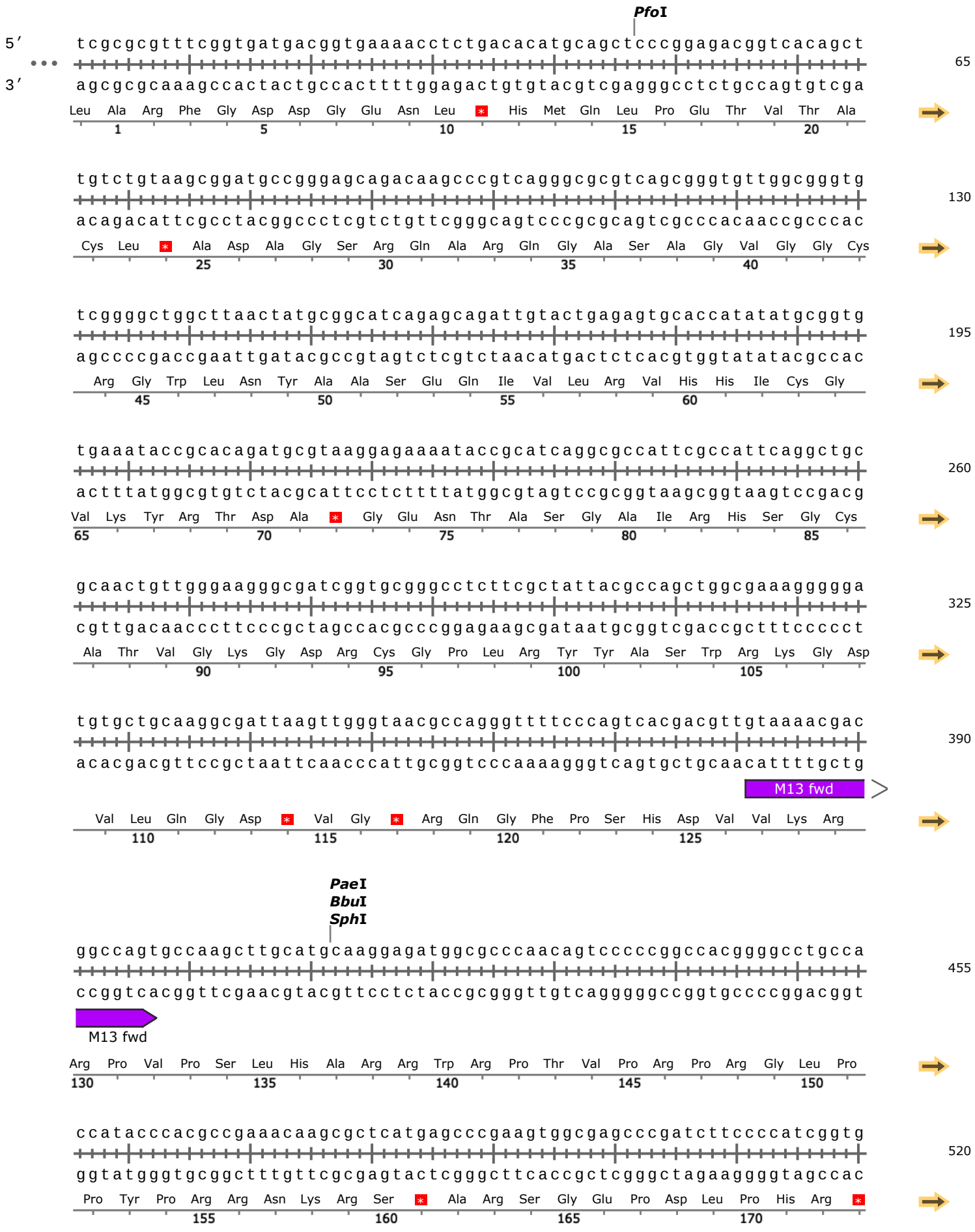


Sequence: Cloned1.dna (Circular / 6717 bp)
Enzymes: Unique 6+ Cutters (62 of 666 total)
Features: 12 total
Primers: 2 total

