SEQUENCE LISTING

<110> Poseida Therapeutics
OSTERTAG, Eric
SHEDLOCK, Devon

<120> MODIFIED STEM CELL MEMORY T CELLS, METHODS OF MAKING AND METHODS OF USING SAME

<130> POTH-012/01WO

<150> 62/402,707
<151> 2016-09-30

<150> 62/553,058
<151> 2017-08-31

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<151> 2017-09-08

<150> 62/502,508
<151> 2017-05-05

<160> 42

<170> PatentIn version 3.5

<210> 1
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> FN3 domain consensus sequence

<400> 1

Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp Ser
1 5 10 15

Leu Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe Leu
20 25 30

Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu Thr
35 40 45

Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro Gly
50 55 60

Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val Lys Gly Gly His Arg Ser
65 70 75 80

Asn Pro Leu Ser Ala Glu Phe Thr Thr
85

<210> 2
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> FN3 consensus sequence

<400> 2

Met Leu Pro Ala Pro Lys Asn Leu Val Val Ser Glu Val Thr Glu Asp
1 5 10 15

Ser Leu Arg Leu Ser Trp Thr Ala Pro Asp Ala Ala Phe Asp Ser Phe
20 25 30

Leu Ile Gln Tyr Gln Glu Ser Glu Lys Val Gly Glu Ala Ile Asn Leu
35 40 45

Thr Val Pro Gly Ser Glu Arg Ser Tyr Asp Leu Thr Gly Leu Lys Pro
50 55 60

Gly Thr Glu Tyr Thr Val Ser Ile Tyr Gly Val Lys Gly Gly His Arg
65 70 75 80

Ser Asn Pro Leu Ser Ala Glu Phe Thr Thr
85 90

<210> 3
<211> 270
<212> DNA
<213> Artificial Sequence

<220>
<223> FN3 consensus sequence

<400> 3
atgctgcctg caccaaagaa cctggtggtg tctcatgtga cagaggatag tgccagactg 60

tcatggactg ctcccgacgc agccttcgat agttttatca tcgtgtaccg ggagaacatc 120

gaaaccggcg aggccattgt cctgacagtg ccagggtccg aacgctctta tgacctgaca 180

gatctgaagc ccggaactga gtactatgtg cagatcgccg gcgtcaaagg aggcaatatc 240

agcttccctc tgtccgcaat cttcaccaca 270

<210> 4
<211> 594
<212> PRT
<213> Trichoplusia ni

<400> 4

Met Gly Ser Ser Leu Asp Asp Glu His Ile Leu Ser Ala Leu Leu Gln
1 5 10 15

Ser Asp Asp Glu Leu Val Gly Glu Asp Ser Asp Ser Glu Ile Ser Asp
20 25 30

His Val Ser Glu Asp Asp Val Gln Ser Asp Thr Glu Glu Ala Phe Ile
35 40 45

Asp Glu Val His Glu Val Gln Pro Thr Ser Ser Gly Ser Glu Ile Leu
50 55 60

Asp Glu Gln Asn Val Ile Glu Gln Pro Gly Ser Ser Leu Ala Ser Asn
65 70 75 80

Arg Ile Leu Thr Leu Pro Gln Arg Thr Ile Arg Gly Lys Asn Lys His
85 90 95

Cys Trp Ser Thr Ser Lys Ser Thr Arg Arg Ser Arg Val Ser Ala Leu
100 105 110

Asn Ile Val Arg Ser Gln Arg Gly Pro Thr Arg Met Cys Arg Asn Ile
115 120 125

Tyr Asp Pro Leu Leu Cys Phe Lys Leu Phe Phe Thr Asp Glu Ile Ile
130 135 140

Ser Glu Ile Val Lys Trp Thr Asn Ala Glu Ile Ser Leu Lys Arg Arg
145 150 155 160

Glu Ser Met Thr Gly Ala Thr Phe Arg Asp Thr Asn Glu Asp Glu Ile
165 170 175

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

His Met Ser Thr Asp Asp Leu Phe Asp Arg Ser Leu Ser Met Val Tyr
195 200 205

Val Ser Val Met Ser Arg Asp Arg Phe Asp Phe Leu Ile Arg Cys Leu
210 215 220

Arg Met Asp Asp Lys Ser Ile Arg Pro Thr Leu Arg Glu Asn Asp Val
225 230 235 240

Phe Thr Pro Val Arg Lys Ile Trp Asp Leu Phe Ile His Gln Cys Ile
245 250 255

Gln Asn Tyr Thr Pro Gly Ala His Leu Thr Ile Asp Glu Gln Leu Leu
260 265 270

Gly Phe Arg Gly Arg Cys Pro Phe Arg Met Tyr Ile Pro Asn Lys Pro
275 280 285

Ser Lys Tyr Gly Ile Lys Ile Leu Met Met Cys Asp Ser Gly Tyr Lys
290 295 300

Tyr Met Ile Asn Gly Met Pro Tyr Leu Gly Arg Gly Thr Gln Thr Asn
305 310 315 320

Gly Val Pro Leu Gly Glu Tyr Tyr Val Lys Glu Leu Ser Lys Pro Val
325 330 335

His Gly Ser Cys Arg Asn Ile Thr Cys Asp Asn Trp Phe Thr Ser Ile
340 345 350

Pro Leu Ala Lys Asn Leu Leu Gln Glu Pro Tyr Lys Leu Thr Ile Val
355 360 365

Gly Thr Val Arg Ser Asn Lys Arg Glu Ile Pro Glu Val Leu Lys Asn
370 375 380

Ser Arg Ser Arg Pro Val Gly Thr Ser Met Phe Cys Phe Asp Gly Pro
385 390 395 400

Leu Thr Leu Val Ser Tyr Lys Pro Lys Pro Ala Lys Met Val Tyr Leu
405 410 415

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

Pro Gln Met Val Met Tyr Tyr Asn Gln Thr Lys Gly Gly Val Asp Thr
435 440 445

Leu Asp Gln Met Cys Ser Val Met Thr Cys Ser Arg Lys Thr Asn Arg
450 455 460

Trp Pro Met Ala Leu Leu Tyr Gly Met Ile Asn Ile Ala Cys Ile Asn
465 470 475 480

Ser Phe Ile Ile Tyr Ser His Asn Val Ser Ser Lys Gly Glu Lys Val
485 490 495

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

Ser Phe Met Arg Lys Arg Leu Glu Ala Pro Thr Leu Lys Arg Tyr Leu
515 520 525

Arg Asp Asn Ile Ser Asn Ile Leu Pro Asn Glu Val Pro Gly Thr Ser

530 535 540

Asp Asp Ser Thr Glu Glu Pro Val Met Lys Lys Arg Thr Tyr Cys Thr
545 550 555 560

Tyr Cys Pro Ser Lys Ile Arg Arg Lys Ala Asn Ala Ser Cys Lys Lys
565 570 575

Cys Lys Lys Val Ile Cys Arg Glu His Asn Ile Asp Met Cys Gln Ser
580 585 590

Cys Phe

<210> 5
<211> 594
<212> PRT
<213> Artificial Sequence

<220>
<223> Super Piggybac Transposase

<400> 5

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1 5 10 15

Ser Asp Asp Glu Leu Val Gly Glu Asp Ser Asp Ser Glu Val Ser Asp
20 25 30

His Val Ser Glu Asp Asp Val Gln Ser Asp Thr Glu Glu Ala Phe Ile
35 40 45

Asp Glu Val His Glu Val Gln Pro Thr Ser Ser Gly Ser Glu Ile Leu
50 55 60

Asp Glu Gln Asn Val Ile Glu Gln Pro Gly Ser Ser Leu Ala Ser Asn
65 70 75 80

Arg Ile Leu Thr Leu Pro Gln Arg Thr Ile Arg Gly Lys Asn Lys His
85 90 95

Cys Trp Ser Thr Ser Lys Ser Thr Arg Arg Ser Arg Val Ser Ala Leu
100 105 110

Asn Ile Val Arg Ser Gln Arg Gly Pro Thr Arg Met Cys Arg Asn Ile
115 120 125

Tyr Asp Pro Leu Leu Cys Phe Lys Leu Phe Phe Thr Asp Glu Ile Ile
