24

Lys Glu Thr Trp Trp Glu Thr Trp Trp Thr Glu Trp Ser Gln Pro Lys
1 5 10 15

Lys Lys Arg Lys Val
20

<210> 25

<211> 11

<212> PRT

<213> Artificial Sequence

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

<400> 25
 Tyr Ala Arg Ala Ala Ala Arg Gln Ala Arg Ala
 1 5 10

<210> 26
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 26
 Thr His Arg Leu Pro Arg Arg Arg Arg Arg Arg
 1 5 10

<210> 27
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 27
 Gly Gly Arg Arg Ala Arg Arg Arg Arg Arg Arg
 1 5 10

<210> 28
 <211> 12
 <212> PRT
 <213> Artificial Sequence

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

<400> 28

Arg Arg Gln Arg Arg Thr Ser Lys Leu Met Lys Arg
1 5 10

<210> 29

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 29

Gly Trp Thr Leu Asn Ser Ala Gly Tyr Leu Leu Gly Lys Ile Asn Leu
1 5 10 15

Lys Ala Leu Ala Ala Leu Ala Lys Lys Ile Leu
20 25

<210> 30

<211> 33

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 30

Lys Ala Leu Ala Trp Glu Ala Lys Leu Ala Lys Ala Leu Ala Lys Ala
1 5 10 15

Leu Ala Lys His Leu Ala Lys Ala Leu Ala Lys Ala Leu Lys Cys Glu
20 25 30

Ala

<210> 31

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 31

Arg Gln Ile Lys Ile Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys
1 5 10 15

<210> 32

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic 6xHis tag"

<400> 32

His His His His His His
1 5

<210> 33

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 33

Leu Glu Gly Gly Gly Ser
1 5

<210> 34

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 34
 Thr Gly Ser Gly
 1

<210> 35
 <211> 8
 <212> PRT
 <213> Artificial Sequence

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

<400> 35
 Gly Gly Ser Gly Gly Gly Ser Gly
 1 5

<210> 36
 <211> 20
 <212> PRT
 <213> Artificial Sequence

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

<220>
 <221> SITE
 <222> (1)..(20)
 <223> /note="This sequence may encompass 1-4 'Gly Gly Gly Gly Ser'
 repeating units"

<400> 36
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser
 20

<210> 37
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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 <222> (1)..(8)
 <223> /note="This sequence may encompass 6-8 residues"

<400> 37
 Gly Gly Gly Gly Gly Gly Gly Gly
 1 5

<210> 38
 <211> 20
 <212> PRT
 <213> Artificial Sequence

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

<220>
 <221> SITE
 <222> (1)..(20)
 <223> /note="This sequence may encompass 1-4 'Glu Ala Ala Ala Lys' repeating units"

<400> 38
 Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu
 1 5 10 15

Ala Ala Ala Lys
 20

<210> 39
 <211> 27
 <212> PRT
 <213> Artificial Sequence

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

<220>
 <221> SITE
 <222> (2)..(26)
 <223> /note="This region may encompass 2-5 'Glu Ala Ala Ala Lys'
 repeating units"

<400> 39
 Ala Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys
 1 5 10 15

Glu Ala Ala Ala Lys Glu Ala Ala Ala Lys Ala
 20 25

<210> 40
 <211> 5
 <212> PRT
 <213> Artificial Sequence

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

<400> 40
 Pro Ala Pro Ala Pro
 1 5

<210> 41
 <211> 16
 <212> PRT
 <213> Artificial Sequence

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

<220>
 <221> SITE
 <222> (1)..(16)
 <223> /note="This sequence may encompass 6-8 'Ala Pro'
 repeating units"

<400> 41
 Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro

1	5	10	15	
<210> 42				
<211> 20				
<212> RNA				
<213> Artificial Sequence				
<220>				
<221> source				
<223> /note="Description of Artificial Sequence: Synthetic oligonucleotide"				
<400> 42				
ggcacugcgg cuggaggugg				20
<210> 43				
<211> 59				
<212> DNA				
<213> Artificial Sequence				
<220>				
<221> source				
<223> /note="Description of Artificial Sequence: Synthetic primer"				
<220>				
<221> modified_base				
<222> (34)..(39)				
<223> a, c, t, g, unknown or other				
<400> 43				
tcgtcggcag cgtcagatgt gtataagaga cagnnnnnng gaaccaggt agccagaga				59
<210> 44				
<211> 57				
<212> DNA				
<213> Artificial Sequence				
<220>				
<221> source				
<223> /note="Description of Artificial Sequence: Synthetic primer"				
<220>				
<221> modified_base				
<222> (35)..(40)				

<223> a, c, t, g, unknown or other

<400> 44

gtctcgtggg ctcggagatg tgtataagag acagnnnnnn ggggtggggt cagacgt 57

<210> 45

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<220>

<221> modified_base

<222> (34)..(39)