Blunt Cutters **Green**, Unique Cutters **Bold**



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tacagccgctatatatccgcggtcgttggcgtggacaccgcgggcactacggccgggtgctacgcagg
Cys Arg Arg Tyr Arg Arg Gln Gln Pro His Leu Trp Arg Arg * Cys Arg Pro Arg Cys Val
175 180 185 190

ggcgtagaggatcgagatctcgatcccgcgaaatttaatacgactcactatagggagaccacaacg
ccgcatctcctagctctagagctagggcgctttaattatgctgagtgatatccctctgggtgttc
T7 promoter
Arg Arg Arg Gly Ser Arg Ser Arg Ser Arg Glu Ile Asn Thr Thr His Tyr Arg Glu Thr Thr Thr
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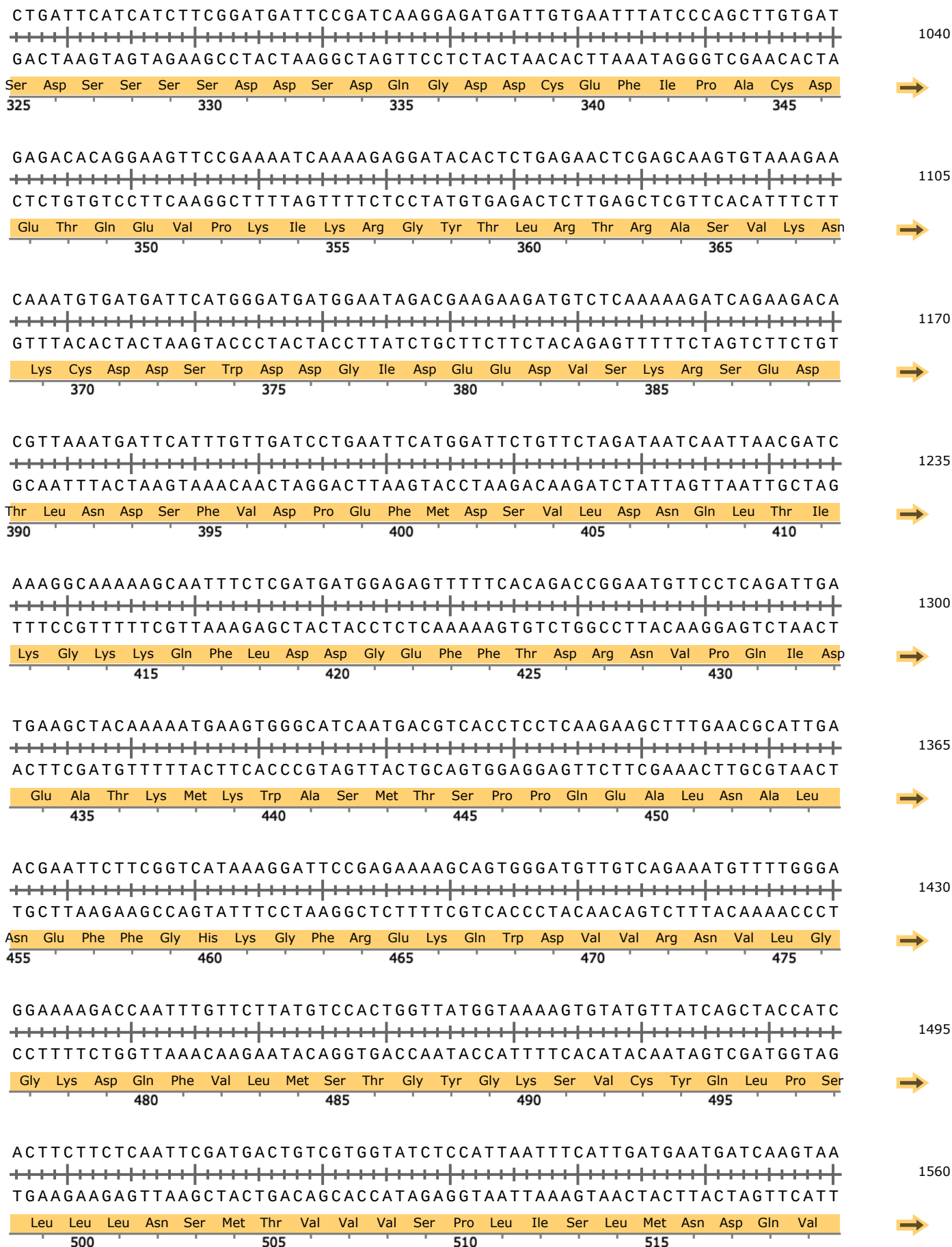
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caaagggagatctttattaaacaaattgaaattcttcctctatatggtaccggtgTATACTATTC
Val Ser Leu * Lys * Phe Cys Leu Thr Leu Arg Arg Arg Tyr Thr Met Ala His Met Ile Ser
220 225 230 235

