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Seoul National University R&DB Foundation

<120> NOVEL CRISPR ASSOCIATED PROTEIN AND USE THEREOF

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aagaaaccat cgaaagaaat tatggcgggc aaagaggatt gttcagaaca tgcatatgca 1740

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aagaaaggaa tacaggacta tcacccatca tcatatattg ttgaaggata taatgaaaag 1860

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cggaatagca ggatagataa tccggattac gatagaatta tctcaccggt attgaataaa 3600

aatggagaat tttttgattc tgatgaatat aattcatata ttgatgcgca aaaggcaccg 3660

ttaccgatag atgccgatgc aaatggcgca ttttgcattg cattaaaagg aatgtatact 3720

gccaatcaga tcaaagaaaa ctgggttgaa ggggagaaac ttccggcgga ttgcttgaag 3780

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Gln Phe Ile Val Lys Asn Gly Ile Ile Lys Glu Asp Glu Leu Arg Gly
35 40 45

Glu Asn Arg Gln Ile Leu Lys Asp Ile Met Asp Asp Tyr Tyr Arg Gly
50 55 60

Phe Ile Ser Glu Thr Leu Ser Ser Ile Asp Asp Ile Asp Trp Thr Ser

65 70 75 80

Leu Phe Glu Lys Met Glu Ile Gln Leu Lys Asn Gly Asp Asn Lys Asp
85 90 95

Thr Leu Ile Lys Glu Gln Ala Glu Lys Arg Lys Ala Ile Tyr Lys Lys
100 105 110

Phe Ala Asp Asp Asp Arg Phe Lys Asn Met Phe Ser Ala Lys Leu Ile
115 120 125

Ser Asp Ile Leu Pro Glu Phe Val Ile His Asn Asn Asn Tyr Ser Ala
130 135 140

Ser Glu Lys Glu Glu Lys Thr Gln Val Ile Lys Leu Phe Ser Arg Phe
145 150 155 160

Ala Thr Ser Phe Lys Asp Tyr Phe Lys Asn Arg Ala Asn Cys Phe Ser
165 170 175

Ala Asp Asp Ile Ser Ser Ser Ser Cys His Arg Ile Val Asn Asp Asn
180 185 190

Ala Glu Ile Phe Phe Ser Asn Ala Leu Val Tyr Arg Arg Ile Val Lys
195 200 205

Asn Leu Ser Asn Asp Asp Ile Asn Lys Ile Ser Gly Asp Ile Lys Asp
210 215 220

Ser Leu Lys Glu Met Ser Leu Glu Glu Ile Tyr Ser Tyr Glu Lys Tyr
225 230 235 240

Gly Glu Phe Ile Thr Gln Glu Gly Ile Ser Phe Tyr Asn Asp Ile Cys
245 250 255

Gly Lys Val Asn Ser Phe Met Asn Leu Tyr Cys Gln Lys Asn Lys Glu
260 265 270

Asn Lys Asn Leu Tyr Lys Leu Arg Lys Leu His Lys Gln Ile Leu Cys
275 280 285

Ile Ala Asp Thr Ser Tyr Glu Val Pro Tyr Lys Phe Glu Ser Asp Glu
290 295 300

Glu Val Tyr Gln Ser Val Asn Gly Phe Leu Asp Asn Ile Ser Ser Lys
305 310 315 320

His Ile Val Glu Arg Leu Arg Lys Ile Gly Asp Asn Tyr Asn Gly Tyr
325 330 335

Asn Leu Asp Lys Ile Tyr Ile Val Ser Lys Phe Tyr Glu Ser Val Ser
340 345 350

Gln Lys Thr Tyr Arg Asp Trp Glu Thr Ile Asn Thr Ala Leu Glu Ile
355 360 365

His Tyr Asn Asn Ile Leu Pro Gly Asn Gly Lys Ser Lys Ala Asp Lys
370 375 380

Val Lys Lys Ala Val Lys Asn Asp Leu Gln Lys Ser Ile Thr Glu Ile
385 390 395 400

Asn Glu Leu Val Ser Asn Tyr Lys Leu Cys Pro Asp Asp Asn Ile Lys
405 410 415

Ala Glu Thr Tyr Ile His Glu Ile Ser His Ile Leu Asn Asn Phe Glu
420 425 430

Ala Gln Glu Leu Lys Tyr Asn Pro Glu Ile His Leu Val Glu Ser Glu
435 440 445

Leu Lys Ala Ser Glu Leu Lys Asn Val Leu Asp Val Ile Met Asn Ala
450 455 460

Phe His Trp Cys Ser Val Phe Met Thr Glu Glu Leu Val Asp Lys Asp
465 470 475 480

Asn Asn Phe Tyr Ala Glu Leu Glu Glu Ile Tyr Asp Glu Ile Tyr Thr
485 490 495

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

Tyr Ser Thr Lys Lys Ile Lys Leu Asn Phe Gly Ile Pro Thr Leu Ala
515 520 525

Asp Gly Trp Ser Lys Ser Lys Glu Tyr Ser Asn Asn Ala Ile Ile Leu
530 535 540

Met Arg Asp Asn Leu Tyr Tyr Leu Gly Ile Phe Asn Ala Lys Asn Lys
545 550 555 560

Pro Asp Lys Lys Ile Ile Glu Gly Asn Thr Ser Glu Asn Lys Gly Asp
565 570 575

Tyr Lys Lys Met Ile Tyr Asn Leu Leu Pro Gly Pro Asn Lys Met Ile
580 585 590

Pro Lys Val Phe Leu Ser Ser Lys Thr Gly Val Glu Thr Tyr Lys Pro
595 600 605

Ser Ala Tyr Ile Leu Glu Gly Tyr Lys Gln Asn Lys His Leu Lys Ser
610 615 620

Ser Lys Asp Phe Asp Ile Thr Phe Cys His Asp Leu Ile Asp Tyr Phe
625 630 635 640

Lys Asn Cys Ile Ala Ile His Pro Glu Trp Lys Asn Phe Gly Phe Asp
645 650 655

Phe Ser Asp Thr Ser Thr Tyr Glu Asp Ile Ser Gly Phe Tyr Arg Glu
660 665 670

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

Asp Ile Asp Leu Leu Gln Glu Lys Gly Gln Leu Tyr Leu Phe Gln Ile
690 695 700

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

Thr Met Tyr Leu Lys Asn Leu Phe Ser Glu Glu Asn Leu Lys Asp Ile
725 730 735

Val Leu Lys Leu Asn Gly Glu Ala Glu Ile Phe Phe Arg Lys Ser Ser
740 745 750

Ile Lys Asn Pro Ile Ile His Lys Lys Gly Ser Ile Leu Val Asn Arg
755 760 765

Thr Tyr Glu Ala Glu Glu Lys Asp Gln Phe Gly Asn Ile Gln Ile Val
770 775 780

Arg Lys Thr Ile Pro Glu Asn Ile Tyr Gln Glu Leu Tyr Lys Tyr Phe
785 790 795 800

Asn Asp Lys Ser Asp Lys Glu Leu Ser Asp Glu Ala Ala Lys Leu Lys
805 810 815

Asn Val Val Gly His His Glu Ala Ala Thr Asn Ile Val Lys Asp Tyr
820 825 830

Arg Tyr Thr Tyr Asp Lys Tyr Phe Leu His Met Pro Ile Thr Ile Asn
835 840 845

Phe Lys Ala Asn Lys Thr Ser Phe Ile Asn Asp Arg Ile Leu Gln Tyr
850 855 860

Ile Ala Lys Glu Lys Asn Leu His Val Ile Gly Ile Asp Arg Gly Glu
865 870 875 880

Arg Asn Leu Ile Tyr Val Ser Val Ile Asp Thr Cys Gly Asn Ile Val
885 890 895

Glu Gln Lys Ser Phe Asn Ile Val Asn Gly Tyr Asp Tyr Gln Ile Lys
900 905 910

Leu Lys Gln Gln Glu Gly Ala Arg Gln Ile Ala Arg Gln Glu Trp Lys
915 920 925

Glu Ile Gly Lys Ile Lys Glu Ile Lys Glu Gly Tyr Leu Ser Leu Val
930 935 940

Ile His Glu Ile Ser Lys Met Val Ile Lys Tyr Asn Ala Ile Ile Ala
945 950 955 960

Met Glu Asp Leu Ser Tyr Gly Phe Lys Lys Gly Arg Phe Lys Val Glu
965 970 975

Arg Gln Val Tyr Gln Lys Phe Glu Thr Met Leu Ile Asn Lys Leu Asn
980 985 990

Tyr Leu Val Phe Lys Asp Ile Ser Ile Thr Glu Asn Gly Gly Leu Leu
995 1000 1005

Lys Gly Tyr Gln Leu Thr Tyr Ile Pro Asp Lys Leu Lys Asn Val Gly
1010 1015 1020

His Gln Cys Gly Cys Ile Phe Tyr Val Pro Ala Ala Tyr Thr Ser Lys
1025 1030 1035 1040

Ile Asp Pro Thr Thr Gly Phe Val Asn Ile Phe Lys Phe Lys Asp Leu
1045 1050 1055

Thr Val Asp Ala Lys Arg Glu Phe Ile Lys Lys Phe Asp Ser Ile Arg
1060 1065 1070

Tyr Asp Ser Glu Lys Lys Leu Phe Cys Phe Thr Phe Asp Tyr Asn Asn
1075 1080 1085

Phe Ile Thr Gln Asn Thr Val Met Ser Lys Ser Ser Trp Ser Val Tyr
1090 1095 1100

Thr Tyr Gly Val Arg Ile Lys Arg Arg Phe Val Asn Gly Arg Phe Ser
1105 1110 1115 1120

Asn Glu Ser Asp Thr Ile Asp Ile Thr Lys Asp Met Glu Lys Thr Leu
1125 1130 1135

Glu Met Thr Asp Ile Asn Trp Arg Asp Gly His Asp Leu Arg Gln Asp
1140 1145 1150

Ile Ile Asp Tyr Glu Ile Val Gln His Ile Phe Glu Ile Phe Arg Leu

1155 1160 1165

Thr Val Gln Met Arg Asn Ser Leu Ser Glu Leu Glu Asp Arg Asp Tyr
1170 1175 1180

Asp Arg Leu Ile Ser Pro Val Leu Asn Glu Asn Asn Ile Phe Tyr Asp
1185 1190 1195 1200