130 135 140

Ser Glu Ile Val Lys Trp Thr Asn Ala Glu Ile Ser Leu Lys Arg Arg
145 150 155 160

Glu Ser Met Thr Ser Ala Thr Phe Arg Asp Thr Asn Glu Asp Glu Ile
165 170 175

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

His Met Ser Thr Asp Asp Leu Phe Asp Arg Ser Leu Ser Met Val Tyr
195 200 205

Val Ser Val Met Ser Arg Asp Arg Phe Asp Phe Leu Ile Arg Cys Leu
210 215 220

Arg Met Asp Asp Lys Ser Ile Arg Pro Thr Leu Arg Glu Asn Asp Val
225 230 235 240

Phe Thr Pro Val Arg Lys Ile Trp Asp Leu Phe Ile His Gln Cys Ile
245 250 255

Gln Asn Tyr Thr Pro Gly Ala His Leu Thr Ile Asp Glu Gln Leu Leu
260 265 270

Gly Phe Arg Gly Arg Cys Pro Phe Arg Val Tyr Ile Pro Asn Lys Pro
275 280 285

Ser Lys Tyr Gly Ile Lys Ile Leu Met Met Cys Asp Ser Gly Thr Lys

290 295 300

Tyr Met Ile Asn Gly Met Pro Tyr Leu Gly Arg Gly Thr Gln Thr Asn
305 310 315 320

Gly Val Pro Leu Gly Glu Tyr Tyr Val Lys Glu Leu Ser Lys Pro Val
325 330 335

His Gly Ser Cys Arg Asn Ile Thr Cys Asp Asn Trp Phe Thr Ser Ile
340 345 350

Pro Leu Ala Lys Asn Leu Leu Gln Glu Pro Tyr Lys Leu Thr Ile Val
355 360 365

Gly Thr Val Arg Ser Asn Lys Arg Glu Ile Pro Glu Val Leu Lys Asn
370 375 380

Ser Arg Ser Arg Pro Val Gly Thr Ser Met Phe Cys Phe Asp Gly Pro
385 390 395 400

Leu Thr Leu Val Ser Tyr Lys Pro Lys Pro Ala Lys Met Val Tyr Leu
405 410 415

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

Pro Gln Met Val Met Tyr Tyr Asn Gln Thr Lys Gly Gly Val Asp Thr
435 440 445

Leu Asp Gln Met Cys Ser Val Met Thr Cys Ser Arg Lys Thr Asn Arg
450 455 460

Trp Pro Met Ala Leu Leu Tyr Gly Met Ile Asn Ile Ala Cys Ile Asn
465 470 475 480

Ser Phe Ile Ile Tyr Ser His Asn Val Ser Ser Lys Gly Glu Lys Val
485 490 495

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

Ser Phe Met Arg Lys Arg Leu Glu Ala Pro Thr Leu Lys Arg Tyr Leu
515 520 525

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

Asp Asp Ser Thr Glu Glu Pro Val Met Lys Lys Arg Thr Tyr Cys Thr
545 550 555 560

Tyr Cys Pro Ser Lys Ile Arg Arg Lys Ala Asn Ala Ser Cys Lys Lys
565 570 575

Cys Lys Lys Val Ile Cys Arg Glu His Asn Ile Asp Met Cys Gln Ser
580 585 590

Cys Phe

<210> 6
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> Sleeping Beauty Transposase

<400> 6

Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Lys Ile Val
1 5 10 15

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
20 25 30

Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
35 40 45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Tyr Leu

50 55 60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
65 70 75 80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
85 90 95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
100 105 110

Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
115 120 125

Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
130 135 140

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
145 150 155 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
165 170 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
180 185 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
195 200 205

Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
210 215 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225 230 235 240

Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
245 250 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
260 265 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
275 280 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
290 295 300

Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
305 310 315 320

Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
325 330 335

Ala Thr Lys Tyr
340

<210> 7
<211> 340
<212> PRT
<213> Artificial Sequence

<220>
<223> hyperactive sleeping beauty transposase

<400> 7

Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Arg Ile Val
1 5 10 15

Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
20 25 30

Ala Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
35 40 45

His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Tyr Leu
50 55 60

Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro

65 70 75 80

Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
85 90 95

Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
100 105 110

Lys Gly His Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
115 120 125

Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
130 135 140

Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
145 150 155 160

Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
165 170 175

Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
180 185 190

Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
195 200 205

Ile Asp Gly Ile Met Asp Ala Val Gln Tyr Val Asp Ile Leu Lys Gln
210 215 220

His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
225 230 235 240

Phe Gln His Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
245 250 255

Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
260 265 270

Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
275 280 285

Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
290 295 300

Gln Glu Glu Trp Ala Lys Ile His Pro Asn Tyr Cys Gly Lys Leu Val
305 310 315 320

Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
325 330 335

Ala Thr Lys Tyr
340

<210> 8
<211> 21
<212> PRT
<213> Homo sapiens

<400> 8

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro
20

<210> 9
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence for human CD8alpha signal peptide