forward primer
TGATGATGACGATCTACC
TGATGATGACGATCTACCATCTACTCGCCCGGGATCTGTGAATGAGGAATTACCAGAAACCGAAC
ACTACTACTGCTAGATGGTAGATGAGCGGGCCCTAGACACTTACTCCTTAATGGTCTTTGGCTTG
Asp Asp Asp Asp Leu Pro Ser Thr Arg Pro Gly Ser Val Asn Glu Glu Leu Pro Glu Thr Glu
240 245 250 255

CCGAAGATAATGATGAGTTGCCTGAAACAGAACCTGAAAGCGATTCCGATAAACCTACCGTAACC
GGCTTCTATTACTACTCAACGGACTTTGTCTTGGACTTTCGCTAAGGCTATTTGGATGGCATTGG
Pro Glu Asp Asn Asp Glu Leu Pro Glu Thr Glu Pro Glu Ser Asp Ser Asp Lys Pro Thr Val Thr
260 265 270 275 280

TCGAATAAACAGAAAACCAAGTTGCTGATGAAGATTATGATTCATTCGACGATTTTGTGCCAG
AGCTTATTTTGTCTTTTGGTTCAACGACTACTTCTAATACTAAGTAAGCTGCTAAAACACGGGTC
Ser Asn Lys Thr Glu Asn Gln Val Ala Asp Glu Asp Tyr Asp Ser Phe Asp Asp Phe Val Pro Ser
285 290 295 300

TCAAACACACACAGCCTCCAAAATACCTGTAAAAAATAAACGAGCCAAAAGTGCCTGTAGAAT
AGTTTGTGTGTGTCGGAGGTTTTATGGACATTTTTTATTGCTCGGTTTTTACGTTGACATCTTA
Gln Thr His Thr Ala Ser Lys Ile Pro Val Lys Asn Lys Arg Ala Lys Lys Cys Thr Val Glu
305 310 315 320



CTACATTGGTTTCTAAAGGTATTGATGCAGTGAAACTAGATGGACATTCTACACAAATTGAATGG
 1625
 GATGTAACCAAAGATTTCCATAACTACGTCACCTTGATCTACCTGTAAGATGTGTTTAACTTACC
 Thr Thr Leu Val Ser Lys Gly Ile Asp Ala Val Lys Leu Asp Gly His Ser Thr Gln Ile Glu Trp →
 520 525 530 535 540

GATCAAGTTGCGAATAATATGCACCGAATTAGGTTTCATCTACATGTCACCTGAAATGGTTACGAG
 1690
 CTAGTTCAACGCTTATTATACGTGGCTTAATCCAAGTAGATGTACAGTGGACTTTACCAATGCTC
 Asp Gln Val Ala Asn Asn Met His Arg Ile Arg Phe Ile Tyr Met Ser Pro Glu Met Val Thr Ser →
 545 550 555 560

CCAAAAGGGTTTGGAATTATTAACCTTCTTGCCGAAAACATATCTCCCTCCTCGCTATTGATGAAG
 1755
 GGTTTTCCCAAACCTTAATAATTGAAGAACGGCTTTTGTATAGAGGGAGGAGCGATAACTACTTC
 Gln Lys Gly Leu Glu Leu Leu Thr Ser Cys Arg Lys His Ile Ser Leu Leu Ala Ile Asp Glu →
 565 570 575 580