Ser Ala Lys Ala Gly Asp Ala Leu Pro Lys Asp Ala Asp Ala Asn Gly
1205 1210 1215

Ala Tyr Cys Ile Ala Leu Lys Gly Leu Tyr Glu Ile Lys Gln Ile Thr
1220 1225 1230

Glu Asn Trp Lys Glu Asp Gly Lys Phe Ser Arg Asp Lys Leu Lys Ile
1235 1240 1245

Ser Asn Lys Asp Trp Phe Asp Phe Ile Gln Asn Lys Arg Tyr Leu
1250 1255 1260

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Asn Ile Thr Gln Leu Asp Leu Leu Thr Glu Asp Glu Ile Arg Ala Gln
35 40 45

Asn Arg Glu Lys Leu Lys Glu Met Met Asp Asp Tyr Tyr Arg Asn Val
50 55 60

Ile Asp Ser Thr Leu His Val Gly Ile Ala Val Asp Trp Ser Tyr Leu
65 70 75 80

Phe Ser Cys Met Arg Asn His Leu Arg Glu Asn Ser Lys Glu Ser Lys
85 90 95

Arg Glu Leu Glu Arg Thr Gln Asp Ser Ile Arg Ser Gln Ile His Asn
100 105 110

Lys Phe Ala Glu Arg Ala Asp Phe Lys Asp Met Phe Gly Ala Ser Ile
115 120 125

Ile Thr Lys Leu Leu Pro Thr Tyr Ile Lys Gln Asn Ser Glu Tyr Ser
130 135 140

Glu Arg Tyr Asp Glu Ser Met Glu Ile Leu Lys Leu Tyr Gly Lys Phe
145 150 155 160

Thr Thr Ser Leu Thr Asp Tyr Phe Glu Thr Arg Lys Asn Ile Phe Ser
165 170 175

Lys Glu Lys Ile Ser Ser Ala Val Gly Tyr Arg Ile Val Glu Glu Asn
180 185 190

Ala Glu Ile Phe Leu Gln Asn Gln Asn Ala Tyr Asp Arg Ile Cys Lys
195 200 205

Ile Ala Gly Leu Asp Leu His Gly Leu Asp Asn Glu Ile Thr Ala Tyr
210 215 220

Val Asp Gly Lys Thr Leu Lys Glu Val Cys Ser Asp Glu Gly Phe Ala
225 230 235 240

Lys Ala Ile Thr Gln Glu Gly Ile Asp Arg Tyr Asn Glu Ala Ile Gly
245 250 255

Ala Val Asn Gln Tyr Met Asn Leu Leu Cys Gln Lys Asn Lys Ala Leu
260 265 270

Lys Pro Gly Gln Phe Lys Met Lys Arg Leu His Lys Gln Ile Leu Cys
275 280 285

Lys Gly Thr Thr Ser Phe Asp Ile Pro Lys Lys Phe Glu Asn Asp Lys
290 295 300

Gln Val Tyr Asp Ala Val Asn Ser Phe Thr Glu Ile Val Thr Lys Asn
305 310 315 320

Asn Asp Leu Lys Arg Leu Leu Asn Ile Thr Gln Asn Ala Asn Asp Tyr
325 330 335

Asp Met Asn Lys Ile Tyr Val Val Ala Asp Ala Tyr Ser Met Ile Ser
340 345 350

Gln Phe Ile Ser Lys Lys Trp Asn Leu Ile Glu Glu Cys Leu Leu Asp
355 360 365

Tyr Tyr Ser Asp Asn Leu Pro Gly Lys Gly Asn Ala Lys Glu Asn Lys
370 375 380

Val Lys Lys Ala Val Lys Glu Glu Thr Tyr Arg Ser Val Ser Gln Leu
385 390 395 400

Asn Glu Val Ile Glu Lys Tyr Tyr Val Glu Lys Thr Gly Gln Ser Val
405 410 415

Trp Lys Val Glu Ser Tyr Ile Ser Ser Leu Ala Glu Met Ile Lys Leu
420 425 430

Glu Leu Cys His Glu Ile Asp Asn Asp Glu Lys His Asn Leu Ile Glu
435 440 445

Asp Asp Glu Lys Ile Ser Glu Ile Lys Glu Leu Leu Asp Met Tyr Met
450 455 460

Asp Val Phe His Ile Ile Lys Val Phe Arg Val Asn Glu Val Leu Asn
465 470 475 480

Phe Asp Glu Thr Phe Tyr Ser Glu Met Asp Glu Ile Tyr Gln Asp Met
485 490 495

Gln Glu Ile Val Pro Leu Tyr Asn His Val Arg Asn Tyr Val Thr Gln
500 505 510

Lys Pro Tyr Lys Gln Glu Lys Tyr Arg Leu Tyr Phe His Thr Pro Thr
515 520 525

Leu Ala Asn Gly Trp Ser Lys Ser Lys Glu Tyr Asp Asn Asn Ala Ile
530 535 540

Ile Leu Val Arg Glu Asp Lys Tyr Tyr Leu Gly Ile Leu Asn Ala Lys

545 550 555 560

Lys Lys Pro Ser Lys Glu Ile Met Ala Gly Lys Glu Asp Cys Ser Glu
565 570 575

His Ala Tyr Ala Lys Met Asn Tyr Tyr Leu Leu Pro Gly Ala Asn Lys
580 585 590

Met Leu Pro Lys Val Phe Leu Ser Lys Lys Gly Ile Gln Asp Tyr His
595 600 605

Pro Ser Ser Tyr Ile Val Glu Gly Tyr Asn Glu Lys Lys His Ile Lys
610 615 620

Gly Ser Lys Asn Phe Asp Ile Arg Phe Cys Arg Asp Leu Ile Asp Tyr
625 630 635 640

Phe Lys Glu Cys Ile Lys Lys His Pro Asp Trp Asn Lys Phe Asn Phe
645 650 655

Glu Phe Ser Ala Thr Glu Thr Tyr Glu Asp Ile Ser Val Phe Tyr Arg
660 665 670

Glu Val Glu Lys Gln Gly Tyr Arg Val Glu Trp Thr Tyr Ile Asn Ser
675 680 685

Glu Asp Ile Gln Lys Leu Glu Glu Asp Gly Gln Leu Phe Leu Phe Gln
690 695 700

Ile Tyr Asn Lys Asp Phe Ala Val Gly Ser Thr Gly Lys Pro Asn Leu
705 710 715 720

His Thr Leu Tyr Leu Lys Asn Leu Phe Ser Glu Glu Asn Leu Arg Asp
725 730 735

Ile Val Leu Lys Leu Asn Gly Glu Ala Glu Ile Phe Phe Arg Lys Ser
740 745 750

Ser Val Gln Lys Pro Val Ile His Lys Cys Gly Ser Ile Leu Val Asn
755 760 765

Arg Thr Tyr Glu Ile Thr Glu Ser Gly Thr Thr Arg Val Gln Ser Ile
770 775 780

Pro Glu Ser Glu Tyr Met Glu Leu Tyr Arg Tyr Phe Asn Ser Glu Lys
785 790 795 800

Gln Ile Glu Leu Ser Asp Glu Ala Lys Lys Tyr Leu Asp Lys Val Gln
805 810 815

Cys Asn Lys Ala Lys Thr Asp Ile Val Lys Asp Tyr Arg Tyr Thr Met
820 825 830

Asp Lys Phe Phe Ile His Leu Pro Ile Thr Ile Asn Phe Lys Val Asp
835 840 845

Lys Gly Asn Asn Val Asn Ala Ile Ala Gln Gln Tyr Ile Ala Gly Arg
850 855 860

Lys Asp Leu His Val Ile Gly Ile Asp Arg Gly Glu Arg Asn Leu Ile
865 870 875 880

Tyr Val Ser Val Ile Asp Met Tyr Gly Arg Ile Leu Glu Gln Lys Ser
885 890 895

Phe Asn Leu Val Glu Gln Val Ser Ser Gln Gly Thr Lys Arg Tyr Tyr
900 905 910

Asp Tyr Lys Glu Lys Leu Gln Asn Arg Glu Glu Glu Arg Asp Lys Ala
915 920 925

Arg Gln Ser Trp Lys Thr Ile Gly Lys Ile Lys Glu Leu Lys Glu Gly
930 935 940

Tyr Leu Ser Ser Val Ile His Glu Ile Ala Gln Met Val Val Lys Tyr
945 950 955 960

Asn Ala Ile Ile Ala Met Glu Asp Leu Asn Tyr Gly Phe Lys Arg Gly
965 970 975

Arg Phe Lys Val Glu Arg Gln Val Tyr Gln Lys Phe Glu Thr Met Leu
980 985 990

Ile Ser Lys Leu Asn Tyr Leu Ala Asp Lys Ser Gln Ala Val Asp Glu
995 1000 1005

Pro Gly Gly Ile Leu Arg Gly Tyr Gln Met Thr Tyr Val Pro Asp Asn
1010 1015 1020

Ile Lys Asn Val Gly Arg Gln Cys Gly Ile Ile Phe Tyr Val Pro Ala
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Ala Tyr Thr Ser Lys Ile Asp Pro Thr Thr Gly Phe Ile Asn Ala Phe
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Lys Arg Asp Val Val Ser Thr Asn Asp Ala Lys Glu Asn Phe Leu Met
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Lys Phe Asp Ser Ile Gln Tyr Asp Ile Glu Lys Gly Leu Phe Lys Phe
1075 1080 1085

Ser Phe Asp Tyr Lys Asn Phe Ala Thr His Lys Leu Thr Leu Ala Lys
1090 1095 1100

Thr Lys Trp Asp Val Tyr Thr Asn Gly Thr Arg Ile Gln Asn Met Lys
1105 1110 1115 1120

Val Glu Gly His Trp Leu Ser Met Glu Val Glu Leu Thr Thr Lys Met
1125 1130 1135

Lys Glu Leu Leu Asp Asp Ser His Ile Pro Tyr Glu Glu Gly Gln Asn
1140 1145 1150

Ile Leu Asp Asp Leu Arg Glu Met Lys Asp Ile Thr Thr Ile Val Asn
1155 1160 1165

Gly Ile Leu Glu Ile Phe Trp Leu Thr Val Gln Leu Arg Asn Ser Arg
1170 1175 1180

Ile Asp Asn Pro Asp Tyr Asp Arg Ile Ile Ser Pro Val Leu Asn Lys
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Asn Gly Glu Phe Phe Asp Ser Asp Glu Tyr Asn Ser Tyr Ile Asp Ala
1205 1210 1215