<400> 9
atggcactgc cagtcaccgc cctgctgctg cctctggctc tgctgctgca cgcagctaga 60

cca 63

<210> 10
<211> 24

<212> PRT
<213> Homo sapiens

<400> 10

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr Leu Tyr Cys
20

<210> 11
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence coding for human CD8alpha transmembrane domain

<400> 11
atctacattt gggcaccact ggccgggacc tgtggagtgc tgctgctgag cctggtcatc 60

acactgtact gc 72

<210> 12
<211> 112
<212> PRT
<213> Homo sapiens

<400> 12

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Lys Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 13
<211> 336
<212> DNA
<213> Artificial Sequenec

<220>
<223> nucleotide sequence encoding the CD28 costimulatory domain

<400> 13
cgcgtgaagt ttagtcgatc agcagatgcc ccagcttaca aacagggaca gaaccagctg 60

tataacgagc tgaatctggg ccgccgagag gaatatgacg tgctggataa gcggagagga 120

cgcgaccccg aaatgggagg caagcccagg cgcaaaaacc ctcaggaagg cctgtataac 180

gagctgcaga aggacaaaat ggcagaagcc tattctgaga tcggcatgaa gggggagcga 240

cggagaggca aagggcacga tgggctgtac cagggactga gcaccgccac aaaggacacc 300

tatgatgctc tgcatatgca ggcactgcct ccaagg 336

<210> 14
<211> 42
<212> PRT
<213> Homo sapiens

<400> 14

Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
20 25 30

Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
35 40

<210> 15
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding the 4-1BB costimulatory domain

<400> 15
aagagaggca ggaagaaact gctgtatatt ttcaaacagc ccttcatgcg ccccgtgcag 60

actacccagg aggaagacgg gtgctcctgt cgattccctg aggaagagga aggcgggtgt 120

gagctg 126

<210> 16
<211> 45
<212> PRT
<213> Homo sapiens

<400> 16

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 17
<211> 135
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotide sequence encoding human CD8alpha hinge

<400> 17
actaccacac cagcacctag accaccaact ccagctccaa ccatcgcgag tcagcccctg 60

agtctgagac ctgaggcctg caggccagct gcaggaggag ctgtgcacac caggggcctg 120

gacttcgcct gcgac 135

<210> 18
<211> 18
<212> PRT
<213> Thosea asigna

<400> 18

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

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

<220>
<223> GSG-T2A

<400> 19

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15

Glu Asn Pro Gly Pro
20

<210> 20
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> GSG-T2A

<400> 20
ggatctggag agggaagggg aagcctgctg acctgtggag acgtggagga aaacccagga 60

cca 63

<210> 21
<211> 20

<212> PRT
<213> Equine rhinitis A

<400> 21

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 22
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> GSG-E2A peptide

<400> 22

Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1 5 10 15

Val Glu Ser Asn Pro Gly Pro
20

<210> 23
<211> 22
<212> PRT
<213> Foot and nout disease virus type O

<400> 23

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 24
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> GSG-F2A peptide

<400> 24

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15

Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 25
<211> 19
<212> PRT
<213> Porcine teschovirus-1

<400> 25

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 26
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> GSG-P2A peptide

<400> 26

Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
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<210> 27
<211> 5296
<212> DNA
<213> Artificial Sequence

<220>
<223> Helraiser transposon

<400> 27
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gcatacgcag gtgtcaagcg ccccaggagg caacggcggc cgcgggctcc caggaccttc 180

gctggccccg ggaggcgagg ccggccgcgc ctagccacac ccgcgggctc ccgggacctt 240

cgccagcaga gagcagagcg ggagagcggg cggagagcgg gaggtttgga ggacttggca 300

gagcaggagg ccgctggaca tagagcagag cgagagagag ggtggcttgg agggcgtggc 360

tccctctgtc accccagctt cctcatcaca gctgtggaaa ctgacagcag ggaggaggaa 420

gtcccacccc cacagaatca gccagaatca gccgttggtc agacagctct cagcggcctg 480

acagccagga ctctcattca cctgcatctc agaccgtgac agtagagagg tgggactatg 540

tctaaagaac aactgttgat acaacgtagc tctgcagccg aaagatgccg gcgttatcga 600

cagaaaatgt ctgcagagca acgtgcgtct gatcttgaaa gaaggcggcg cctgcaacag 660

aatgtatctg aagagcagct actggaaaaa cgtcgctctg aagccgaaaa acagcggcgt 720

catcgacaga aaatgtctaa agaccaacgt gcctttgaag ttgaaagaag gcggtggcga 780

cgacagaata tgtctagaga acagtcatca acaagtacta ccaataccgg taggaactgc 840

cttctcagca aaaatggagt acatgaggat gcaattctcg aacatagttg tggtggaatg 900

actgttcgat gtgaattttg cctatcacta aatttctctg atgaaaaacc atccgatggg 960

aaatttactc gatgttgtag caaagggaaa gtctgtccaa atgatataca ttttccagat 1020

tacccggcat atttaaaaag attaatgaca aacgaagatt ctgacagtaa aaatttcatg 1080

gaaaatattc gttccataaa tagttctttt gcttttgctt ccatgggtgc aaatattgca 1140

tcgccatcag gatatgggcc atactgtttt agaatacacg gacaagttta tcaccgtact 1200

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ctcatgatca acatcaacaa cctcatgcat gaaataaatg aattaacaaa atcgtacaag 1380

atgctacatg aggtagaaaa ggaagcccaa tctgaagcag cagcaaaagg tattgctccc 1440

acagaagtaa caatggcgat taaatacgat cgtaacagtg acccaggtag atataattct 1500

ccccgtgtaa ccgaggttgc tgtcatattc agaaacgaag atggagaacc tccttttgaa 1560

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caaatcagta tcctgtttcc tacattagat gcaatgacat atcctattct ttttccacat 1680

ggtgaaaaag gctggggaac agatattgca ttaagactca gagacaacag tgtaatcgac 1740

aataatacta gacaaaatgt aaggacacga gtcacacaaa tgcagtatta tggatttcat 1800

ctctctgtgc gggacacgtt caatcctatt ttaaatgcag gaaaattaac tcaacagttt 1860

attgtggatt catattcaaa aatggaggcc aatcggataa atttcatcaa agcaaaccaa 1920

tctaagttga gagttgaaaa atatagtggt ttgatggatt atctcaaatc tagatctgaa 1980

aatgacaatg tgccgattgg taaaatgata atacttccat catcttttga gggtagtccc 2040

agaaatatgc agcagcgata tcaggatgct atggcaattg taacgaagta tggcaagccc 2100

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agatctggta gcaccatgtc tattggaaat aaagttgtcg ataacacttg gattgtccct 2640