CTCATTGTGTTTCTCAATGGGGACACGACTTTCGAAACTCGTACAGGCATCTCGCAGAAATTAGA
 1820
 GAGTAACACAAAGAGTTACCCCTGTGCTGAAAGCTTTGAGCATGTCCGTAGAGCGTCTTTAATCT
 Ala His Cys Val Ser Gln Trp Gly His Asp Phe Arg Asn Ser Tyr Arg His Leu Ala Glu Ile Arg →
 585 590 595 600 605

AACCGATCTGATCTATGCAATATTCCAATGATTGCTCTTACCGCTACTGCCACAGTTAGAGTTCCG
 1885
 TTGGCTAGACTAGATACGTTATAAGGTTACTAACGAGAATGGCGATGACGGTGTCAATCTCAAGC
 Asn Arg Ser Asp Leu Cys Asn Ile Pro Met Ile Ala Leu Thr Ala Thr Ala Thr Val Arg Val Arg →
 610 615 620 625

TGATGACGTCATTGCTAATTTAAGACTCCGCAAGCCATTAATCACAACTACGTCGTTTGATAGAA
 1950
 ACTACTGCAGTAACGATTAATTTCTGAGGCGTTCGGTAATTAGTGTGATGCAGCAAACCTATCTT
 Asp Asp Val Ile Ala Asn Leu Arg Leu Arg Lys Pro Leu Ile Thr Thr Thr Ser Phe Asp Arg →
 630 635 640 645

PctI
BsmI
BsaMI
MvaI269I

AGAATCTCTACATTTCTGTGCATTCTTCAAAGGACATGGCTGAAGATTTAGGATTATTCATGAAA
 2015
 TCTTAGAGATGTAAAGACACGTAAGAAGTTTCTGTACCGACTTCTAAATCCTAATAAGTACTTT
 Lys Asn Leu Tyr Ile Ser Val His Ser Ser Lys Asp Met Ala Glu Asp Leu Gly Leu Phe Met Lys →
 650 655 660 665 670

OliI
AleI

ACCGATGAAGTTAAAGGAAGACACTTGGTGGACCTACTATTATTTATTGCCAAACGAAACAAAT
 2080
 TGGCTACTTCAATTTCTTCTGTGAAACCACCTGGATGATAATAAATAACGGTTTGCTTTGTTTA
 Thr Asp Glu Val Lys Gly Arg His Phe Gly Gly Pro Thr Ile Ile Tyr Cys Gln Thr Lys Gln Met →
 675 680 685 690

GGTCGATGATGTGAACTGTGTTTTGAGAAGAATCGGAGTTCGTTCTGCTCATTATCACGCAGGAC 2145
+++++
CCAGCTACTACACTTGACACAAAACCTCTTCTTAGCCTCAAGCAAGACGAGTAATAGTGCGTCCTG
Val Asp Asp Val Asn Cys Val Leu Arg Arg Ile Gly Val Arg Ser Ala His Tyr His Ala Gly →
695 700 705 710

TCACTAAAAATCAACGAGAAAAAGCACACACCGATTTTATGAGAGATAAGATTACAACAATCGTT 2210
+++++
AGTGATTTTTAGTTGCTCTTTTTTCGTGTGTGGCTAAAATACTCTCTATTCTAATGTTGTTAGCAA
Leu Thr Lys Asn Gln Arg Glu Lys Ala His Thr Asp Phe Met Arg Asp Lys Ile Thr Thr Ile Val →
715 720 725 730 735

GCGACAGTTGCATTTGGTATGGGAATTGACAAACCCGACGTTTCGAAATGTGATTCATTACGGATG 2275
+++++
CGCTGTCAACGTAAACCATACCTTAACTGTTTGGGCTGCAAGCTTTACACTAAGTAATGCCTAC
Ala Thr Val Ala Phe Gly Met Gly Ile Asp Lys Pro Asp Val Arg Asn Val Ile His Tyr Gly Cys →
740 745 750 755

CCCGAACAAATATCGAATCATATTATCAAGAAATCGGAAGAGCTGGTCGAGATGGATCTCCAAGTA 2340
+++++
GGGCTTGTTATAGCTTAGTATAATAGTTCTTTAGCCTTCTCGACCAGCTCTACCTAGAGGTTTCAT
Pro Asn Asn Ile Glu Ser Tyr Tyr Gln Glu Ile Gly Arg Ala Gly Arg Asp Gly Ser Pro Ser →
760 765 770 775