Gln Lys Ala Pro Leu Pro Ile Asp Ala Asp Ala Asn Gly Ala Phe Cys
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Ile Ala Leu Lys Gly Met Tyr Thr Ala Asn Gln Ile Lys Glu Asn Trp
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Val Glu Gly Glu Lys Leu Pro Ala Asp Cys Leu Lys Ile Glu His Ala
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Ser Trp Leu Ala Phe Met Gln Gly Glu Arg Gly
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tgcttcactt ttgattataa caatttcatc acccagaaca cagtcatgag taaatctagc 3300

tggtccgtgt acacctatgg ggtacgcatt aagcggcgct ttgtgaatgg ccggttctca 3360

aacgaaagcg acactataga tatcaccaaa gacatggaga agacacttga aatgaccgat 3420

attaattggc gcgacggtca cgatctgcgg caggacatca ttgattacga gatagttcaa 3480

catatctttg aaattttccg cttgactgtc cagatgcgga acagtctgtc tgagctcgaa 3540

gaccgcgatt atgaccggct tatcagccct gtgctgaatg agaacaatat tttttacgat 3600

tccgccaaag ctggcgacgc cttgcccaag gatgcagacg ccaacggagc ttattgtata 3660

gccctgaaag ggctctacga aatcaagcag attaccgaga attggaaaga agatggcaag 3720

ttctcacgcg acaaacttaa gatcagcaac aaagattggt ttgacttcat tcaaaataag 3780

cggtatctg 3789

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<211> 3825
<212> DNA
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<220>
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actgaagatg agatccgcgc ccagaaccgg gaaaagctca aagagatgat ggacgattat 180

taccgcaatg ttattgacag taccccttcac gtcgggatcg ctgtggattg gtcttatctg 240

ttcagctgca tgcggaacca tttgcgcgaa aattccaagg agtcaaaacg ggaactggag 300

cgcacacagg acagcattcg gagtcagata cacaacaagt ttgccgaacg cgcagatttc 360

aaagacatgt ttggcgcctc tatcattacc aagctccttc ctacttacat caaacaaaat 420

agcgagtatt ccgaacggta cgatgagtca atggaaattc tgaagttgta tggtaaattc 480

accacaagcc tgaccgacta ctttgagact cgcaagaaca tattcagtaa agaaaagatc 540

tctagcgctg taggctatcg gattgtggag gaaaatgccg agatctttct ccagaaccag 600

aatgcatacg atcgcatttg taaaatagcc ggacttgacc tgcatgggtt ggataacgaa 660

atcaccgctt atgttgacgg caagacactg aaagaggtct gctccgatga aggtttcgcc 720

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tatatgaatc tcctttgtca gaaaaacaag gccctgaaac ccgggcaatt taagatgaaa 840

cgcttgcaca agcagatact gtgcaaaggc actacctcat tcgatatccc gaagaaattt 900

gagaatgaca agcaggtata cgatgcagtg aacagcttca cagaaattgt taccaaaaat 960

aacgacctca agcggcttct gaatatcact caaaacgcca atgattatga catgaacaaa 1020

atttacgtcg tggctgatgc ctatagtatg atatctcagt ttatcagcaa gaaatggaat 1080

ttgattgagg aatgtctgct cgactactat tccgataacc ttccaggtaa gggcaatgca 1140

aaagagaaca aggtaaaaaa ggccgtgaaa gaagagacct accgctcagt tagccagctg 1200

aatgaagtca tcgagaagta ttacgtggaa aaaacaggac aaagtgtatg gaaggtggag 1260

tcttatatta gctccttggc tgaaatgata aaactggagc tctgccatga aatcgacaac 1320

gatgagaagc acaatcttat tgaagacgat gagaaaatct cagaaattaa ggagctgttg 1380

gacatgtaca tggatgtttt ccatataatc aaagtctttc gggtgaacga agtactgaat 1440

ttcgacgaga cctttttatag cgaaatggat gagatttacc aggacatgca ggaaatcgtg 1500

cccctctata accacgttcg caattacgtc actcaaaagc cgtataaaca ggagaagtac 1560

cggctttatt tccatacccc tacactggcc aacgggtgga gtaaatctaa ggaatacgat 1620

aataacgcaa ttatattggt gcgcgaggac aaatattacc tgggcatcct caatgccaag 1680

aaaaagccca gcaaagaaat tatggctggt aaggaggatt gttccgaaca cgcctatgca 1740

aaaatgaact actatcttct gccgggcgcc aataagatgt tgccaaaagt atttctgtca 1800

aagaaaggaa tccaggacta ccatcccagc agttatattg tggaggggta caacgaaaag 1860

aaacacataa agggctctaa aaatttcgat atccggtttt gccgcgacct cattgattat 1920

ttcaaggagt gtatcaaaaa gcatccggac tggaacaaat ttaatttcga atttagcgct 1980

accgagactt acgaagatat ttccgttttc tatcgggagg tcgaaaagca aggttaccgc 2040

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tttttgttcc aaatttacaa taaggacttt gccgtaggaa gcacagggaa acctaacctg 2160

cacaccctct atcttaagaa tctgttcagt gaggaaaact tgcgggatat cgtgctgaaa 2220

ctcaatggcg aggcagaaat ttttttccgc aagtctagcg ttcagaaacc cgtcatacat 2280

aagtgcggtt ccatccttgt gaaccggact tacgagatta ccgaatcagg cacaacccgc 2340

gtacagagca tcccggagag tgaatatatg gagctgtacc ggtattttaa ttctgaaaaa 2400

caaattgagt tgagcgacga agccaagaaa tacctggata aggtgcagtg taacaaagct 2460

aagactgaca tagttaaaga ttatcgctac accatggaca agttctttat ccacctccca 2520

attacaatca atttcaaagt cgataaggga aacaatgtga acgccattgc acagcaatat 2580

atagccgggc ggaaagacct tcatgtaatc ggcattgatc gcggtgagcg gaatctgatc 2640

tacgtgtccg ttattgacat gtatggccgc atattggaac agaagtcatt taacctggtc 2700

gagcaggtga gcagtcaagg aaccaaacgg tactatgatt acaaggaaaa actccagaat 2760

cgcgaggaag agcgggacaa ggctcgccag tcttggaaaa ctatcgggaa gattaaagaa 2820

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aacgcaataa tcgccatgga ggatttgaat tatggtttca agcggggccg ctttaaagtc 2940

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gacaagagcc aagccgtaga tgaacccgga gggattctgc gcggctacca gatgacatat 3060

gtgccggaca atattaaaaa cgttggtcgg cagtgcggca taatctttta cgtccctgca 3120

gcctatacca gtaagattga tcccactacc ggattcatca atgcttttaa acgcgacgtg 3180

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atagaaaagg ggctgttcaa attttccttc gactataaga actttgcaac ccataaactc 3300

actcttgcca agaccaaatg ggatgtgtac acaaatggca cccggattca gaacatgaag 3360

gttgagggtc actggctgtc aatggaagtc gagttgacta ccaaaatgaa ggaactgctc 3420

gacgatagcc atattccgta tgaggaaggc cagaatatcc ttgacgatct gcgcgagatg 3480

aaagacatta caaccatagt gaacggaatc ttggaaattt tctggctgac tgtacaactc 3540

cggaatagtc gcatcgataa cccagactac gatcggatta tatctcccgt gcttaataag 3600

aacggggagt ttttcgacag cgatgaatat aattcctaca tcgacgctca gaaagccccg 3660

ctgcctattg atgcagacgc caacggcgct ttttgtatcg ccttgaaggg tatgtatacc 3720

gcaaatcaga ttaaagagaa ctgggttgaa ggcgagaagc tgcccgccga ttgcctcaaa 3780

atagaacacg cttcatggct tgccttcatg caaggagagc gcggg 3825

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<212> PRT
<213> Artificial Sequence

<220>
<223> AsCas12a

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Glu Gln Gly Phe Ile Glu Glu Asp Lys Ala Arg Asn Asp His Tyr Lys
35 40 45