tataacccgt atttgtgcct taaatataac tgtcatataa atgttgaagt ctgtgcatca 2700

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ttcttattga atagagaaga ttctgatgca cgtaattatt attattggga gattccacag 3060

cattatgtgt ttaataattc tttgtggaca aaacgccgaa agggtgggaa taaagtatta 3120

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35 40 45

Leu Glu Lys Arg Arg Ser Glu Ala Glu Lys Gln Arg Arg His Arg Gln
50 55 60

Lys Met Ser Lys Asp Gln Arg Ala Phe Glu Val Glu Arg Arg Arg Trp
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Arg Arg Gln Asn Met Ser Arg Glu Gln Ser Ser Thr Ser Thr Thr Asn
85 90 95

Thr Gly Arg Asn Cys Leu Leu Ser Lys Asn Gly Val His Glu Asp Ala
100 105 110

Ile Leu Glu His Ser Cys Gly Gly Met Thr Val Arg Cys Glu Phe Cys
115 120 125

Leu Ser Leu Asn Phe Ser Asp Glu Lys Pro Ser Asp Gly Lys Phe Thr
130 135 140

Arg Cys Cys Ser Lys Gly Lys Val Cys Pro Asn Asp Ile His Phe Pro
145 150 155 160

Asp Tyr Pro Ala Tyr Leu Lys Arg Leu Met Thr Asn Glu Asp Ser Asp
165 170 175

Ser Lys Asn Phe Met Glu Asn Ile Arg Ser Ile Asn Ser Ser Phe Ala
180 185 190

Phe Ala Ser Met Gly Ala Asn Ile Ala Ser Pro Ser Gly Tyr Gly Pro
195 200 205

Tyr Cys Phe Arg Ile His Gly Gln Val Tyr His Arg Thr Gly Thr Leu
210 215 220

His Pro Ser Asp Gly Val Ser Arg Lys Phe Ala Gln Leu Tyr Ile Leu
225 230 235 240

Asp Thr Ala Glu Ala Thr Ser Lys Arg Leu Ala Met Pro Glu Asn Gln
245 250 255

Gly Cys Ser Glu Arg Leu Met Ile Asn Ile Asn Asn Leu Met His Glu
260 265 270

Ile Asn Glu Leu Thr Lys Ser Tyr Lys Met Leu His Glu Val Glu Lys
275 280 285

Glu Ala Gln Ser Glu Ala Ala Ala Lys Gly Ile Ala Pro Thr Glu Val
290 295 300

Thr Met Ala Ile Lys Tyr Asp Arg Asn Ser Asp Pro Gly Arg Tyr Asn
305 310 315 320

Ser Pro Arg Val Thr Glu Val Ala Val Ile Phe Arg Asn Glu Asp Gly
325 330 335

Glu Pro Pro Phe Glu Arg Asp Leu Leu Ile His Cys Lys Pro Asp Pro
340 345 350

Asn Asn Pro Asn Ala Thr Lys Met Lys Gln Ile Ser Ile Leu Phe Pro
355 360 365

Thr Leu Asp Ala Met Thr Tyr Pro Ile Leu Phe Pro His Gly Glu Lys
370 375 380

Gly Trp Gly Thr Asp Ile Ala Leu Arg Leu Arg Asp Asn Ser Val Ile
385 390 395 400

Asp Asn Asn Thr Arg Gln Asn Val Arg Thr Arg Val Thr Gln Met Gln
405 410 415

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

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

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Arg Val Glu Lys Tyr Ser Gly Leu Met Asp Tyr Leu Lys Ser Arg Ser
465 470 475 480

Glu Asn Asp Asn Val Pro Ile Gly Lys Met Ile Ile Leu Pro Ser Ser
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Phe Glu Gly Ser Pro Arg Asn Met Gln Gln Arg Tyr Gln Asp Ala Met
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Ala Ile Val Thr Lys Tyr Gly Lys Pro Asp Leu Phe Ile Thr Met Thr
515 520 525