TTTGTGCGTGATTCTGGGCTCCGAAAGATTTGAATACTATAAAATTTAAACTTCGAAATTCGCAG 2405
+++++
AAACAGCACATAAGACCCGAGGCTTTCTAAACTTATGATATTTTAAATTTGAAGCTTTAAGCGTC
Ile Cys Arg Val Phe Trp Ala Pro Lys Asp Leu Asn Thr Ile Lys Phe Lys Leu Arg Asn Ser Gln →
780 785 790 795 800

CAAAAAGAAGAAGTAGTTGAAAATCTTACAATGATGCTAAGACAACCTCGAGTTGGTTCTGACAAC 2470
+++++
GTTTTTCTTCTTCATCAACTTTTAGAATGTTACTACGATTCTGTTGAGCTCAACCAAGACTGTTG
Gln Lys Glu Glu Val Val Glu Asn Leu Thr Met Met Leu Arg Gln Leu Glu Leu Val Leu Thr Thr →
805 810 815 820

CGTTGGATGTAGAAGATACCAACTTCTGAAGCACTTTGACCCATCATACGCGAAACCTCCAACTA 2535
+++++
GCAACCTACATCTTCTATGGTTGAAGACTTCGTGAAACTGGGTAGTATGCGCTTTGGAGGTTGAT
Val Gly Cys Arg Arg Tyr Gln Leu Leu Lys His Phe Asp Pro Ser Tyr Ala Lys Pro Pro Thr →
825 830 835 840

TGCAAGCTGATTGTTGTGATAGATGTAAGTCTCAATGGAATCAAGATTCATCATCCAGT 2600
+++++
ACGTTTCGACTAACAACTATCTACATGACTTTACGAGTTACCTTTAGTTCTAAGTAGTAGGTCA
Met Gln Ala Asp Cys Cys Asp Arg Cys Thr Glu Met Leu Asn Gly Asn Gln Asp Ser Ser Ser Ser →
845 850 855 860 865

ATTGTTGATGTTACAACAGAATCGAAGTGGTTGTTTCAAGTTATTAACGAAATGTACAACGGGAA 2665
+++++
TAACAACTACAATGTTGTCTTAGCTTCACCAACAAAGTTCAATAATTGCTTTACATGTTGCCCTT
Ile Val Asp Val Thr Thr Glu Ser Lys Trp Leu Phe Gln Val Ile Asn Glu Met Tyr Asn Gly Lys →
870 875 880 885

AACTGGTATCGGAAAACCAATCGAATTTCTGAGGGGATCGAGTAAAGAAGACTGGCGAATCAAGA 2730
 TTGACCATAGCCTTTTGGTTAGCTTAAAGACTCCCCTAGCTCATTCTTCTGACCGCTTAGTTCT
 Thr Gly Ile Gly Lys Pro Ile Glu Phe Leu Arg Gly Ser Ser Lys Glu Asp Trp Arg Ile Lys →
 890 895 900 905

CCACATCTCAACAAAAATTGTTTGGAAATTGGAAAACATATTCCTGATAAATGGTGGAAAGCACTT 2795
 GGTGTAGAGTTGTTTTTAAACAAACCTTAAACCTTTTGTATAAGGACTATTTACCACCTTTCTGTGAA
 Thr Thr Ser Gln Gln Lys Leu Phe Gly Ile Gly Lys His Ile Pro Asp Lys Trp Trp Lys Ala Leu →
 910 915 920 925 930

GCAGCATCACTTCGAATTGCTGGTTATCTTGGAGAAGTTAGGCTGATGCAAATGAAATTTGGAAG 2860
 CGTCGTAGTGAAGCTTAAACGACCAATAGAACCCTTCAATCCGACTACGTTTACTTTAAACCTTC
 Ala Ala Ser Leu Arg Ile Ala Gly Tyr Leu Gly Glu Val Arg Leu Met Gln Met Lys Phe Gly Ser →
 935 940 945 950