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

Cys Leu Gln Leu Val Gln Leu Asp Trp Glu Asn Leu Ser Ala Ala Ile
65 70 75 80

Asp Ser Tyr Arg Lys Glu Lys Thr Glu Glu Thr Arg Asn Ala Leu Ile
85 90 95

Glu Glu Gln Ala Thr Tyr Arg Asn Ala Ile His Asp Tyr Phe Ile Gly
100 105 110

Arg Thr Asp Asn Leu Thr Asp Ala Ile Asn Lys Arg His Ala Glu Ile
115 120 125

Tyr Lys Gly Leu Phe Lys Ala Glu Leu Phe Asn Gly Lys Val Leu Lys
130 135 140

Gln Leu Gly Thr Val Thr Thr Thr Glu His Glu Asn Ala Leu Leu Arg
145 150 155 160

Ser Phe Asp Lys Phe Thr Thr Tyr Phe Ser Gly Phe Tyr Glu Asn Arg
165 170 175

Lys Asn Val Phe Ser Ala Glu Asp Ile Ser Thr Ala Ile Pro His Arg
180 185 190

Ile Val Gln Asp Asn Phe Pro Lys Phe Lys Glu Asn Cys His Ile Phe
195 200 205

Thr Arg Leu Ile Thr Ala Val Pro Ser Leu Arg Glu His Phe Glu Asn
210 215 220

Val Lys Lys Ala Ile Gly Ile Phe Val Ser Thr Ser Ile Glu Glu Val
225 230 235 240

Phe Ser Phe Pro Phe Tyr Asn Gln Leu Leu Thr Gln Thr Gln Ile Asp
245 250 255

Leu Tyr Asn Gln Leu Leu Gly Gly Ile Ser Arg Glu Ala Gly Thr Glu
260 265 270

Lys Ile Lys Gly Leu Asn Glu Val Leu Asn Leu Ala Ile Gln Lys Asn
275 280 285

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

Leu Phe Lys Gln Ile Leu Ser Asp Arg Asn Thr Leu Ser Phe Ile Leu
305 310 315 320

Glu Glu Phe Lys Ser Asp Glu Glu Val Ile Gln Ser Phe Cys Lys Tyr
325 330 335

Lys Thr Leu Leu Arg Asn Glu Asn Val Leu Glu Thr Ala Glu Ala Leu
340 345 350

Phe Asn Glu Leu Asn Ser Ile Asp Leu Thr His Ile Phe Ile Ser His
355 360 365

Lys Lys Leu Glu Thr Ile Ser Ser Ala Leu Cys Asp His Trp Asp Thr
370 375 380

Leu Arg Asn Ala Leu Tyr Glu Arg Arg Ile Ser Glu Leu Thr Gly Lys
385 390 395 400

Ile Thr Lys Ser Ala Lys Glu Lys Val Gln Arg Ser Leu Lys His Glu
405 410 415

Asp Ile Asn Leu Gln Glu Ile Ile Ser Ala Ala Gly Lys Glu Leu Ser
420 425 430

Glu Ala Phe Lys Gln Lys Thr Ser Glu Ile Leu Ser His Ala His Ala
435 440 445

Ala Leu Asp Gln Pro Leu Pro Thr Thr Leu Lys Lys Gln Glu Glu Lys
450 455 460

Glu Ile Leu Lys Ser Gln Leu Asp Ser Leu Leu Gly Leu Tyr His Leu
465 470 475 480

Leu Asp Trp Phe Ala Val Asp Glu Ser Asn Glu Val Asp Pro Glu Phe
485 490 495

Ser Ala Arg Leu Thr Gly Ile Lys Leu Glu Met Glu Pro Ser Leu Ser
500 505 510

Phe Tyr Asn Lys Ala Arg Asn Tyr Ala Thr Lys Lys Pro Tyr Ser Val
515 520 525

Glu Lys Phe Lys Leu Asn Phe Gln Met Pro Thr Leu Ala Ser Gly Trp
530 535 540

Asp Val Asn Lys Glu Lys Asn Asn Gly Ala Ile Leu Phe Val Lys Asn
545 550 555 560

Gly Leu Tyr Tyr Leu Gly Ile Met Pro Lys Gln Lys Gly Arg Tyr Lys
565 570 575

Ala Leu Ser Phe Glu Pro Thr Glu Lys Thr Ser Glu Gly Phe Asp Lys
580 585 590

Met Tyr Tyr Asp Tyr Phe Pro Asp Ala Ala Lys Met Ile Pro Lys Cys
595 600 605

Ser Thr Gln Leu Lys Ala Val Thr Ala His Phe Gln Thr His Thr Thr
610 615 620

Pro Ile Leu Leu Ser Asn Asn Phe Ile Glu Pro Leu Glu Ile Thr Lys

625 630 635 640

Glu Ile Tyr Asp Leu Asn Asn Pro Glu Lys Glu Pro Lys Lys Phe Gln
645 650 655

Thr Ala Tyr Ala Lys Lys Thr Gly Asp Gln Lys Gly Tyr Arg Glu Ala
660 665 670

Leu Cys Lys Trp Ile Asp Phe Thr Arg Asp Phe Leu Ser Lys Tyr Thr
675 680 685

Lys Thr Thr Ser Ile Asp Leu Ser Ser Leu Arg Pro Ser Ser Gln Tyr
690 695 700

Lys Asp Leu Gly Glu Tyr Tyr Ala Glu Leu Asn Pro Leu Leu Tyr His
705 710 715 720

Ile Ser Phe Gln Arg Ile Ala Glu Lys Glu Ile Met Asp Ala Val Glu
725 730 735

Thr Gly Lys Leu Tyr Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ala Lys
740 745 750

Gly His His Gly Lys Pro Asn Leu His Thr Leu Tyr Trp Thr Gly Leu
755 760 765

Phe Ser Pro Glu Asn Leu Ala Lys Thr Ser Ile Lys Leu Asn Gly Gln
770 775 780

Ala Glu Leu Phe Tyr Arg Pro Lys Ser Arg Met Lys Arg Met Ala His
785 790 795 800

Arg Leu Gly Glu Lys Met Leu Asn Lys Lys Leu Lys Asp Gln Lys Thr
805 810 815

Pro Ile Pro Asp Thr Leu Tyr Gln Glu Leu Tyr Asp Tyr Val Asn His
820 825 830

Arg Leu Ser His Asp Leu Ser Asp Glu Ala Arg Ala Leu Leu Pro Asn
835 840 845

Val Ile Thr Lys Glu Val Ser His Glu Ile Ile Lys Asp Arg Arg Phe
850 855 860

Thr Ser Asp Lys Phe Phe Phe His Val Pro Ile Thr Leu Asn Tyr Gln
865 870 875 880

Ala Ala Asn Ser Pro Ser Lys Phe Asn Gln Arg Val Asn Ala Tyr Leu
885 890 895

Lys Glu His Pro Glu Thr Pro Ile Ile Gly Ile Asp Arg Gly Glu Arg
900 905 910

Asn Leu Ile Tyr Ile Thr Val Ile Asp Ser Thr Gly Lys Ile Leu Glu
915 920 925

Gln Arg Ser Leu Asn Thr Ile Gln Gln Phe Asp Tyr Gln Lys Lys Leu
930 935 940

Asp Asn Arg Glu Lys Glu Arg Val Ala Ala Arg Gln Ala Trp Ser Val
945 950 955 960

Val Gly Thr Ile Lys Asp Leu Lys Gln Gly Tyr Leu Ser Gln Val Ile
965 970 975

His Glu Ile Val Asp Leu Met Ile His Tyr Gln Ala Val Val Val Leu
980 985 990

Glu Asn Leu Asn Phe Gly Phe Lys Ser Lys Arg Thr Gly Ile Ala Glu
995 1000 1005

Lys Ala Val Tyr Gln Gln Phe Glu Lys Met Leu Ile Asp Lys Leu Asn
1010 1015 1020

Cys Leu Val Leu Lys Asp Tyr Pro Ala Glu Lys Val Gly Gly Val Leu
1025 1030 1035 1040

Asn Pro Tyr Gln Leu Thr Asp Gln Phe Thr Ser Phe Ala Lys Met Gly
1045 1050 1055

Thr Gln Ser Gly Phe Leu Phe Tyr Val Pro Ala Pro Tyr Thr Ser Lys
1060 1065 1070

Ile Asp Pro Leu Thr Gly Phe Val Asp Pro Phe Val Trp Lys Thr Ile
1075 1080 1085

Lys Asn His Glu Ser Arg Lys His Phe Leu Glu Gly Phe Asp Phe Leu
1090 1095 1100

His Tyr Asp Val Lys Thr Gly Asp Phe Ile Leu His Phe Lys Met Asn
1105 1110 1115 1120

Arg Asn Leu Ser Phe Gln Arg Gly Leu Pro Gly Phe Met Pro Ala Trp
1125 1130 1135

Asp Ile Val Phe Glu Lys Asn Glu Thr Gln Phe Asp Ala Lys Gly Thr
1140 1145 1150

Pro Phe Ile Ala Gly Lys Arg Ile Val Pro Val Ile Glu Asn His Arg
1155 1160 1165

Phe Thr Gly Arg Tyr Arg Asp Leu Tyr Pro Ala Asn Glu Leu Ile Ala
1170 1175 1180

Leu Leu Glu Glu Lys Gly Ile Val Phe Arg Asp Gly Ser Asn Ile Leu
1185 1190 1195 1200

Pro Lys Leu Leu Glu Asn Asp Asp Ser His Ala Ile Asp Thr Met Val
1205 1210 1215

Ala Leu Ile Arg Ser Val Leu Gln Met Arg Asn Ser Asn Ala Ala Thr
1220 1225 1230

Gly Glu Asp Tyr Ile Asn Ser Pro Val Arg Asp Leu Asn Gly Val Cys
1235 1240 1245

Phe Asp Ser Arg Phe Gln Asn Pro Glu Trp Pro Met Asp Ala Asp Ala
1250 1255 1260

Asn Gly Ala Tyr His Ile Ala Leu Lys Gly Gln Leu Leu Leu Asn His
1265 1270 1275 1280

Leu Lys Glu Ser Lys Asp Leu Lys Leu Gln Asn Gly Ile Ser Asn Gln
1285 1290 1295

Asp Trp Leu Ala Tyr Ile Gln Glu Leu Arg Asn
1300 1305

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<213> Artificial Sequence

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Asp Asn Lys Arg Leu Leu Val Glu Asp Glu Lys Arg Ala Glu Asp Tyr
35 40 45