Cys Asn Pro Lys Trp Ala Asp Ile Thr Asn Asn Leu Gln Arg Trp Gln
530 535 540

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

Leu Asn Ala Leu Leu Asn Asp Ile Cys Lys Phe His Leu Phe Gly Lys
565 570 575

Val Ile Ala Lys Ile His Val Ile Glu Phe Gln Lys Arg Gly Leu Pro
580 585 590

His Ala His Ile Leu Leu Ile Leu Asp Ser Glu Ser Lys Leu Arg Ser
595 600 605

Glu Asp Asp Ile Asp Arg Ile Val Lys Ala Glu Ile Pro Asp Glu Asp
610 615 620

Gln Cys Pro Arg Leu Phe Gln Ile Val Lys Ser Asn Met Val His Gly
625 630 635 640

Pro Cys Gly Ile Gln Asn Pro Asn Ser Pro Cys Met Glu Asn Gly Lys
645 650 655

Cys Ser Lys Gly Tyr Pro Lys Glu Phe Gln Asn Ala Thr Ile Gly Asn
660 665 670

Ile Asp Gly Tyr Pro Lys Tyr Lys Arg Arg Ser Gly Ser Thr Met Ser
675 680 685

Ile Gly Asn Lys Val Val Asp Asn Thr Trp Ile Val Pro Tyr Asn Pro
690 695 700

Tyr Leu Cys Leu Lys Tyr Asn Cys His Ile Asn Val Glu Val Cys Ala
705 710 715 720

Ser Ile Lys Ser Val Lys Tyr Leu Phe Lys Tyr Ile Tyr Lys Gly His
725 730 735

Asp Cys Ala Asn Ile Gln Ile Ser Glu Lys Asn Ile Ile Asn His Asp
740 745 750

Glu Val Gln Asp Phe Ile Asp Ser Arg Tyr Val Ser Ala Pro Glu Ala
755 760 765

Val Trp Arg Leu Phe Ala Met Arg Met His Asp Gln Ser His Ala Ile
770 775 780

Thr Arg Leu Ala Ile His Leu Pro Asn Asp Gln Asn Leu Tyr Phe His
785 790 795 800

Thr Asp Asp Phe Ala Glu Val Leu Asp Arg Ala Lys Arg His Asn Ser
805 810 815

Thr Leu Met Ala Trp Phe Leu Leu Asn Arg Glu Asp Ser Asp Ala Arg
820 825 830

Asn Tyr Tyr Tyr Trp Glu Ile Pro Gln His Tyr Val Phe Asn Asn Ser
835 840 845

Leu Trp Thr Lys Arg Arg Lys Gly Gly Asn Lys Val Leu Gly Arg Leu
850 855 860

Phe Thr Val Ser Phe Arg Glu Pro Glu Arg Tyr Tyr Leu Arg Leu Leu
865 870 875 880

Leu Leu His Val Lys Gly Ala Ile Ser Phe Glu Asp Leu Arg Thr Val
885 890 895

Gly Gly Val Thr Tyr Asp Thr Phe His Glu Ala Ala Lys His Arg Gly
900 905 910

Leu Leu Leu Asp Asp Thr Ile Trp Lys Asp Thr Ile Asp Asp Ala Ile
915 920 925

Ile Leu Asn Met Pro Lys Gln Leu Arg Gln Leu Phe Ala Tyr Ile Cys
930 935 940

Val Phe Gly Cys Pro Ser Ala Ala Asp Lys Leu Trp Asp Glu Asn Lys
945 950 955 960

Ser His Phe Ile Glu Asp Phe Cys Trp Lys Leu His Arg Arg Glu Gly
965 970 975

Ala Cys Val Asn Cys Glu Met His Ala Leu Asn Glu Ile Gln Glu Val
980 985 990

Phe Thr Leu His Gly Met Lys Cys Ser His Phe Lys Leu Pro Asp Tyr
995 1000 1005

Pro Leu Leu Met Asn Ala Asn Thr Cys Asp Gln Leu Tyr Glu Gln
1010 1015 1020

Gln Gln Ala Glu Val Leu Ile Asn Ser Leu Asn Asp Glu Gln Leu
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Ala Ala Phe Gln Thr Ile Thr Ser Ala Ile Glu Asp Gln Thr Val
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His Pro Lys Cys Phe Phe Leu Asp Gly Pro Gly Gly Ser Gly Lys
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Thr Tyr Leu Tyr Lys Val Leu Thr His Tyr Ile Arg Gly Arg Gly
1070 1075 1080

Gly Thr Val Leu Pro Thr Ala Ser Thr Gly Ile Ala Ala Asn Leu
1085 1090 1095

Leu Leu Gly Gly Arg Thr Phe His Ser Gln Tyr Lys Leu Pro Ile
1100 1105 1110

Pro Leu Asn Glu Thr Ser Ile Ser Arg Leu Asp Ile Lys Ser Glu
1115 1120 1125

Val Ala Lys Thr Ile Lys Lys Ala Gln Leu Leu Ile Ile Asp Glu
1130 1135 1140

Cys Thr Met Ala Ser Ser His Ala Ile Asn Ala Ile Asp Arg Leu
1145 1150 1155

Leu Arg Glu Ile Met Asn Leu Asn Val Ala Phe Gly Gly Lys Val
1160 1165 1170

Leu Leu Leu Gly Gly Asp Phe Arg Gln Cys Leu Ser Ile Val Pro
1175 1180 1185

His Ala Met Arg Ser Ala Ile Val Gln Thr Ser Leu Lys Tyr Cys
1190 1195 1200

Asn Val Trp Gly Cys Phe Arg Lys Leu Ser Leu Lys Thr Asn Met
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Arg Ser Glu Asp Ser Ala Tyr Ser Glu Trp Leu Val Lys Leu Gly
1220 1225 1230

Asp Gly Lys Leu Asp Ser Ser Phe His Leu Gly Met Asp Ile Ile
1235 1240 1245

Glu Ile Pro His Glu Met Ile Cys Asn Gly Ser Ile Ile Glu Ala

1250 1255 1260

Thr Phe Gly Asn Ser Ile Ser Ile Asp Asn Ile Lys Asn Ile Ser
1265 1270 1275

Lys Arg Ala Ile Leu Cys Pro Lys Asn Glu His Val Gln Lys Leu
1280 1285 1290

Asn Glu Glu Ile Leu Asp Ile Leu Asp Gly Asp Phe His Thr Tyr
1295 1300 1305

Leu Ser Asp Asp Ser Ile Asp Ser Thr Asp Asp Ala Glu Lys Glu
1310 1315 1320

Asn Phe Pro Ile Glu Phe Leu Asn Ser Ile Thr Pro Ser Gly Met
1325 1330 1335

Pro Cys His Lys Leu Lys Leu Lys Val Gly Ala Ile Ile Met Leu
1340 1345 1350

Leu Arg Asn Leu Asn Ser Lys Trp Gly Leu Cys Asn Gly Thr Arg
1355 1360 1365

Phe Ile Ile Lys Arg Leu Arg Pro Asn Ile Ile Glu Ala Glu Val
1370 1375 1380

Leu Thr Gly Ser Ala Glu Gly Glu Val Val Leu Ile Pro Arg Ile
1385 1390 1395

Asp Leu Ser Pro Ser Asp Thr Gly Leu Pro Phe Lys Leu Ile Arg
1400 1405 1410

Arg Gln Phe Pro Val Met Pro Ala Phe Ala Met Thr Ile Asn Lys
1415 1420 1425

Ser Gln Gly Gln Thr Leu Asp Arg Val Gly Ile Phe Leu Pro Glu
1430 1435 1440

Pro Val Phe Ala His Gly Gln Leu Tyr Val Ala Phe Ser Arg Val
1445 1450 1455

Arg Arg Ala Cys Asp Val Lys Val Lys Val Val Asn Thr Ser Ser
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Gln Gly Lys Leu Val Lys His Ser Glu Ser Val Phe Thr Leu Asn
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Val Val Tyr Arg Glu Ile Leu Glu
1490 1495

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<213> Oryzias latipes

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Asn Gln Pro Gln Asp Gln Glu His Pro Trp Pro Tyr Leu Arg Glu Phe
20 25 30