TTGTATCACTTTGTCCGAACCTCGGGGAACGATGGCTTTTACTGGAAAAGAGATGAAAATCGATG 2925
 AACATAGTGAACAGGCTTGAGCCCCTTGCTACCGAAAACCTGACCTTTTCTCTACTTTTAGCTAC
 Cys Ile Thr Leu Ser Glu Leu Gly Glu Arg Trp Leu Leu Thr Gly Lys Glu Met Lys Ile Asp →
 955 960 965 970

CGACACCGATTTTATTGCAAGGGAAGAAAGAAAAGCCGCACCTTCAACTGTCCCGGAGCTTCA 2990
 GCTGTGGCTAAAATAACGTTCCCTTCTTTCTTTTTCGGCGTGGAAGTTGACAGGGGCCTCGAAGT
 Ala Thr Pro Ile Leu Leu Gln Gly Lys Lys Glu Lys Ala Ala Pro Ser Thr Val Pro Gly Ala Ser →
 975 980 985 990 995

AGATCTCAGTCAACTAAATCAAGTACAGAGATTCCAACCAAGATTCTCGGAGCGAATAAGATTCC 3055
 TCTAGAGTCAGTTGATTTAGTTTCATGTCTCTAAGGTTGTTCTAAGAGCCTCGCTTATTCTAAGC
 Arg Ser Gln Ser Thr Lys Ser Ser Thr Glu Ile Pro Thr Lys Ile Leu Gly Ala Asn Lys Ile Arg →
 1000 1005 1010 1015

TGAATACGAGCCTGCAAATGAAAACGAGCAGCTGATGAACTTGAAAAGCAAGAAGTCACTGGTC 3120
 ACTTATGCTCGGACGTTTACTTTTGTCTCGTCTGACTACTTGAACCTTTTTCGTTCTTCAGTGACCAG
 Glu Tyr Glu Pro Ala Asn Glu Asn Glu Gln Leu Met Asn Leu Lys Lys Gln Glu Val Thr Gly →
 1020 1025 1030 1035

TTCCAGAGAAGATTGATCAACTGCGCTCTCGTCTTGACGACATTCGTGTAGGAATTGCAAACATG 3185
 AAGGTCTCTTCTAACTAGTTGACGCGAGAGCAGAAGCTGCTGTAAGCACATCCTTAACGTTTGTAC
 Leu Pro Glu Lys Ile Asp Gln Leu Arg Ser Arg Leu Asp Asp Ile Arg Val Gly Ile Ala Asn Met →
 1040 1045 1050 1055 1060

NsiI
Zsp2I
EcoT22I
Mph1103I

CATGAAGTAGCACCATTCCAAATTGTATCGAATACTGTTCTTGATTGTTTTGCCAACTTGAGACC 3250
 GTACTTCATCGTGGTAAGGTTTAAACATAGCTTATGACAAGAAGCTAACAAAACGGTTGAACTCTGG
 His Glu Val Ala Pro Phe Gln Ile Val Ser Asn Thr Val Leu Asp Cys Phe Ala Asn Leu Arg Pro →
 1065 1070 1075 1080

BbvCI
Bpu10I

TACCTCAGCCTCGAATCTCGAAATGATTGATGGAATGTCGGCTCAGCAGAAATCTAGATACGGAA
 ATGGAGTCGGAGCTTAGAGCTTTACTAACTACCTTACAGCCGAGTCGTCCTTTAGATCTATGCCTT
 Thr Ser Ala Ser Asn Leu Glu Met Ile Asp Gly Met Ser Ala Gln Gln Lys Ser Arg Tyr Gly
 1085 1090 1095 1100

3315



AACGATTTGTCGATTGTGTTGTACAATTTTCAAAGGAAACTGGCATTGCAACAAACGTCAATGCC
 TTGCTAAACAGCTAACACAACATGTTAAAAGTTTCTTTGACCGTAACGTTGTTTGCAGTTACGG
 Lys Arg Phe Val Asp Cys Val Val Gln Phe Ser Lys Glu Thr Gly Ile Ala Thr Asn Val Asn Ala
 1105 1110 1115 1120 1125

