

SEQUENCE LISTING

<110> Logomix, Inc.
Tokyo Institute of Technology

<120> Genome modification method and genome modification Kit

<130> PL19-9001W0

<150> JP 2020-068266

<151> 2020-04-06

<150> JP 2020-141335

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<160> 73

<170> PatentIn version 3.5

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<211> 1423

<212> PRT

<213> Staphylococcus pyogenes

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Met Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp
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Tyr Lys Asp Asp Asp Asp Lys Met Ala Pro Lys Lys Lys Arg Lys Val
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35 40 45

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

Lys Val Pro Ser Lys Lys Phe Lys Val Leu Gly Asn Thr Asp Arg His
65 70 75 80

Ser Ile Lys Lys Asn Leu Ile Gly Ala Leu Leu Phe Asp Ser Gly Glu
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Thr Ala Glu Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr
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Arg Arg Lys Asn Arg Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu
115 120 125

Met Ala Lys Val Asp Asp Ser Phe Phe His Arg Leu Glu Glu Ser Phe
130 135 140

Leu Val Glu Glu Asp Lys Lys His Glu Arg His Pro Ile Phe Gly Asn
145 150 155 160

Ile Val Asp Glu Val Ala Tyr His Glu Lys Tyr Pro Thr Ile Tyr His
165 170 175

Leu Arg Lys Lys Leu Val Asp Ser Thr Asp Lys Ala Asp Leu Arg Leu
180 185 190

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195 200 205

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210 215 220

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225 230 235 240

Asn Ala Ser Gly Val Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser
245 250 255

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

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

Lys Tyr Lys Glu Ile Phe Phe Asp Gln Ser Lys Asn Gly Tyr Ala Gly
385 390 395 400

Tyr Ile Asp Gly Gly Ala Ser Gln Glu Glu Phe Tyr Lys Phe Ile Lys
405 410 415

Pro Ile Leu Glu Lys Met Asp Gly Thr Glu Glu Leu Leu Val Lys Leu
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Asn Arg Glu Asp Leu Leu Arg Lys Gln Arg Thr Phe Asp Asn Gly Ser
435 440 445

Ile Pro His Gln Ile His Leu Gly Glu Leu His Ala Ile Leu Arg Arg
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465 470 475 480

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

Gly Asn Ser Arg Phe Ala Trp Met Thr Arg Lys Ser Glu Glu Thr Ile
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515 520 525

Ser Phe Ile Glu Arg Met Thr Asn Phe Asp Lys Asn Leu Pro Asn Glu
530 535 540

Lys Val Leu Pro Lys His Ser Leu Leu Tyr Glu Tyr Phe Thr Val Tyr
545 550 555 560

Asn Glu Leu Thr Lys Val Lys Tyr Val Thr Glu Gly Met Arg Lys Pro
565 570 575

Ala Phe Leu Ser Gly Glu Gln Lys Lys Ala Ile Val Asp Leu Leu Phe
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625 630 635 640

Lys Asp Lys Asp Phe Leu Asp Asn Glu Glu Asn Glu Asp Ile Leu Glu
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Glu Arg Leu Lys Thr Tyr Ala His Leu Phe Asp Asp Lys Val Met Lys
675 680 685