Lys Gly Val Lys Lys Leu Leu Asp Arg Tyr Tyr Leu Ser Phe Ile Asn
50 55 60

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

Leu Phe Arg Lys Lys Thr Arg Thr Glu Lys Glu Asn Lys Glu Leu Glu
85 90 95

Asn Leu Glu Ile Asn Leu Arg Lys Glu Ile Ala Lys Ala Phe Lys Gly
100 105 110

Ala Ala Gly Tyr Lys Ser Leu Phe Lys Lys Asp Ile Ile Glu Thr Ile
115 120 125

Leu Pro Glu Ala Ala Asp Asp Lys Asp Glu Ile Ala Leu Val Asn Ser
130 135 140

Phe Asn Gly Phe Thr Thr Ala Phe Thr Gly Phe Phe Asp Asn Arg Glu
145 150 155 160

Asn Xaa Phe Ser Glu Glu Ala Lys Ser Thr Ser Ile Ala Phe Arg Cys
165 170 175

Ile Asn Glu Asn Leu Thr Arg Tyr Ile Ser Asn Xaa Asp Ile Phe Glu
180 185 190

Lys Val Asp Ala Ile Phe Asp Lys His Glu Val Gln Glu Ile Lys Glu
195 200 205

Lys Ile Leu Asn Ser Asp Tyr Asp Val Glu Asp Phe Phe Glu Gly Glu
210 215 220

Phe Phe Asn Phe Val Leu Thr Gln Glu Gly Ile Asp Val Tyr Asn Ala
225 230 235 240

Ile Ile Gly Gly Phe Val Thr Glu Ser Gly Glu Lys Ile Lys Gly Leu
245 250 255

Asn Glu Tyr Ile Asn Leu Tyr Asn Ala Lys Thr Lys Gln Ala Leu Pro
260 265 270

Lys Phe Lys Pro Leu Tyr Lys Gln Val Leu Ser Asp Arg Glu Ser Leu
275 280 285

Ser Phe Tyr Gly Glu Gly Tyr Thr Ser Asp Glu Glu Val Leu Glu Val
290 295 300

Phe Arg Asn Thr Leu Asn Lys Asn Ser Glu Ile Phe Ser Ser Ile Lys
305 310 315 320

Lys Leu Glu Lys Leu Phe Lys Asn Phe Asp Glu Tyr Ser Ser Ala Gly
325 330 335

Ile Phe Val Lys Asn Gly Pro Ala Ile Ser Thr Ile Ser Lys Asp Ile
340 345 350

Phe Gly Glu Trp Asn Leu Ile Arg Asp Lys Trp Asn Ala Glu Tyr Asp
355 360 365

Asp Ile His Leu Lys Lys Lys Ala Val Val Thr Glu Lys Tyr Glu Asp
370 375 380

Asp Arg Arg Lys Ser Phe Lys Lys Ile Gly Ser Phe Ser Leu Glu Gln
385 390 395 400

Leu Gln Glu Tyr Ala Asp Ala Asp Leu Ser Val Val Glu Lys Leu Lys
405 410 415

Glu Ile Ile Ile Gln Lys Val Asp Glu Ile Tyr Lys Val Tyr Gly Ser
420 425 430

Ser Glu Lys Leu Phe Asp Ala Asp Phe Val Leu Glu Lys Ser Leu Lys
435 440 445

Lys Asn Asp Ala Val Val Ala Ile Xaa Lys Asp Leu Leu Asp Ser Val
450 455 460

Lys Ser Phe Glu Asn Tyr Ile Lys Ala Phe Phe Gly Glu Gly Lys Glu
465 470 475 480

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

Ile Leu Leu Lys Val Asp His Ile Tyr Asp Ala Ile Arg Asn Tyr Val
500 505 510

Thr Gln Lys Pro Tyr Ser Lys Asp Lys Phe Lys Leu Tyr Phe Gln Asn
515 520 525

Pro Gln Phe Xaa Gly Gly Trp Asp Lys Asp Lys Glu Thr Asp Tyr Arg
530 535 540

Ala Thr Ile Leu Arg Tyr Gly Ser Lys Tyr Tyr Leu Ala Ile Xaa Asp
545 550 555 560

Lys Lys Tyr Ala Lys Cys Leu Gln Lys Ile Asp Lys Asp Asp Val Asn
565 570 575

Gly Asn Tyr Glu Lys Ile Asn Tyr Lys Leu Leu Pro Gly Pro Asn Lys
580 585 590

Xaa Leu Pro Lys Val Phe Phe Ser Lys Lys Trp Xaa Ala Tyr Tyr Asn
595 600 605

Pro Ser Glu Asp Ile Gln Lys Ile Tyr Lys Asn Gly Thr Phe Lys Lys
610 615 620

Gly Asp Xaa Phe Asn Leu Asn Asp Cys His Lys Leu Ile Asp Phe Phe
625 630 635 640

Lys Asp Ser Ile Ser Arg Tyr Pro Lys Trp Ser Asn Ala Tyr Asp Phe
645 650 655

Asn Phe Ser Glu Thr Glu Lys Tyr Lys Asp Ile Ala Gly Phe Tyr Arg
660 665 670

Glu Val Glu Glu Gln Gly Tyr Lys Val Ser Phe Glu Ser Ala Ser Lys
675 680 685

Lys Glu Val Asp Lys Leu Val Glu Glu Gly Lys Leu Tyr Xaa Phe Gln
690 695 700

Ile Tyr Asn Lys Asp Phe Ser Asp Lys Ser His Gly Thr Pro Asn Leu

705 710 715 720

His Thr Xaa Tyr Phe Lys Leu Leu Phe Asp Glu Asn Asn His Gly Gln
725 730 735

Ile Arg Leu Ser Gly Gly Ala Glu Leu Phe Xaa Arg Arg Ala Ser Leu
740 745 750

Lys Lys Glu Glu Leu Val Val His Pro Ala Asn Ser Pro Ile Ala Asn
755 760 765

Lys Asn Pro Asp Asn Pro Lys Lys Thr Thr Thr Leu Ser Tyr Asp Val
770 775 780

Tyr Lys Asp Lys Arg Phe Ser Glu Asp Gln Tyr Glu Leu His Ile Pro
785 790 795 800

Ile Ala Ile Asn Lys Cys Pro Lys Asn Ile Phe Lys Ile Asn Thr Glu
805 810 815

Val Arg Val Leu Leu Lys His Asp Asp Asn Pro Tyr Val Ile Gly Ile
820 825 830

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

Gly Asn Ile Val Glu Gln Tyr Ser Leu Asn Glu Ile Ile Asn Asn Phe
850 855 860

Asn Gly Ile Arg Ile Lys Thr Asp Tyr His Ser Leu Leu Asp Lys Lys
865 870 875 880

Glu Lys Glu Arg Phe Glu Ala Arg Gln Asn Trp Thr Ser Ile Glu Asn
885 890 895

Ile Lys Glu Leu Lys Ala Gly Tyr Ile Ser Gln Val Val His Lys Ile
900 905 910

Cys Glu Leu Val Glu Lys Tyr Asp Ala Val Ile Ala Leu Glu Asp Leu
915 920 925

Asn Ser Gly Phe Lys Asn Ser Arg Val Lys Val Glu Lys Gln Val Tyr
930 935 940

Gln Lys Phe Glu Lys Xaa Leu Ile Asp Lys Leu Asn Tyr Xaa Val Asp
945 950 955 960

Lys Lys Ser Asn Pro Cys Ala Thr Gly Gly Ala Leu Lys Gly Tyr Gln
965 970 975

Ile Thr Asn Lys Phe Glu Ser Phe Lys Ser Xaa Ser Thr Gln Asn Gly
980 985 990

Phe Ile Phe Tyr Ile Pro Ala Trp Leu Thr Ser Lys Ile Asp Pro Ser
995 1000 1005

Thr Gly Phe Val Asn Leu Leu Lys Thr Lys Tyr Thr Ser Ile Ala Asp
1010 1015 1020

Ser Lys Lys Phe Ile Ser Ser Phe Asp Arg Ile Xaa Tyr Val Pro Glu
1025 1030 1035 1040

Glu Asp Leu Phe Glu Phe Ala Leu Asp Tyr Lys Asn Phe Ser Arg Thr
1045 1050 1055

Asp Ala Asp Tyr Ile Lys Lys Trp Lys Leu Tyr Ser Tyr Gly Asn Arg
1060 1065 1070

Ile Arg Ile Phe Ala Ala Ala Lys Lys Asn Asn Val Phe Ala Trp Glu
1075 1080 1085

Glu Val Cys Leu Thr Ser Ala Tyr Lys Glu Leu Phe Asn Lys Tyr Gly
1090 1095 1100

Ile Asn Tyr Gln Gln Gly Asp Ile Arg Ala Leu Leu Cys Glu Gln Ser
1105 1110 1115 1120

Asp Lys Ala Phe Tyr Ser Ser Phe Xaa Ala Leu Xaa Ser Leu Xaa Leu
1125 1130 1135

Gln Xaa Arg Asn Ser Ile Thr Gly Arg Thr Asp Val Asp Phe Leu Ile
1140 1145 1150

Ser Pro Val Lys Asn Ser Asp Gly Ile Phe Tyr Asp Ser Arg Asn Tyr
1155 1160 1165

Glu Ala Gln Glu Asn Ala Ile Leu Pro Lys Asn Ala Asp Ala Asn Gly
1170 1175 1180

Ala Tyr Asn Ile Ala Arg Lys Val Leu Trp Ala Ile Gly Gln Phe Lys
1185 1190 1195 1200

Lys Ala Glu Asp Glu Lys Leu Asp Lys Val Lys Ile Ala Ile Ser Asn
1205 1210 1215

Lys Glu Trp Leu Glu Tyr Ala Gln Thr Ser Val Lys
1220 1225

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<213> Artificial Sequence

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Ala Arg Gly Leu Ile Leu Asp Asp Glu Lys Arg Ala Lys Asp Tyr Lys
35 40 45