3380



AACGATATGATACCCCTGAACTTATTTCAAAAATGCAGAAAGTTCTCTCGGATGCGGTGAGAAG
 TTGCTATACTATGGGGGACTTGAATAAAGTTTTTACGTCTTTCAAGAGAGCCTACGCCACTCTTC
 Asn Asp Met Ile Pro Pro Glu Leu Ile Ser Lys Met Gln Lys Val Leu Ser Asp Ala Val Arg Arg
 1130 1135 1140 1145

3445



BssNAI
BstZ17I
Bst1107I

AGTATACACAGAGCATCTTATTTTCGAGATCCACTGCGAAAGAAGTGGCAACTGCTCGAGGAATTA
 TCATATGTGTCTCGTAGAATAAAGCTCTAGGTGACGCTTTCTTCACCGTTGACGAGCTCCTTAAT
 Val Tyr Thr Glu His Leu Ile Ser Arg Ser Thr Ala Lys Glu Val Ala Thr Ala Arg Gly Ile
 1150 1155 1160 1165

3510



RruI
NruI
BtuMI
Bsp68I

GTGAGGGTACTGTATATTCATATCTCGCGATGGCGGTAGAAAAAGGATTACCTCTTCACTTAGAC
 CACTCCCATGACATATAAGTATAGAGCGCTACCGCCATCTTTTCTTAATGGAGAAGTGAATCTG
 Ser Glu Gly Thr Val Tyr Ser Tyr Leu Ala Met Ala Val Glu Lys Gly Leu Pro Leu His Leu Asp
 1170 1175 1180 1185 1190

3575



AAGTTAAATGTCTCCAGAAAGAATATTGCAATGGCTCTAAATGCAGTTAGAGTACATTTAGGATC
 TTCAATTTACAGAGGTCTTTCTTATAACGTTACCGAGATTTACGTCAATCTCATGTAAATCCTAG
 Lys Leu Asn Val Ser Arg Lys Asn Ile Ala Met Ala Leu Asn Ala Val Arg Val His Leu Gly Ser
 1195 1200 1205 1210

3640



AAATGTTGCCGTA CTGACACCATGGGTTGAAGCTATGGGAGTCGTACCTGATTTTAATCAGTTGA
 TTTACAACGGCATGACTGTGGTACCCAACCTTCGATACCCTCAGCATGGACTAAAATTAGTCAACT
 Asn Val Ala Val Leu Thr Pro Trp Val Glu Ala Met Gly Val Val Pro Asp Phe Asn Gln Leu
 1215 1220 1225 1230

3705



AATTGATCCGGGCAATTCTTATTTACGAATATGGATTGGATACGAGTGAGAACCAAGAGAAGCCA
 TTAAGTGGCCCGTTAAGAATAAATGCTTATACCTAACCTATGCTCACTCTTGGTTCTCTTCGGT
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3770

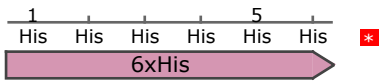


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 Asp Ile Gln Ser Met Pro Ser Thr Ser Asn Pro Ser Thr Ile Lys Thr Val Pro Ser Thr Pro Ser
 1260 1265 1270 1275

ATCCTCTCTCAGAGCTCCTCCATTGAAGAAATTCAACTTNGt c g a c t c g a g c g a g c t c c c g g g g
 TAGGAGAGAGTCTCGAGGAGGTAACCTCTTTAAGTTTGAANCagctgagctcgctcgagggcccc
 Ser Ser Leu Arg Ala Pro Pro Leu Lys Lys Phe Lys Leu ? Arg Leu Glu Arg Ala Pro Gly
 1280 1285 1290 1295

CGAGGAGGTAACCTCTTTAAGTTTGAANCAGCTGNN (P)
 reverse primer

ggggttctcatcatcatcatcatcattaataaaagggcggaattccagcacactggcggccggttac
 cccaagagtagtagtagtagtaattattttcccgcttaaggctcgtgtgaccgccggcaatg
 EagI
 EclXI
 BstZI
 BseX3I
 Eco52I
 AhI
 BcuI
 SpeI
 BstXI