Phe Ser Leu Ser Gly Val Asn Lys Asp Ser Phe Lys Met Lys Cys Val
35 40 45

Leu Cys Leu Pro Leu Asn Lys Glu Ile Ser Ala Phe Lys Ser Ser Pro
50 55 60

Ser Asn Leu Arg Lys His Ile Glu Arg Met His Pro Asn Tyr Leu Lys
65 70 75 80

Asn Tyr Ser Lys Leu Thr Ala Gln Lys Arg Lys Ile Gly Thr Ser Thr
85 90 95

His Ala Ser Ser Ser Lys Gln Leu Lys Val Asp Ser Val Phe Pro Val
100 105 110

Lys His Val Ser Pro Val Thr Val Asn Lys Ala Ile Leu Arg Tyr Ile
115 120 125

Ile Gln Gly Leu His Pro Phe Ser Thr Val Asp Leu Pro Ser Phe Lys
130 135 140

Glu Leu Ile Ser Thr Leu Gln Pro Gly Ile Ser Val Ile Thr Arg Pro
145 150 155 160

Thr Leu Arg Ser Lys Ile Ala Glu Ala Ala Leu Ile Met Lys Gln Lys
165 170 175

Val Thr Ala Ala Met Ser Glu Val Glu Trp Ile Ala Thr Thr Thr Asp
180 185 190

Cys Trp Thr Ala Arg Arg Lys Ser Phe Ile Gly Val Thr Ala His Trp
195 200 205

Ile Asn Pro Gly Ser Leu Glu Arg His Ser Ala Ala Leu Ala Cys Lys
210 215 220

Arg Leu Met Gly Ser His Thr Phe Glu Val Leu Ala Ser Ala Met Asn
225 230 235 240

Asp Ile His Ser Glu Tyr Glu Ile Arg Asp Lys Val Val Cys Thr Thr
245 250 255

Thr Asp Ser Gly Ser Asn Phe Met Lys Ala Phe Arg Val Phe Gly Val
260 265 270

Glu Asn Asn Asp Ile Glu Thr Glu Ala Arg Arg Cys Glu Ser Asp Asp
275 280 285

Thr Asp Ser Glu Gly Cys Gly Glu Gly Ser Asp Gly Val Glu Phe Gln
290 295 300

Asp Ala Ser Arg Val Leu Asp Gln Asp Asp Gly Phe Glu Phe Gln Leu
305 310 315 320

Pro Lys His Gln Lys Cys Ala Cys His Leu Leu Asn Leu Val Ser Ser
325 330 335

Val Asp Ala Gln Lys Ala Leu Ser Asn Glu His Tyr Lys Lys Leu Tyr
340 345 350

Arg Ser Val Phe Gly Lys Cys Gln Ala Leu Trp Asn Lys Ser Ser Arg
355 360 365

Ser Ala Leu Ala Ala Glu Ala Val Glu Ser Glu Ser Arg Leu Gln Leu
370 375 380

Leu Arg Pro Asn Gln Thr Arg Trp Asn Ser Thr Phe Met Ala Val Asp
385 390 395 400

Arg Ile Leu Gln Ile Cys Lys Glu Ala Gly Glu Gly Ala Leu Arg Asn
405 410 415

Ile Cys Thr Ser Leu Glu Val Pro Met Phe Asn Pro Ala Glu Met Leu
420 425 430

Phe Leu Thr Glu Trp Ala Asn Thr Met Arg Pro Val Ala Lys Val Leu
435 440 445

Asp Ile Leu Gln Ala Glu Thr Asn Thr Gln Leu Gly Trp Leu Leu Pro
450 455 460

Ser Val His Gln Leu Ser Leu Lys Leu Gln Arg Leu His His Ser Leu
465 470 475 480

Arg Tyr Cys Asp Pro Leu Val Asp Ala Leu Gln Gln Gly Ile Gln Thr
485 490 495

Arg Phe Lys His Met Phe Glu Asp Pro Glu Ile Ile Ala Ala Ala Ile
500 505 510

Leu Leu Pro Lys Phe Arg Thr Ser Trp Thr Asn Asp Glu Thr Ile Ile
515 520 525

Lys Arg Gly Met Asp Tyr Ile Arg Val His Leu Glu Pro Leu Asp His
530 535 540

Lys Lys Glu Leu Ala Asn Ser Ser Ser Asp Asp Glu Asp Phe Phe Ala
545 550 555 560

Ser Leu Lys Pro Thr Thr His Glu Ala Ser Lys Glu Leu Asp Gly Tyr
565 570 575

Leu Ala Cys Val Ser Asp Thr Arg Glu Ser Leu Leu Thr Phe Pro Ala
580 585 590

Ile Cys Ser Leu Ser Ile Lys Thr Asn Thr Pro Leu Pro Ala Ser Ala
595 600 605

Ala Cys Glu Arg Leu Phe Ser Thr Ala Gly Leu Leu Phe Ser Pro Lys
610 615 620

Arg Ala Arg Leu Asp Thr Asn Asn Phe Glu Asn Gln Leu Leu Leu Lys
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Leu Asn Leu Arg Phe Tyr Asn Phe Glu
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tg 4682

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<211> 1053
<212> PRT
<213> Artificial Sequence