Gln Leu Lys Arg Arg Arg Tyr Thr Gly Trp Gly Arg Leu Ser Arg Lys
690 695 700

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705 710 715 720

Phe Leu Lys Ser Asp Gly Phe Ala Asn Arg Asn Phe Met Gln Leu Ile
725 730 735

His Asp Asp Ser Leu Thr Phe Lys Glu Asp Ile Gln Lys Ala Gln Val
740 745 750

Ser Gly Gln Gly Asp Ser Leu His Glu His Ile Ala Asn Leu Ala Gly
755 760 765

Ser Pro Ala Ile Lys Lys Gly Ile Leu Gln Thr Val Lys Val Val Asp
770 775 780

Glu Leu Val Lys Val Met Gly Arg His Lys Pro Glu Asn Ile Val Ile
785 790 795 800

Glu Met Ala Arg Glu Asn Gln Thr Thr Gln Lys Gly Gln Lys Asn Ser
805 810 815

Arg Glu Arg Met Lys Arg Ile Glu Glu Gly Ile Lys Glu Leu Gly Ser
820 825 830

Gln Ile Leu Lys Glu His Pro Val Glu Asn Thr Gln Leu Gln Asn Glu
835 840 845

Lys Leu Tyr Leu Tyr Tyr Leu Gln Asn Gly Arg Asp Met Tyr Val Asp
850 855 860

Gln Glu Leu Asp Ile Asn Arg Leu Ser Asp Tyr Asp Val Asp His Ile
865 870 875 880

Val Pro Gln Ser Phe Leu Lys Asp Asp Ser Ile Asp Asn Lys Val Leu
885 890 895

Thr Arg Ser Asp Lys Asn Arg Gly Lys Ser Asp Asn Val Pro Ser Glu
900 905 910

Glu Val Val Lys Lys Met Lys Asn Tyr Trp Arg Gln Leu Leu Asn Ala
915 920 925

Lys Leu Ile Thr Gln Arg Lys Phe Asp Asn Leu Thr Lys Ala Glu Arg
930 935 940

Gly Gly Leu Ser Glu Leu Asp Lys Ala Gly Phe Ile Lys Arg Gln Leu
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Val Glu Thr Arg Gln Ile Thr Lys His Val Ala Gln Ile Leu Asp Ser
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Arg Met Asn Thr Lys Tyr Asp Glu Asn Asp Lys Leu Ile Arg Glu Val
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995 1000 1005

Phe Gln Phe Tyr Lys Val Arg Glu Ile Asn Asn Tyr His His Ala
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Lys Tyr Pro Lys Leu Glu Ser Glu Phe Val Tyr Gly Asp Tyr Lys
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Val Tyr Asp Val Arg Lys Met Ile Ala Lys Ser Glu Gln Glu Ile
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Gly Lys Ala Thr Ala Lys Tyr Phe Phe Tyr Ser Asn Ile Met Asn
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Phe	Ser	Lys	Glu	Ser	Ile	Leu	Pro	Lys	Arg	Asn	Ser	Asp	Lys	Leu
1145						1150					1155			
Ile	Ala	Arg	Lys	Lys	Asp	Trp	Asp	Pro	Lys	Lys	Tyr	Gly	Gly	Phe
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Asp	Ser	Pro	Thr	Val	Ala	Tyr	Ser	Val	Leu	Val	Val	Ala	Lys	Val
1175						1180					1185			
Glu	Lys	Gly	Lys	Ser	Lys	Lys	Leu	Lys	Ser	Val	Lys	Glu	Leu	Leu
1190						1195					1200			
Gly	Ile	Thr	Ile	Met	Glu	Arg	Ser	Ser	Phe	Glu	Lys	Asn	Pro	Ile
1205						1210					1215			
Asp	Phe	Leu	Glu	Ala	Lys	Gly	Tyr	Lys	Glu	Val	Lys	Lys	Asp	Leu
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Arg	Lys	Arg	Met	Leu	Ala	Ser	Ala	Gly	Glu	Leu	Gln	Lys	Gly	Asn
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Ala Asn Leu Asp Lys Val Leu Ser Ala Tyr Asn Lys His Arg Asp
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Ala Thr Leu Ile His Gln Ser Ile Thr Gly Leu Tyr Glu Thr Arg
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attccccct tgaatttggg cttttatcca tcccatcaca ccctcagcat ctctcctggg	780
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 caggatcagg gaaaggtgag 20

<210> 64
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer for APP 3' junction PCR

<400> 64
 gaacggctac gaaaatccaa 20

<210> 65
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer for APP 3' junction PCR

<400> 65
 ctcttctccc cacccaaaa 19

<210> 66
 <211> 20
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 <213> Artificial Sequence

<220>
 <223> Forward primer for Puromycin 5' junction PCR-4

<400> 66
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<210> 67
 <211> 20
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<220>
 <223> Reverse primer for Puromycin 5' junction PCR-4

<400> 67
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<210> 68
 <211> 19
 <212> DNA
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<220>
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<400> 68
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<210> 69
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<220>
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<400> 69
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<210> 70
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 <220>
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 <220>
 <223> Reverse primer for Blasticidin 5' junction PCR-4

 <400> 71
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 <210> 72
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 <210> 73
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 <212> DNA
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 <220>
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 <400> 73
 ctcttctccc cacccaaaa 19