Lys Ala Lys Gln Ile Ile Asp Lys Tyr His Gln Phe Phe Ile Glu Glu
50 55 60

Ile Leu Ser Ser Val Cys Ile Ser Glu Asp Leu Leu Gln Asn Tyr Ser
65 70 75 80

Asp Val Tyr Phe Lys Leu Lys Lys Ser Asp Asp Asp Asn Leu Gln Lys
85 90 95

Asp Phe Lys Ser Ala Lys Asp Thr Ile Lys Lys Gln Ile Ser Glu Tyr
100 105 110

Ile Lys Asp Ser Glu Lys Phe Lys Asn Leu Phe Asn Gln Asn Leu Ile
115 120 125

Asp Ala Lys Lys Gly Gln Glu Ser Asp Leu Ile Leu Trp Leu Lys Gln
130 135 140

Ser Lys Asp Asn Gly Ile Glu Leu Phe Lys Ala Asn Ser Asp Ile Thr
145 150 155 160

Asp Ile Asp Glu Ala Leu Glu Ile Ile Lys Ser Phe Lys Gly Trp Thr
165 170 175

Thr Tyr Phe Lys Gly Phe His Glu Asn Arg Lys Asn Val Tyr Ser Ser
180 185 190

Asn Asp Ile Pro Thr Ser Ile Ile Tyr Arg Ile Val Asp Asp Asn Leu
195 200 205

Pro Lys Phe Leu Glu Asn Lys Ala Lys Tyr Glu Ser Leu Lys Asp Lys
210 215 220

Ala Pro Glu Ala Ile Asn Tyr Glu Gln Ile Lys Lys Asp Leu Ala Glu
225 230 235 240

Glu Leu Thr Phe Asp Ile Asp Tyr Lys Thr Ser Glu Val Asn Gln Arg
245 250 255

Val Phe Ser Leu Asp Glu Val Phe Glu Ile Ala Asn Phe Asn Asn Tyr
260 265 270

Leu Asn Gln Ser Gly Ile Thr Lys Phe Asn Thr Ile Ile Gly Gly Lys
275 280 285

Phe Val Asn Gly Glu Asn Thr Lys Arg Lys Gly Ile Asn Glu Tyr Ile
290 295 300

Asn Leu Tyr Ser Gln Gln Ile Asn Asp Lys Thr Leu Lys Lys Tyr Lys
305 310 315 320

Met Ser Val Leu Phe Lys Gln Ile Leu Ser Asp Thr Glu Ser Lys Ser
325 330 335

Phe Val Ile Asp Lys Leu Glu Asp Asp Ser Asp Val Val Thr Thr Met
340 345 350

Gln Ser Phe Tyr Glu Gln Ile Ala Ala Phe Lys Thr Val Glu Glu Lys
355 360 365

Ser Ile Lys Glu Thr Leu Ser Leu Leu Phe Asp Asp Leu Lys Ala Gln
370 375 380

Lys Leu Asp Leu Ser Lys Ile Tyr Phe Lys Asn Asp Lys Ser Leu Thr
385 390 395 400

Asp Leu Ser Gln Gln Val Phe Asp Asp Tyr Ser Val Ile Gly Thr Ala
405 410 415

Val Leu Glu Tyr Ile Thr Gln Gln Ile Ala Pro Lys Asn Leu Asp Asn
420 425 430

Pro Ser Lys Lys Glu Gln Glu Leu Ile Ala Lys Lys Thr Glu Lys Ala
435 440 445

Lys Tyr Leu Ser Leu Glu Thr Ile Lys Leu Ala Leu Glu Glu Phe Asn
450 455 460

Lys His Arg Asp Ile Asp Lys Gln Cys Arg Phe Glu Glu Ile Leu Ala
465 470 475 480

Asn Phe Ala Ala Ile Pro Met Ile Phe Asp Glu Ile Ala Gln Asn Lys
485 490 495

Asp Asn Leu Ala Gln Ile Ser Ile Lys Tyr Gln Asn Gln Gly Lys Lys
500 505 510

Asp Leu Leu Gln Ala Ser Ala Glu Asp Asp Val Lys Ala Ile Lys Asp
515 520 525

Leu Leu Asp Gln Thr Asn Asn Leu Leu His Lys Leu Lys Ile Phe His
530 535 540

Ile Ser Gln Ser Glu Asp Lys Ala Asn Ile Leu Asp Lys Asp Glu His
545 550 555 560

Phe Tyr Leu Val Phe Glu Glu Cys Tyr Phe Glu Leu Ala Asn Ile Val
565 570 575

Pro Leu Tyr Asn Lys Ile Arg Asn Tyr Ile Thr Gln Lys Pro Tyr Ser
580 585 590

Asp Glu Lys Phe Lys Leu Asn Phe Glu Asn Ser Thr Leu Ala Asn Gly
595 600 605

Trp Asp Lys Asn Lys Glu Pro Asp Asn Thr Ala Ile Leu Phe Ile Lys
610 615 620

Asp Asp Lys Tyr Tyr Leu Gly Val Met Asn Lys Lys Asn Asn Lys Ile
625 630 635 640

Phe Asp Asp Lys Ala Ile Lys Glu Asn Lys Gly Glu Gly Tyr Lys Lys
645 650 655

Ile Val Tyr Lys Leu Leu Pro Gly Ala Asn Lys Met Leu Pro Lys Val
660 665 670

Phe Phe Ser Ala Lys Ser Ile Lys Phe Tyr Asn Pro Ser Glu Asp Ile
675 680 685

Leu Arg Ile Arg Asn His Ser Thr His Thr Lys Asn Gly Ser Pro Gln
690 695 700

Lys Gly Tyr Glu Lys Phe Glu Phe Asn Ile Glu Asp Cys Arg Lys Phe
705 710 715 720

Ile Asp Phe Tyr Lys Gln Ser Ile Ser Lys His Pro Glu Trp Lys Asp
725 730 735

Phe Gly Phe Arg Phe Ser Asp Thr Gln Arg Tyr Asn Ser Ile Asp Glu
740 745 750

Phe Tyr Arg Glu Val Glu Asn Gln Gly Tyr Lys Leu Thr Phe Glu Asn
755 760 765

Ile Ser Glu Ser Tyr Ile Asp Ser Val Val Asn Gln Gly Lys Leu Tyr
770 775 780

Leu Phe Gln Ile Tyr Asn Lys Asp Phe Ser Ala Tyr Ser Lys Gly Arg
785 790 795 800

Pro Asn Leu His Thr Leu Tyr Trp Lys Ala Leu Phe Asp Glu Arg Asn
805 810 815

Leu Gln Asp Val Val Tyr Lys Leu Asn Gly Glu Ala Glu Leu Phe Tyr
820 825 830

Arg Lys Gln Ser Ile Pro Lys Lys Ile Thr His Pro Ala Lys Glu Ala
835 840 845

Ile Ala Asn Lys Asn Lys Asp Asn Pro Lys Lys Glu Ser Val Phe Glu
850 855 860

Tyr Asp Leu Ile Lys Asp Lys Arg Phe Thr Glu Asp Lys Phe Phe Phe

865 870 875 880

His Cys Pro Ile Thr Ile Asn Phe Lys Ser Ser Gly Ala Asn Lys Phe
885 890 895

Asn Asp Glu Ile Asn Leu Leu Leu Lys Glu Lys Ala Asn Asp Val His
900 905 910

Ile Leu Ser Ile Asp Arg Gly Glu Arg His Leu Ala Tyr Tyr Thr Leu
915 920 925

Val Asp Gly Lys Gly Asn Ile Ile Lys Gln Asp Thr Phe Asn Ile Ile
930 935 940

Gly Asn Asp Arg Met Lys Thr Asn Tyr His Asp Lys Leu Ala Ala Ile
945 950 955 960

Glu Lys Asp Arg Asp Ser Ala Arg Lys Asp Trp Lys Lys Ile Asn Asn
965 970 975

Ile Lys Glu Met Lys Glu Gly Tyr Leu Ser Gln Val Val His Glu Ile
980 985 990

Ala Lys Leu Val Ile Glu Tyr Asn Ala Ile Val Val Phe Glu Asp Leu
995 1000 1005

Asn Phe Gly Phe Lys Arg Gly Arg Phe Lys Val Glu Lys Gln Val Tyr
1010 1015 1020

Gln Lys Leu Glu Lys Met Leu Ile Glu Lys Leu Asn Tyr Leu Val Phe
1025 1030 1035 1040

Lys Asp Asn Glu Phe Asp Lys Thr Gly Gly Val Leu Arg Ala Tyr Gln
1045 1050 1055

Leu Thr Ala Pro Phe Glu Thr Phe Lys Lys Met Gly Lys Gln Thr Gly
1060 1065 1070

Ile Ile Tyr Tyr Val Pro Ala Gly Phe Thr Ser Lys Ile Cys Pro Val
1075 1080 1085

Thr Gly Phe Val Asn Gln Leu Tyr Pro Lys Tyr Glu Ser Val Ser Lys
1090 1095 1100

Ser Gln Glu Phe Phe Ser Lys Phe Asp Lys Ile Cys Tyr Asn Leu Asp
1105 1110 1115 1120

Lys Gly Tyr Phe Glu Phe Ser Phe Asp Tyr Lys Asn Phe Gly Asp Lys
1125 1130 1135

Ala Ala Lys Gly Lys Trp Thr Ile Ala Ser Phe Gly Ser Arg Leu Ile
1140 1145 1150

Asn Phe Arg Asn Ser Asp Lys Asn His Asn Trp Asp Thr Arg Glu Val
1155 1160 1165

Tyr Pro Thr Lys Glu Leu Glu Lys Leu Leu Lys Asp Tyr Ser Ile Glu
1170 1175 1180

Tyr Gly His Gly Glu Cys Ile Lys Ala Ala Ile Cys Gly Glu Ser Asp
1185 1190 1195 1200

Lys Lys Phe Phe Ala Lys Leu Thr Ser Val Leu Asn Thr Ile Leu Gln
1205 1210 1215

Met Arg Asn Ser Lys Thr Gly Thr Glu Leu Asp Tyr Leu Ile Ser Pro
1220 1225 1230

Val Ala Asp Val Asn Gly Asn Phe Phe Asp Ser Arg Gln Ala Pro Lys
1235 1240 1245

Asn Met Pro Gln Asp Ala Asp Ala Asn Gly Ala Tyr His Ile Gly Leu
1250 1255 1260

Lys Gly Leu Met Leu Leu Gly Arg Ile Lys Asn Asn Gln Glu Gly Lys
1265 1270 1275 1280

Lys Leu Asn Leu Val Ile Lys Asn Glu Glu Tyr Phe Glu Phe Val Gln
1285 1290 1295

Asn Arg Asn Asn
1300

<210> 12
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<212> RNA
<213> Artificial Sequence

<220>
<223> 5'-handle RNA

<400> 12
aauuucuacu guuguagau 19

<210> 13
<211> 1263
<212> PRT
<213> Artificial Sequence

<220>
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<400> 13
Met Asn Asn Gly Thr Asn Asn Phe Gln Asn Phe Ile Gly Ile Ser Ser
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Leu Gln Lys Thr Leu Arg Asn Ala Leu Ile Pro Thr Glu Thr Thr Gln
20 25 30