<220>
<223> dSaCas9

<400> 32

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

Val Arg Leu Phe Lys Glu Ala Asn Val Glu Asn Asn Glu Gly Arg Arg
35 40 45

Ser Lys Arg Gly Ala Arg Arg Leu Lys Arg Arg Arg Arg His Arg Ile
50 55 60

Gln Arg Val Lys Lys Leu Leu Phe Asp Tyr Asn Leu Leu Thr Asp His
65 70 75 80

Ser Glu Leu Ser Gly Ile Asn Pro Tyr Glu Ala Arg Val Lys Gly Leu
85 90 95

Ser Gln Lys Leu Ser Glu Glu Glu Phe Ser Ala Ala Leu Leu His Leu
100 105 110

Ala Lys Arg Arg Gly Val His Asn Val Asn Glu Val Glu Glu Asp Thr
115 120 125

Gly Asn Glu Leu Ser Thr Lys Glu Gln Ile Ser Arg Asn Ser Lys Ala
130 135 140

Leu Glu Glu Lys Tyr Val Ala Glu Leu Gln Leu Glu Arg Leu Lys Lys
145 150 155 160

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

Val Lys Glu Ala Lys Gln Leu Leu Lys Val Gln Lys Ala Tyr His Gln
180 185 190

Leu Asp Gln Ser Phe Ile Asp Thr Tyr Ile Asp Leu Leu Glu Thr Arg
195 200 205

Arg Thr Tyr Tyr Glu Gly Pro Gly Glu Gly Ser Pro Phe Gly Trp Lys
210 215 220

Asp Ile Lys Glu Trp Tyr Glu Met Leu Met Gly His Cys Thr Tyr Phe
225 230 235 240

Pro Glu Glu Leu Arg Ser Val Lys Tyr Ala Tyr Asn Ala Asp Leu Tyr
245 250 255

Asn Ala Leu Asn Asp Leu Asn Asn Leu Val Ile Thr Arg Asp Glu Asn
260 265 270

Glu Lys Leu Glu Tyr Tyr Glu Lys Phe Gln Ile Ile Glu Asn Val Phe
275 280 285

Lys Gln Lys Lys Lys Pro Thr Leu Lys Gln Ile Ala Lys Glu Ile Leu
290 295 300

Val Asn Glu Glu Asp Ile Lys Gly Tyr Arg Val Thr Ser Thr Gly Lys
305 310 315 320

Pro Glu Phe Thr Asn Leu Lys Val Tyr His Asp Ile Lys Asp Ile Thr
325 330 335

Ala Arg Lys Glu Ile Ile Glu Asn Ala Glu Leu Leu Asp Gln Ile Ala

340 345 350

Lys Ile Leu Thr Ile Tyr Gln Ser Ser Glu Asp Ile Gln Glu Glu Leu
355 360 365

Thr Asn Leu Asn Ser Glu Leu Thr Gln Glu Glu Ile Glu Gln Ile Ser
370 375 380

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

Asn Leu Ile Leu Asp Glu Leu Trp His Thr Asn Asp Asn Gln Ile Ala
405 410 415

Ile Phe Asn Arg Leu Lys Leu Val Pro Lys Lys Val Asp Leu Ser Gln
420 425 430

Gln Lys Glu Ile Pro Thr Thr Leu Val Asp Asp Phe Ile Leu Ser Pro
435 440 445

Val Val Lys Arg Ser Phe Ile Gln Ser Ile Lys Val Ile Asn Ala Ile
450 455 460

Ile Lys Lys Tyr Gly Leu Pro Asn Asp Ile Ile Ile Glu Leu Ala Arg
465 470 475 480

Glu Lys Asn Ser Lys Asp Ala Gln Lys Met Ile Asn Glu Met Gln Lys
485 490 495

Arg Asn Arg Gln Thr Asn Glu Arg Ile Glu Glu Ile Ile Arg Thr Thr
500 505 510

Gly Lys Glu Asn Ala Lys Tyr Leu Ile Glu Lys Ile Lys Leu His Asp
515 520 525

Met Gln Glu Gly Lys Cys Leu Tyr Ser Leu Glu Ala Ile Pro Leu Glu
530 535 540

Asp Leu Leu Asn Asn Pro Phe Asn Tyr Glu Val Asp His Ile Ile Pro
545 550 555 560

Arg Ser Val Ser Phe Asp Asn Ser Phe Asn Asn Lys Val Leu Val Lys
565 570 575

Gln Glu Glu Ala Ser Lys Lys Gly Asn Arg Thr Pro Phe Gln Tyr Leu
580 585 590

Ser Ser Ser Asp Ser Lys Ile Ser Tyr Glu Thr Phe Lys Lys His Ile
595 600 605

Leu Asn Leu Ala Lys Gly Lys Gly Arg Ile Ser Lys Thr Lys Lys Glu
610 615 620

Tyr Leu Leu Glu Glu Arg Asp Ile Asn Arg Phe Ser Val Gln Lys Asp
625 630 635 640

Phe Ile Asn Arg Asn Leu Val Asp Thr Arg Tyr Ala Thr Arg Gly Leu
645 650 655

Met Asn Leu Leu Arg Ser Tyr Phe Arg Val Asn Asn Leu Asp Val Lys
660 665 670

Val Lys Ser Ile Asn Gly Gly Phe Thr Ser Phe Leu Arg Arg Lys Trp
675 680 685

Lys Phe Lys Lys Glu Arg Asn Lys Gly Tyr Lys His His Ala Glu Asp
690 695 700

Ala Leu Ile Ile Ala Asn Ala Asp Phe Ile Phe Lys Glu Trp Lys Lys
705 710 715 720

Leu Asp Lys Ala Lys Lys Val Met Glu Asn Gln Met Phe Glu Glu Lys
725 730 735

Gln Ala Glu Ser Met Pro Glu Ile Glu Thr Glu Gln Glu Tyr Lys Glu
740 745 750

Ile Phe Ile Thr Pro His Gln Ile Lys His Ile Lys Asp Phe Lys Asp
755 760 765

Tyr Lys Tyr Ser His Arg Val Asp Lys Lys Pro Asn Arg Glu Leu Ile
770 775 780

Asn Asp Thr Leu Tyr Ser Thr Arg Lys Asp Asp Lys Gly Asn Thr Leu
785 790 795 800

Ile Val Asn Asn Leu Asn Gly Leu Tyr Asp Lys Asp Asn Asp Lys Leu
805 810 815

Lys Lys Leu Ile Asn Lys Ser Pro Glu Lys Leu Leu Met Tyr His His
820 825 830

Asp Pro Gln Thr Tyr Gln Lys Leu Lys Leu Ile Met Glu Gln Tyr Gly
835 840 845

Asp Glu Lys Asn Pro Leu Tyr Lys Tyr Tyr Glu Glu Thr Gly Asn Tyr
850 855 860

Leu Thr Lys Tyr Ser Lys Lys Asp Asn Gly Pro Val Ile Lys Lys Ile
865 870 875 880

Lys Tyr Tyr Gly Asn Lys Leu Asn Ala His Leu Asp Ile Thr Asp Asp
885 890 895

Tyr Pro Asn Ser Arg Asn Lys Val Val Lys Leu Ser Leu Lys Pro Tyr
900 905 910

Arg Phe Asp Val Tyr Leu Asp Asn Gly Val Tyr Lys Phe Val Thr Val
915 920 925

Lys Asn Leu Asp Val Ile Lys Lys Glu Asn Tyr Tyr Glu Val Asn Ser
930 935 940

Lys Cys Tyr Glu Glu Ala Lys Lys Leu Lys Lys Ile Ser Asn Gln Ala
945 950 955 960

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

Glu Leu Tyr Arg Val Ile Gly Val Asn Asn Asp Leu Leu Asn Arg Ile
980 985 990

Glu Val Asn Met Ile Asp Ile Thr Tyr Arg Glu Tyr Leu Glu Asn Met
995 1000 1005

Asn Asp Lys Arg Pro Pro Arg Ile Ile Lys Thr Ile Ala Ser Lys
1010 1015 1020

Thr Gln Ser Ile Lys Lys Tyr Ser Thr Asp Ile Leu Gly Asn Leu
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Tyr Glu Val Lys Ser Lys Lys His Pro Gln Ile Ile Lys Lys Gly
1040 1045 1050

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<211> 1368
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<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 33