<223> a, c, t, g, unknown or other

<400> 45

tcgtcggcag cgtcagatgt gtataagaga cagnnnnnnc tagagcaaac cttggcattg 60

tcc 63

<210> 46

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<221> source

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

<220>

<221> modified_base

<222> (35)..(40)

<223> a, c, t, g, unknown or other

<400> 46

gtctcgtggg ctcggagatg tgtataagag acagnnnnnn accctctacc ctccctgatg 60

<210> 47

<211> 1404

<212> PRT

<213> Artificial Sequence

<220>

<221> source

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

<400> 47

Pro Ala Ala Lys Arg Val Lys Leu Asp Gly Gly Gly Gly Ser Thr Gly
1 5 10 15

Met Asp Lys Lys Tyr Ser Ile Gly Leu Asp Ile Gly Thr Asn Ser Val
20 25 30

Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro Ser Lys Lys Phe
35 40 45

Lys Val Leu Gly Thr Asp Arg His Ser Ile Lys Lys Asn Leu Ile Gly
50 55 60

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

Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys Asn Arg Ile Cys Tyr
85 90 95

Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys Val Asp Asp Ser Phe
100 105 110

Phe His Arg Leu Glu Glu Ser Phe Leu Val Glu Glu Asp Lys Lys His
115 120 125

Glu Arg His Pro Ile Phe Gly Asn Ile Val Asp Glu Val Ala Tyr His
130 135 140

Glu Lys Tyr Pro Thr Ile Tyr His Leu Arg Lys Lys Leu Val Asp Ser
145 150 155 160

Thr Asp Lys Ala Asp Leu Arg Leu Ile Tyr Leu Ala Leu Ala His Met
165 170 175

Ile Lys Phe Arg Gly His Phe Leu Ile Glu Gly Asp Leu Asn Pro Asp
 180 185 190

Asn Ser Asp Val Asp Lys Leu Phe Ile Gln Leu Val Gln Thr Tyr Asn
 195 200 205

Gln Leu Phe Glu Glu Asn Pro Ile Asn Ala Ser Gly Val Asp Ala Lys
 210 215 220

Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg Arg Leu Glu Asn Leu
 225 230 235 240

Ile Ala Gln Leu Pro Gly Glu Lys Lys Asn Gly Leu Phe Gly Asn Leu
 245 250 255

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

Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys Asp Thr Tyr Asp Asp
 275 280 285

Asp Leu Asp Asn Leu Leu Ala Gln Ile Gly Asp Gln Tyr Ala Asp Leu
 290 295 300

Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile Leu Leu Ser Asp Ile
 305 310 315 320

Leu Arg Val Asn Thr Glu Ile Thr Lys Ala Pro Leu Ser Ala Ser Met
 325 330 335

Ile Lys Arg Tyr Asp Glu His His Gln Asp Leu Thr Leu Leu Lys Ala
 340 345 350

Leu Val Arg Gln Gln Leu Pro Glu Lys Tyr Lys Glu Ile Phe Phe Asp
 355 360 365

Gln Ser Lys Asn Gly Tyr Ala Gly Tyr Ile Asp Gly Gly Ala Ser Gln
 370 375 380

Glu Glu Phe Tyr Lys Phe Ile Lys Pro Ile Leu Glu Lys Met Asp Gly
 385 390 395 400

Thr Glu Glu Leu Leu Val Lys Leu Asn Arg Glu Asp Leu Leu Arg Lys
 405 410 415

Gln Arg Thr Phe Asp Asn Gly Ser Ile Pro His Gln Ile His Leu Gly
 420 425 430

Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp Phe Tyr Pro Phe Leu
 435 440 445

Lys Asp Asn Arg Glu Lys Ile Glu Lys Ile Leu Thr Phe Arg Ile Pro
 450 455 460

Tyr Tyr Val Gly Pro Leu Ala Arg Gly Asn Ser Arg Phe Ala Trp Met
 465 470 475 480

Thr Arg Lys Ser Glu Glu Thr Ile Thr Pro Trp Asn Phe Glu Glu Val
 485 490 495

Val Asp Lys Gly Ala Ser Ala Gln Ser Phe Ile Glu Arg Met Thr Asn
 500 505 510

Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu Pro Lys His Ser Leu
 515 520 525

Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu Thr Lys Val Lys Tyr
 530 535 540

Val Thr Glu Gly Met Arg Lys Pro Ala Phe Leu Ser Gly Glu Gln Lys
 545 550 555 560

Lys Ala Ile Val Asp Leu Leu Phe Lys Thr Asn Arg Lys Val Thr Val
 565 570 575

Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile Glu Cys Phe Asp Ser

580

585

590

Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn Ala Ser Leu Gly Thr
 595 600 605

Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys Asp Phe Leu Asp Asn
 610 615 620

Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val Leu Thr Leu Thr Leu
 625 630 635 640

Phe Glu Asp Arg Glu Met Ile Glu Glu Arg Leu Lys Thr Tyr Ala His
 645 650 655

Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys Arg Arg Arg Tyr Thr
 660 665 670

Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn Gly Ile Arg Asp Lys
 675 680 685

Gln Ser Gly Lys Thr Ile Leu Asp Phe Leu Lys Ser Asp Gly Phe Ala
 690 695 700

Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp Ser Leu Thr Phe Lys
 705 710 715 720

Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln Gly Asp Ser Leu His
 725 730 735

Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala Ile Lys Lys Gly Ile
 740 745 750

Leu Gln Thr Val Lys Val Val Asp Glu Leu Val Lys Val Met Gly Arg
 755 760 765

His Lys Pro Glu Asn Ile Val Ile Glu Met Ala Arg Glu Asn Gln Thr
 770 775 780

Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg Met Lys Arg Ile Glu
785 790 795 800

Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu Lys Glu His Pro Val
805 810 815

Glu Asn Thr Gln Leu Gln Asn Glu Lys Leu Tyr Leu Tyr Tyr Leu Gln
820 825 830

Asn Gly Arg Asp Met Tyr Val Asp Gln Glu Leu Asp Ile Asn Arg Leu
835 840 845

Ser Asp Tyr Asp Val Asp His Ile Val Pro Gln Ser Phe Leu Lys Asp
850 855 860

Asp Ser Ile Asp Asn Gln Val Leu Thr Arg Ser Asp Lys Asn Arg Gly
865 870 875 880

Lys Ser Asp Asn Val Pro Ser Glu Glu Val Val Lys Lys Met Lys Asn
885 890 895

Tyr Trp Arg Gln Leu Leu Asn Ala Lys Leu Ile Thr Gln Arg Lys Phe
900 905 910

Asp Asn Leu Thr Lys Ala Glu Arg Gly Gly Leu Ser Glu Leu Asp Lys
915 920 925

Ala Gly Phe Ile Lys Arg Gln Leu Val Glu Thr Arg Gln Ile Thr Lys
930 935 940

His Val Ala Gln Ile Leu Asp Ser Arg Met Asn Thr Lys Tyr Asp Glu
945 950 955 960

Asn Asp Lys Leu Ile Arg Glu Val Lys Val Ile Thr Leu Lys Ser Lys
965 970 975

Leu Val Ser Asp Phe Arg Lys Asp Phe Gln Phe Tyr Lys Val Arg Glu
980 985 990

Ile Asn Asn Tyr His His Ala His Asp Ala Tyr Leu Asn Ala Val Val
 995 1000 1005

Gly Thr Ala Leu Ile Lys Lys Tyr Pro Lys Leu Glu Ser Glu Phe
 1010 1015 1020

Val Tyr Gly Asp Tyr Lys Val Tyr Asp Val Arg Lys Met Ile Ala
 1025 1030 1035

Lys Ser Glu Gln Glu Ile Gly Lys Ala Thr Ala Lys Tyr Phe Phe
 1040 1045 1050

Tyr Ser Asn Ile Met Asn Phe Phe Lys Thr Glu Ile Thr Leu Ala
 1055 1060 1065

Asn Gly Glu Ile Arg Lys Arg Pro Leu Ile Glu Thr Asn Gly Glu
 1070 1075 1080

Thr Gly Glu Ile Val Trp Asp Lys Gly Arg Asp Phe Ala Thr Val
 1085 1090 1095

Arg Lys Val Leu Ser Met Pro Gln Val Asn Ile Val Lys Lys Thr
 1100 1105 1110

Glu Val Gln Thr Gly Gly Phe Ser Lys Glu Ser Ile Leu Pro Lys
 1115 1120 1125

Arg Asn Ser Asp Lys Leu Ile Ala Arg Lys Lys Asp Trp Asp Pro
 1130 1135 1140

Lys Lys Tyr Gly Gly Phe Asp Ser Pro Thr Val Ala Tyr Ser Val
 1145 1150 1155

Leu Val Val Ala Lys Val Glu Lys Gly Lys Ser Lys Lys Leu Lys
 1160 1165 1170

Ser Val Lys Glu Leu Leu Gly Ile Thr Ile Met Glu Arg Ser Ser
 1175 1180 1185

Phe Glu Lys Asn Pro Ile Asp Phe Leu Glu Ala Lys Gly Tyr Lys
 1190 1195 1200

Glu Val Lys Lys Asp Leu Ile Ile Lys Leu Pro Lys Tyr Ser Leu
 1205 1210 1215

Phe Glu Leu Glu Asn Gly Arg Lys Arg Met Leu Ala Ser Ala Gly
 1220 1225 1230

Glu Leu Gln Lys Gly Asn Glu Leu Ala Leu Pro Ser Lys Tyr Val
 1235 1240 1245

Asn Phe Leu Tyr Leu Ala Ser His Tyr Glu Lys Leu Lys Gly Ser
 1250 1255 1260

Pro Glu Asp Asn Glu Gln Lys Gln Leu Phe Val Glu Gln His Lys
 1265 1270 1275

His Tyr Leu Asp Glu Ile Ile Glu Gln Ile Ser Glu Phe Ser Lys
 1280 1285 1290

Arg Val Ile Leu Ala Asp Ala Asn Leu Asp Lys Val Leu Ser Ala
 1295 1300 1305

Tyr Asn Lys His Arg Asp Lys Pro Ile Arg Glu Gln Ala Glu Asn
 1310 1315 1320

Ile Ile His Leu Phe Thr Leu Thr Asn Leu Gly Ala Pro Ala Ala
 1325 1330 1335

Phe Lys Tyr Phe Asp Thr Thr Ile Asp Arg Lys Arg Tyr Thr Ser
 1340 1345 1350

Thr Lys Glu Val Leu Asp Ala Thr Leu Ile His Gln Ser Ile Thr
 1355 1360 1365

Gly Leu Tyr Glu Thr Arg Ile Asp Leu Ser Gln Leu Gly Gly Asp

1370

1375

1380

Glu Phe Pro Lys Lys Lys Arg Lys Val Gly Gly Gly Gly Ser Pro
 1385 1390 1395

Lys Lys Lys Arg Lys Val
 1400

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 <211> 20
 <212> RNA
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<220>
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<400> 48
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20

<210> 49
 <211> 20
 <212> RNA
 <213> Artificial Sequence

<220>
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<400> 49