Gln Phe Ile Val Lys Asn Gly Ile Ile Lys Glu Asp Glu Leu Arg Gly
35 40 45

Glu Asn Arg Gln Ile Leu Lys Asp Ile Met Asp Asp Tyr Tyr Arg Gly
50 55 60

Phe Ile Ser Glu Thr Leu Ser Ser Ile Asp Asp Ile Asp Trp Thr Ser
65 70 75 80

Leu Phe Glu Lys Met Glu Ile Gln Leu Lys Asn Gly Asp Asn Lys Asp
85 90 95

Thr Leu Ile Lys Glu Gln Ala Glu Lys Arg Lys Ala Ile Tyr Lys Lys
100 105 110

Phe Ala Asp Asp Asp Arg Phe Lys Asn Met Phe Ser Ala Lys Leu Ile
115 120 125

Ser Asp Ile Leu Pro Glu Phe Val Ile His Asn Asn Asn Tyr Ser Ala
130 135 140

Ser Glu Lys Glu Glu Lys Thr Gln Val Ile Lys Leu Phe Ser Arg Phe
145 150 155 160

Ala Thr Ser Phe Lys Asp Tyr Phe Lys Asn Arg Ala Asn Cys Phe Ser
165 170 175

Ala Asp Asp Ile Ser Ser Ser Ser Cys His Arg Ile Val Asn Asp Asn
180 185 190

Ala Glu Ile Phe Phe Ser Asn Ala Leu Val Tyr Arg Arg Ile Val Lys
195 200 205

Asn Leu Ser Asn Asp Asp Ile Asn Lys Ile Ser Gly Asp Ile Lys Asp
210 215 220

Ser Leu Lys Glu Met Ser Leu Glu Glu Ile Tyr Ser Tyr Glu Lys Tyr
225 230 235 240

Gly Glu Phe Ile Thr Gln Glu Gly Ile Ser Phe Tyr Asn Asp Ile Cys
245 250 255

Gly Lys Val Asn Ser Phe Met Asn Leu Tyr Cys Gln Lys Asn Lys Glu
260 265 270

Asn Lys Asn Leu Tyr Lys Leu Arg Lys Leu His Lys Gln Ile Leu Cys
275 280 285

Ile Ala Asp Thr Ser Tyr Glu Val Pro Tyr Lys Phe Glu Ser Asp Glu
290 295 300

Glu Val Tyr Gln Ser Val Asn Gly Phe Leu Asp Asn Ile Ser Ser Lys
305 310 315 320

His Ile Val Glu Arg Leu Arg Lys Ile Gly Asp Asn Tyr Asn Gly Tyr
325 330 335

Asn Leu Asp Lys Ile Tyr Ile Val Ser Lys Phe Tyr Glu Ser Val Ser
340 345 350

Gln Lys Thr Tyr Arg Asp Trp Glu Thr Ile Asn Thr Ala Leu Glu Ile
355 360 365

His Tyr Asn Asn Ile Leu Pro Gly Asn Gly Lys Ser Lys Ala Asp Lys
370 375 380

Val Lys Lys Ala Val Lys Asn Asp Leu Gln Lys Ser Ile Thr Glu Ile
385 390 395 400

Asn Glu Leu Val Ser Asn Tyr Lys Leu Cys Pro Asp Asp Asn Ile Lys
405 410 415

Ala Glu Thr Tyr Ile His Glu Ile Ser His Ile Leu Asn Asn Phe Glu
420 425 430

Ala Gln Glu Leu Lys Tyr Asn Pro Glu Ile His Leu Val Glu Ser Glu
435 440 445

Leu Lys Ala Ser Glu Leu Lys Asn Val Leu Asp Val Ile Met Asn Ala
450 455 460

Phe His Trp Cys Ser Val Phe Met Thr Glu Glu Leu Val Asp Lys Asp
465 470 475 480

Asn Asn Phe Tyr Ala Glu Leu Glu Glu Ile Tyr Asp Glu Ile Tyr Thr
485 490 495

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

Tyr Ser Thr Lys Lys Ile Lys Leu Asn Phe Gly Ile Pro Thr Leu Ala

515 520 525

Asp Gly Trp Ser Lys Ser Lys Glu Tyr Ser Asn Asn Ala Ile Ile Leu
530 535 540

Met Arg Asp Asn Leu Tyr Tyr Leu Gly Ile Phe Asn Ala Lys Asn Lys
545 550 555 560

Pro Asp Lys Lys Ile Ile Glu Gly Asn Thr Ser Glu Asn Lys Gly Asp
565 570 575

Tyr Lys Lys Met Ile Tyr Asn Leu Leu Pro Gly Pro Asn Lys Met Ile
580 585 590

Pro Lys Val Phe Leu Ser Ser Lys Thr Gly Val Glu Thr Tyr Lys Pro
595 600 605

Ser Ala Tyr Ile Leu Glu Gly Tyr Lys Gln Asn Lys His Leu Lys Ser
610 615 620

Ser Lys Asp Phe Asp Ile Thr Phe Cys His Asp Leu Ile Asp Tyr Phe
625 630 635 640

Lys Asn Cys Ile Ala Ile His Pro Glu Trp Lys Asn Phe Gly Phe Asp
645 650 655

Phe Ser Asp Thr Ser Thr Tyr Glu Asp Ile Ser Gly Phe Tyr Arg Glu
660 665 670

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

Asp Ile Asp Leu Leu Gln Glu Lys Gly Gln Leu Tyr Leu Phe Gln Ile
690 695 700

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

Thr Met Tyr Leu Lys Asn Leu Phe Ser Glu Glu Asn Leu Lys Asp Ile
725 730 735

Val Leu Lys Leu Asn Gly Glu Ala Glu Ile Phe Phe Arg Lys Ser Ser
740 745 750

Ile Lys Asn Pro Ile Ile His Lys Lys Gly Ser Ile Leu Val Asn Arg
755 760 765

Thr Tyr Glu Ala Glu Glu Lys Asp Gln Phe Gly Asn Ile Gln Ile Val
770 775 780

Arg Lys Thr Ile Pro Glu Asn Ile Tyr Gln Glu Leu Tyr Lys Tyr Phe
785 790 795 800

Asn Asp Lys Ser Asp Lys Glu Leu Ser Asp Glu Ala Ala Lys Leu Lys
805 810 815

Asn Val Val Gly His His Glu Ala Ala Thr Asn Ile Val Lys Asp Tyr
820 825 830

Arg Tyr Thr Tyr Asp Lys Tyr Phe Leu His Met Pro Ile Thr Ile Asn
835 840 845

Phe Lys Ala Asn Lys Thr Ser Phe Ile Asn Asp Arg Ile Leu Gln Tyr
850 855 860

Ile Ala Lys Glu Lys Asn Leu His Val Ile Gly Ile Ala Arg Gly Glu
865 870 875 880

Arg Asn Leu Ile Tyr Val Ser Val Ile Asp Thr Cys Gly Asn Ile Val
885 890 895

Glu Gln Lys Ser Phe Asn Ile Val Asn Gly Tyr Asp Tyr Gln Ile Lys
900 905 910

Leu Lys Gln Gln Glu Gly Ala Arg Gln Ile Ala Arg Lys Glu Trp Lys
915 920 925

Glu Ile Gly Lys Ile Lys Glu Ile Lys Glu Gly Tyr Leu Ser Leu Val
930 935 940

Ile His Glu Ile Ser Lys Met Val Ile Lys Tyr Asn Ala Ile Ile Ala
945 950 955 960

Met Glu Asp Leu Ser Tyr Gly Phe Lys Lys Gly Arg Phe Lys Val Glu
965 970 975

Arg Gln Val Tyr Gln Lys Phe Glu Thr Met Leu Ile Asn Lys Leu Asn
980 985 990

Tyr Leu Val Phe Lys Asp Ile Ser Ile Thr Glu Asn Gly Gly Leu Leu
995 1000 1005

Lys Gly Tyr Gln Leu Thr Tyr Ile Pro Asp Lys Leu Lys Asn Val Gly
1010 1015 1020

His Gln Cys Gly Cys Ile Phe Tyr Val Pro Ala Ala Tyr Thr Ser Lys
1025 1030 1035 1040

Ile Asp Pro Thr Thr Gly Phe Val Asn Ile Phe Lys Phe Lys Asp Leu
1045 1050 1055

Thr Val Asp Ala Lys Arg Glu Phe Ile Lys Lys Phe Asp Ser Ile Arg
1060 1065 1070

Tyr Asp Ser Glu Lys Lys Leu Phe Cys Phe Thr Phe Asp Tyr Asn Asn
1075 1080 1085

Phe Ile Thr Gln Asn Thr Val Met Ser Lys Ser Ser Trp Ser Val Tyr
1090 1095 1100

Thr Tyr Gly Val Arg Ile Lys Arg Arg Phe Val Asn Gly Arg Phe Ser
1105 1110 1115 1120

Asn Glu Ser Asp Thr Ile Asp Ile Thr Lys Asp Met Glu Lys Thr Leu
1125 1130 1135

Glu Met Thr Asp Ile Asn Trp Arg Asp Gly His Asp Leu Arg Gln Asp
1140 1145 1150

Ile Ile Asp Tyr Glu Ile Val Gln His Ile Phe Glu Ile Phe Arg Leu
1155 1160 1165

Thr Val Gln Met Arg Asn Ser Leu Ser Glu Leu Glu Asp Arg Asp Tyr
1170 1175 1180

Asp Arg Leu Ile Ser Pro Val Leu Asn Glu Asn Asn Ile Phe Tyr Asp
1185 1190 1195 1200

Ser Ala Lys Ala Gly Asp Ala Leu Pro Lys Asp Ala Asp Ala Asn Gly
1205 1210 1215

Ala Tyr Cys Ile Ala Leu Lys Gly Leu Tyr Glu Ile Lys Gln Ile Thr
1220 1225 1230

Glu Asn Trp Lys Glu Asp Gly Lys Phe Ser Arg Asp Lys Leu Lys Ile
1235 1240 1245

Ser Asn Lys Asp Trp Phe Asp Phe Ile Gln Asn Lys Arg Tyr Leu
1250 1255 1260

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<211> 1275
<212> PRT
<213> Artificial Sequence

<220>
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Gln Lys Thr Leu Arg Asn Glu Leu Ile Pro Thr Glu Thr Thr Lys Lys
20 25 30