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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 Ala 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

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<212> PRT
<213> Clostridium sp. 7_2_43FAA

<400> 34

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Gln Ile Ser His Ile Ser His Glu Tyr Leu Ser Leu Ile Asp Leu Ala
20 25 30

Phe Asp Ser Lys Gln Asn Arg Leu Phe Glu Met Lys Val Leu Glu Leu
35 40 45

Leu Val Asn Glu Tyr Gly Phe Lys Gly Arg His Leu Gly Gly Ser Arg
50 55 60

Lys Pro Asp Gly Ile Val Tyr Ser Thr Thr Leu Glu Asp Asn Phe Gly
65 70 75 80

Ile Ile Val Asp Thr Lys Ala Tyr Ser Glu Gly Tyr Ser Leu Pro Ile
85 90 95

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

Asp Glu Glu Val Asn Pro Asn Lys Trp Trp Glu Asn Phe Ser Glu Glu
115 120 125

Val Lys Lys Tyr Tyr Phe Val Phe Ile Ser Gly Ser Phe Lys Gly Lys
130 135 140

Phe Glu Glu Gln Leu Arg Arg Leu Ser Met Thr Thr Gly Val Asn Gly
145 150 155 160

Ser Ala Val Asn Val Val Asn Leu Leu Leu Gly Ala Glu Lys Ile Arg
165 170 175

Ser Gly Glu Met Thr Ile Glu Glu Leu Glu Arg Ala Met Phe Asn Asn
180 185 190

Ser Glu Phe Ile Leu Lys Tyr
195

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<211> 4897
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tagatattaa gttttattat atttacactt acatactaat aataaattca acaaacaatt 180

tatttatgtt tatttattta ttaaaaaaaa acaaaaactc aaaatttctt ctataaagta 240

acaaaacttt tatcgaatac ctgcagcccg ggggatgcag agggacagcc ccccccccaaa 300

gcccccaggg atgtaattac gtccctcccc cgctaggggg cagcagcgag ccgcccgggg 360

ctccgctccg gtccggcgct ccccccgcat ccccgagccg gcagcgtgcg gggacagccc 420

gggcacgggg aaggtggcac gggatcgctt tcctctgaac gcttctcgct gctctttgag 480

cctgcagaca cctgggggga tacggggaaa agttgactgt gcctttcgat cgaaccatgg 540

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ggatccacgg gtaccgatca catatgcctt taattaaaca ctagttctat agtgtcacct 1980

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tgagaaagcg ccacgcttcc cgaagggaga aaggcggaca ggtatccggt aagcggcagg 3660

gtcggaacag gagagcgcac gagggagctt ccagggggaa acgcctggta tctttatagt 3720

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<213> Artificial Sequence

<220>
<223> EF1a-2r primer

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<210> 37
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<213> Artificial Sequence

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35 40 45

Leu Phe Glu Met Lys Val Leu Glu Leu Leu Val Asn Glu Tyr Gly Phe
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Lys Gly Arg His Leu Gly Gly Ser Arg Lys Pro Asp Gly Ile Val Tyr
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Ser Thr Thr Leu Glu Asp Asn Phe Gly Ile Ile Val Asp Thr Lys Ala
85 90 95

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

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Phe Ile Ser Gly Ser Phe Lys Gly Lys Phe Glu Glu Gln Leu Arg Arg
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Leu Ser Met Thr Thr Gly Val Asn Gly Ser Ala Val Asn Val Val Asn
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Leu Leu Leu Gly Ala Glu Lys Ile Arg Ser Gly Glu Met Thr Ile Glu
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Glu Leu Glu Arg Ala Met Phe Asn Asn Ser Glu Phe Ile Leu Lys Tyr
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Gly Gly Gly Gly Ser Asp Lys Lys Tyr Ser Ile Gly Leu Ala Ile Gly
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Thr Asn Ser Val Gly Trp Ala Val Ile Thr Asp Glu Tyr Lys Val Pro
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Ala Thr Arg Leu Lys Arg Thr Ala Arg Arg Arg Tyr Thr Arg Arg Lys
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Asn Arg Ile Cys Tyr Leu Gln Glu Ile Phe Ser Asn Glu Met Ala Lys
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Gly Val Asp Ala Lys Ala Ile Leu Ser Ala Arg Leu Ser Lys Ser Arg
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Lys Ser Asn Phe Asp Leu Ala Glu Asp Ala Lys Leu Gln Leu Ser Lys
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Gln Tyr Ala Asp Leu Phe Leu Ala Ala Lys Asn Leu Ser Asp Ala Ile
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Gln Ile His Leu Gly Glu Leu His Ala Ile Leu Arg Arg Gln Glu Asp
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Glu Arg Met Thr Asn Phe Asp Lys Asn Leu Pro Asn Glu Lys Val Leu
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Pro Lys His Ser Leu Leu Tyr Glu Tyr Phe Thr Val Tyr Asn Glu Leu
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Arg Lys Val Thr Val Lys Gln Leu Lys Glu Asp Tyr Phe Lys Lys Ile
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Glu Cys Phe Asp Ser Val Glu Ile Ser Gly Val Glu Asp Arg Phe Asn
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Ala Ser Leu Gly Thr Tyr His Asp Leu Leu Lys Ile Ile Lys Asp Lys
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Asp Phe Leu Asp Asn Glu Glu Asn Glu Asp Ile Leu Glu Asp Ile Val
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Lys Thr Tyr Ala His Leu Phe Asp Asp Lys Val Met Lys Gln Leu Lys
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Arg Arg Arg Tyr Thr Gly Trp Gly Arg Leu Ser Arg Lys Leu Ile Asn
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Ser Asp Gly Phe Ala Asn Arg Asn Phe Met Gln Leu Ile His Asp Asp
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Ser Leu Thr Phe Lys Glu Asp Ile Gln Lys Ala Gln Val Ser Gly Gln
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Gly Asp Ser Leu His Glu His Ile Ala Asn Leu Ala Gly Ser Pro Ala
930 935 940

Ile Lys Lys Gly Ile Leu Gln Thr Val Lys Val Val Asp Glu Leu Val

945 950 955 960

Lys Val Met Gly Arg His Lys Pro Glu Asn Ile Val Ile Glu Met Ala
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Arg Glu Asn Gln Thr Thr Gln Lys Gly Gln Lys Asn Ser Arg Glu Arg
980 985 990

Met Lys Arg Ile Glu Glu Gly Ile Lys Glu Leu Gly Ser Gln Ile Leu
995 1000 1005

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