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20

<210> 50
 <211> 59
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 <213> Artificial Sequence

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<210> 51
 <211> 63
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<220>
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 <222> (35)..(40)
 <223> a, c, t, g, unknown or other

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<210> 52
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<210> 53

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 g 61

<210> 54
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 <223> a, c, t, g, unknown or other

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 tat 63

<210> 55
 <211> 61
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primer"

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<223> a, c, t, g, unknown or other

<400> 55

gtctcgtggg ctcggagatg tgtataagag acagnnnnnn ccaatctact cccaggagca 60

g 61

<210> 56

<211> 59

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<222> (34)..(39)

<223> a, c, t, g, unknown or other

<400> 56

tcgtcggcag cgtcagatgt gtataagaga cagnnnnnnt cactggagca gggaggaca 59

<210> 57

<211> 61

<212> DNA

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<400> 57

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g 61

<210> 58

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cucccuccca ggauccucuc 20

<210> 59

<211> 20

<212> RNA

<213> Artificial Sequence

<220>

<221> source

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<400> 59

gccaguagcc agccccgucc 20

<210> 60

<211> 20

<212> RNA

<213> Artificial Sequence

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caggcagucu ucauccccgu 20

<210> 61

<211> 20

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 <400> 61
 gaagcgugau gacaaagagg 20

 <210> 62
 <211> 20
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 <400> 62
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 <210> 63
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 <223> a, c, t, g, unknown or other

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<210> 65
 <211> 61
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 c 61

<210> 66
 <211> 64
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 cact 64

 <210> 67
 <211> 64
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 <223> a, c, t, g, unknown or other

 <400> 67
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 <210> 68
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 <223> a, c, t, g, unknown or other

 <400> 68
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<210> 69
 <211> 60
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<220>
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 <223> a, c, t, g, unknown or other

<400> 69
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<210> 70
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c 61

<210> 71
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<223> a, c, t, g, unknown or other

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g 61

<210> 72

<211> 62

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cc 62

<210> 73

<211> 23

<212> DNA

<213> Homo sapiens

<400> 73

ggcactgcgg ctggaggtgg ggg 23

<210> 74

<211> 23

<212> DNA

<213> Homo sapiens

<400> 74

ggcacgacgg ctggaggtgg ggg 23

<210> 75
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 75
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<210> 76
 <211> 23
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 <213> Homo sapiens

<400> 76
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<210> 77
 <211> 23
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 <213> Homo sapiens

<400> 77
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<210> 78
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<400> 78
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<210> 79
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<400> 79
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<210> 80
 <211> 23
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<213> Homo sapiens

<400> 80

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23

<210> 81

<211> 23

<212> DNA

<213> Homo sapiens

<400> 81

caggcagtct tcatccccgt agg

23

<210> 82

<211> 23

<212> DNA

<213> Homo sapiens

<400> 82

gaagcgtgat gacaaagagg agg

23

<210> 83

<211> 23

<212> DNA

<213> Homo sapiens

<400> 83

attctggtca acgtgtcctt cgg

23