Asn Ile Thr Gln Leu Asp Leu Leu Thr Glu Asp Glu Ile Arg Ala Gln
35 40 45

Asn Arg Glu Lys Leu Lys Glu Met Met Asp Asp Tyr Tyr Arg Asn Val
50 55 60

Ile Asp Ser Thr Leu His Val Gly Ile Ala Val Asp Trp Ser Tyr Leu
65 70 75 80

Phe Ser Cys Met Arg Asn His Leu Arg Glu Asn Ser Lys Glu Ser Lys
85 90 95

Arg Glu Leu Glu Arg Thr Gln Asp Ser Ile Arg Ser Gln Ile His Asn
100 105 110

Lys Phe Ala Glu Arg Ala Asp Phe Lys Asp Met Phe Gly Ala Ser Ile
115 120 125

Ile Thr Lys Leu Leu Pro Thr Tyr Ile Lys Gln Asn Ser Glu Tyr Ser
130 135 140

Glu Arg Tyr Asp Glu Ser Met Glu Ile Leu Lys Leu Tyr Gly Lys Phe
145 150 155 160

Thr Thr Ser Leu Thr Asp Tyr Phe Glu Thr Arg Lys Asn Ile Phe Ser
165 170 175

Lys Glu Lys Ile Ser Ser Ala Val Gly Tyr Arg Ile Val Glu Glu Asn
180 185 190

Ala Glu Ile Phe Leu Gln Asn Gln Asn Ala Tyr Asp Arg Ile Cys Lys
195 200 205

Ile Ala Gly Leu Asp Leu His Gly Leu Asp Asn Glu Ile Thr Ala Tyr
210 215 220

Val Asp Gly Lys Thr Leu Lys Glu Val Cys Ser Asp Glu Gly Phe Ala
225 230 235 240

Lys Ala Ile Thr Gln Glu Gly Ile Asp Arg Tyr Asn Glu Ala Ile Gly
245 250 255

Ala Val Asn Gln Tyr Met Asn Leu Leu Cys Gln Lys Asn Lys Ala Leu
260 265 270

Lys Pro Gly Gln Phe Lys Met Lys Arg Leu His Lys Gln Ile Leu Cys
275 280 285

Lys Gly Thr Thr Ser Phe Asp Ile Pro Lys Lys Phe Glu Asn Asp Lys
290 295 300

Gln Val Tyr Asp Ala Val Asn Ser Phe Thr Glu Ile Val Thr Lys Asn
305 310 315 320

Asn Asp Leu Lys Arg Leu Leu Asn Ile Thr Gln Asn Ala Asn Asp Tyr
325 330 335

Asp Met Asn Lys Ile Tyr Val Val Ala Asp Ala Tyr Ser Met Ile Ser
340 345 350

Gln Phe Ile Ser Lys Lys Trp Asn Leu Ile Glu Glu Cys Leu Leu Asp
355 360 365

Tyr Tyr Ser Asp Asn Leu Pro Gly Lys Gly Asn Ala Lys Glu Asn Lys
370 375 380

Val Lys Lys Ala Val Lys Glu Glu Thr Tyr Arg Ser Val Ser Gln Leu
385 390 395 400

Asn Glu Val Ile Glu Lys Tyr Tyr Val Glu Lys Thr Gly Gln Ser Val
405 410 415

Trp Lys Val Glu Ser Tyr Ile Ser Ser Leu Ala Glu Met Ile Lys Leu
420 425 430

Glu Leu Cys His Glu Ile Asp Asn Asp Glu Lys His Asn Leu Ile Glu
435 440 445

Asp Asp Glu Lys Ile Ser Glu Ile Lys Glu Leu Leu Asp Met Tyr Met
450 455 460

Asp Val Phe His Ile Ile Lys Val Phe Arg Val Asn Glu Val Leu Asn
465 470 475 480

Phe Asp Glu Thr Phe Tyr Ser Glu Met Asp Glu Ile Tyr Gln Asp Met
485 490 495

Gln Glu Ile Val Pro Leu Tyr Asn His Val Arg Asn Tyr Val Thr Gln
500 505 510

Lys Pro Tyr Lys Gln Glu Lys Tyr Arg Leu Tyr Phe His Thr Pro Thr
515 520 525

Leu Ala Asn Gly Trp Ser Lys Ser Lys Glu Tyr Asp Asn Asn Ala Ile
530 535 540

Ile Leu Val Arg Glu Asp Lys Tyr Tyr Leu Gly Ile Leu Asn Ala Lys
545 550 555 560

Lys Lys Pro Ser Lys Glu Ile Met Ala Gly Lys Glu Asp Cys Ser Glu
565 570 575

His Ala Tyr Ala Lys Met Asn Tyr Tyr Leu Leu Pro Gly Ala Asn Lys
580 585 590

Met Leu Pro Lys Val Phe Leu Ser Lys Lys Gly Ile Gln Asp Tyr His
595 600 605

Pro Ser Ser Tyr Ile Val Glu Gly Tyr Asn Glu Lys Lys His Ile Lys
610 615 620

Gly Ser Lys Asn Phe Asp Ile Arg Phe Cys Arg Asp Leu Ile Asp Tyr
625 630 635 640

Phe Lys Glu Cys Ile Lys Lys His Pro Asp Trp Asn Lys Phe Asn Phe
645 650 655

Glu Phe Ser Ala Thr Glu Thr Tyr Glu Asp Ile Ser Val Phe Tyr Arg
660 665 670

Glu Val Glu Lys Gln Gly Tyr Arg Val Glu Trp Thr Tyr Ile Asn Ser
675 680 685

Glu Asp Ile Gln Lys Leu Glu Glu Asp Gly Gln Leu Phe Leu Phe Gln
690 695 700

Ile Tyr Asn Lys Asp Phe Ala Val Gly Ser Thr Gly Lys Pro Asn Leu
705 710 715 720

His Thr Leu Tyr Leu Lys Asn Leu Phe Ser Glu Glu Asn Leu Arg Asp
725 730 735

Ile Val Leu Lys Leu Asn Gly Glu Ala Glu Ile Phe Phe Arg Lys Ser
740 745 750

Ser Val Gln Lys Pro Val Ile His Lys Cys Gly Ser Ile Leu Val Asn
755 760 765

Arg Thr Tyr Glu Ile Thr Glu Ser Gly Thr Thr Arg Val Gln Ser Ile
770 775 780

Pro Glu Ser Glu Tyr Met Glu Leu Tyr Arg Tyr Phe Asn Ser Glu Lys
785 790 795 800

Gln Ile Glu Leu Ser Asp Glu Ala Lys Lys Tyr Leu Asp Lys Val Gln
805 810 815

Cys Asn Lys Ala Lys Thr Asp Ile Val Lys Asp Tyr Arg Tyr Thr Met
820 825 830

Asp Lys Phe Phe Ile His Leu Pro Ile Thr Ile Asn Phe Lys Val Asp
835 840 845

Lys Gly Asn Asn Val Asn Ala Ile Ala Gln Gln Tyr Ile Ala Gly Arg
850 855 860

Lys Asp Leu His Val Ile Gly Ile Ala Arg Gly Glu Arg Asn Leu Ile
865 870 875 880

Tyr Val Ser Val Ile Asp Met Tyr Gly Arg Ile Leu Glu Gln Lys Ser
885 890 895

Phe Asn Leu Val Glu Gln Val Ser Ser Gln Gly Thr Lys Arg Tyr Tyr
900 905 910

Asp Tyr Lys Glu Lys Leu Gln Asn Arg Glu Glu Glu Arg Asp Lys Ala
915 920 925

Arg Lys Ser Trp Lys Thr Ile Gly Lys Ile Lys Glu Leu Lys Glu Gly
930 935 940

Tyr Leu Ser Ser Val Ile His Glu Ile Ala Gln Met Val Val Lys Tyr
945 950 955 960

Asn Ala Ile Ile Ala Met Glu Asp Leu Asn Tyr Gly Phe Lys Arg Gly
965 970 975

Arg Phe Lys Val Glu Arg Gln Val Tyr Gln Lys Phe Glu Thr Met Leu
980 985 990

Ile Ser Lys Leu Asn Tyr Leu Ala Asp Lys Ser Gln Ala Val Asp Glu

995 1000 1005

Pro Gly Gly Ile Leu Arg Gly Tyr Gln Met Thr Tyr Val Pro Asp Asn
1010 1015 1020

Ile Lys Asn Val Gly Arg Gln Cys Gly Ile Ile Phe Tyr Val Pro Ala
1025 1030 1035 1040

Ala Tyr Thr Ser Lys Ile Asp Pro Thr Thr Gly Phe Ile Asn Ala Phe
1045 1050 1055

Lys Arg Asp Val Val Ser Thr Asn Asp Ala Lys Glu Asn Phe Leu Met
1060 1065 1070

Lys Phe Asp Ser Ile Gln Tyr Asp Ile Glu Lys Gly Leu Phe Lys Phe
1075 1080 1085

Ser Phe Asp Tyr Lys Asn Phe Ala Thr His Lys Leu Thr Leu Ala Lys
1090 1095 1100

Thr Lys Trp Asp Val Tyr Thr Asn Gly Thr Arg Ile Gln Asn Met Lys
1105 1110 1115 1120

Val Glu Gly His Trp Leu Ser Met Glu Val Glu Leu Thr Thr Lys Met
1125 1130 1135

Lys Glu Leu Leu Asp Asp Ser His Ile Pro Tyr Glu Glu Gly Gln Asn
1140 1145 1150

Ile Leu Asp Asp Leu Arg Glu Met Lys Asp Ile Thr Thr Ile Val Asn
1155 1160 1165

Gly Ile Leu Glu Ile Phe Trp Leu Thr Val Gln Leu Arg Asn Ser Arg
1170 1175 1180

Ile Asp Asn Pro Asp Tyr Asp Arg Ile Ile Ser Pro Val Leu Asn Lys
1185 1190 1195 1200

Asn Gly Glu Phe Phe Asp Ser Asp Glu Tyr Asn Ser Tyr Ile Asp Ala
1205 1210 1215

Gln Lys Ala Pro Leu Pro Ile Asp Ala Asp Ala Asn Gly Ala Phe Cys
1220 1225 1230

Ile Ala Leu Lys Gly Met Tyr Thr Ala Asn Gln Ile Lys Glu Asn Trp
1235 1240 1245

Val Glu Gly Glu Lys Leu Pro Ala Asp Cys Leu Lys Ile Glu His Ala
1250 1255 1260

Ser Trp Leu Ala Phe Met Gln Gly Glu Arg Gly
1265 1270 1275

<210> 15
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> CCR5 Adapter primer sequence (5'-3')

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tcgtcggcag cgtcagatgt gtataagaga cagggtattt ctgttcagat cac 53

<210> 16

<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> CCR5 Adapter primer sequence (5'-3')

<400> 16
gtctcgtggg ctcggagatg tgtataagag acaggcccat caattataga aagcc 55

<210> 17
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> DNMT1 Adapter primer sequence (5'-3')

<400> 17
tcgtcggcag cgtcagatgt gtataagaga cagctgcaca cagcaggcct ttg 53

<210> 18
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> DNMT1 Adapter primer sequence (5'-3')

<400> 18
gtctcgtggg ctcggagatg tgtataagag acagcccaat aagtggcaga gtgc 54

<210> 19
<211> 28
<212> RNA
<213> Artificial Sequence

<220>
<223> NbFTa14_1/2-2 crRNA sequence(PAM site)

<400> 19
tttggataat ttgtactctt gtcgatgt 28

<210> 20
<211> 28
<212> RNA
<213> Artificial Sequence

<220>
<223> NbFTa14_1/2-4 crRNA sequence(PAM site)

<400> 20
tttagtccac aaacagctaa gcccacat 28

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> NGS NbFTa14_1 Forward primer

<400> 21
tgagctgaag atggattatg 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> NGS NbFTa14_1 Reverse primer

<400> 22
tcatgcttaa gataaaagag 20

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> NGS NbFTa14_2 Forward primer

<400> 23
tcatgagctt aagatggatc 20

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> NGS NbFTa14_2 Reverse primer

<400> 24
gtttaagcta aaagaactac 20

<210> 25
<211> 43
<212> RNA
<213> Artificial Sequence

<220>
<223> LsXTb12 crRNA #1

<400> 25
aatttctact aagtgtagat tcttcatcct caattccatc acc 43

<210> 26
<211> 43
<212> RNA
<213> Artificial Sequence

<220>
<223> LsXTb12 crRNA #2

<400> 26
aatttctact aagtgtagat gcaagcctgt aactctggaa gac 43

<210> 27
<211> 1504
<212> DNA
<213> Artificial Sequence

<220>
<223> HsCCR5 Linear DNA

<400> 27
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tcttcattac acctgcagct ctcattttcc atacagtcag tatcaattct ggaagaattt 120
ccagacatta aagatagtca tcttggggct ggtcctgccg ctgcttgtca tggtcatctg 180
ctactcggga atcctaaaaa ctctgcttcg gtgtcgaaat gagaagaaga ggcacagggc 240
tgtgaggctt atcttcacca tcatgattgt ttattttctc ttctgggctc cctacaacat 300
tgtccttctc ctgaacacct tccaggaatt ctttggcctg aataattgca gtagctctaa 360
caggttggac caagctatgc aggtgacaga gactcttggg atgacgcact gctgcatcaa 420
ccccatcatc tatgcctttg tcggggagaa gttcagaaac tacctcttag tcttcttcca 480
aaagcacatt gccaaacgct tctgcaaatg ctgttctatt ttccagcaag aggctcccga 540
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