Gly Gly Ser His His His His His His Lys Gly Glu Phe Gln His Thr Gly Gly Arg Tyr
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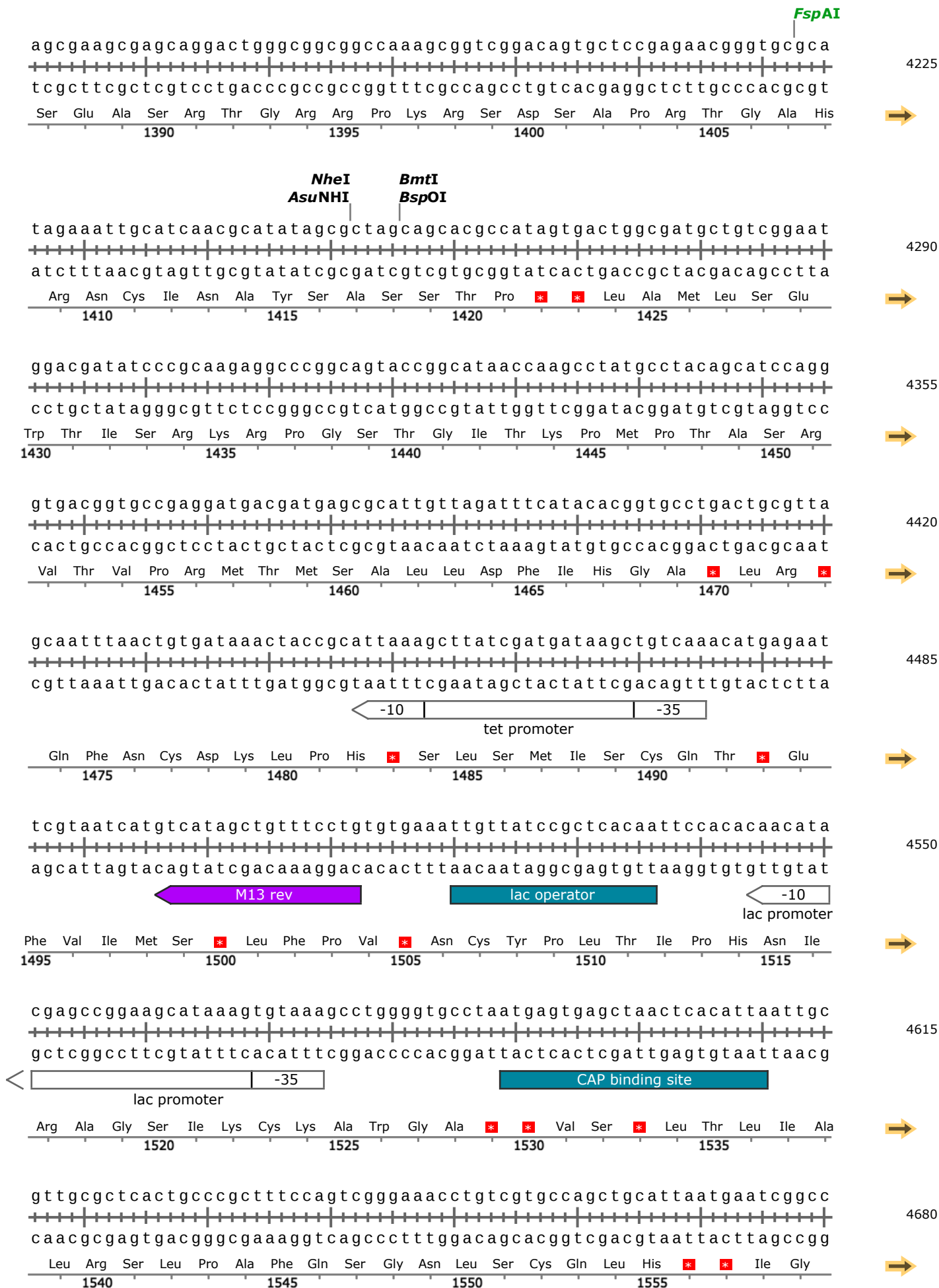
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 1325 1330 1335 1340

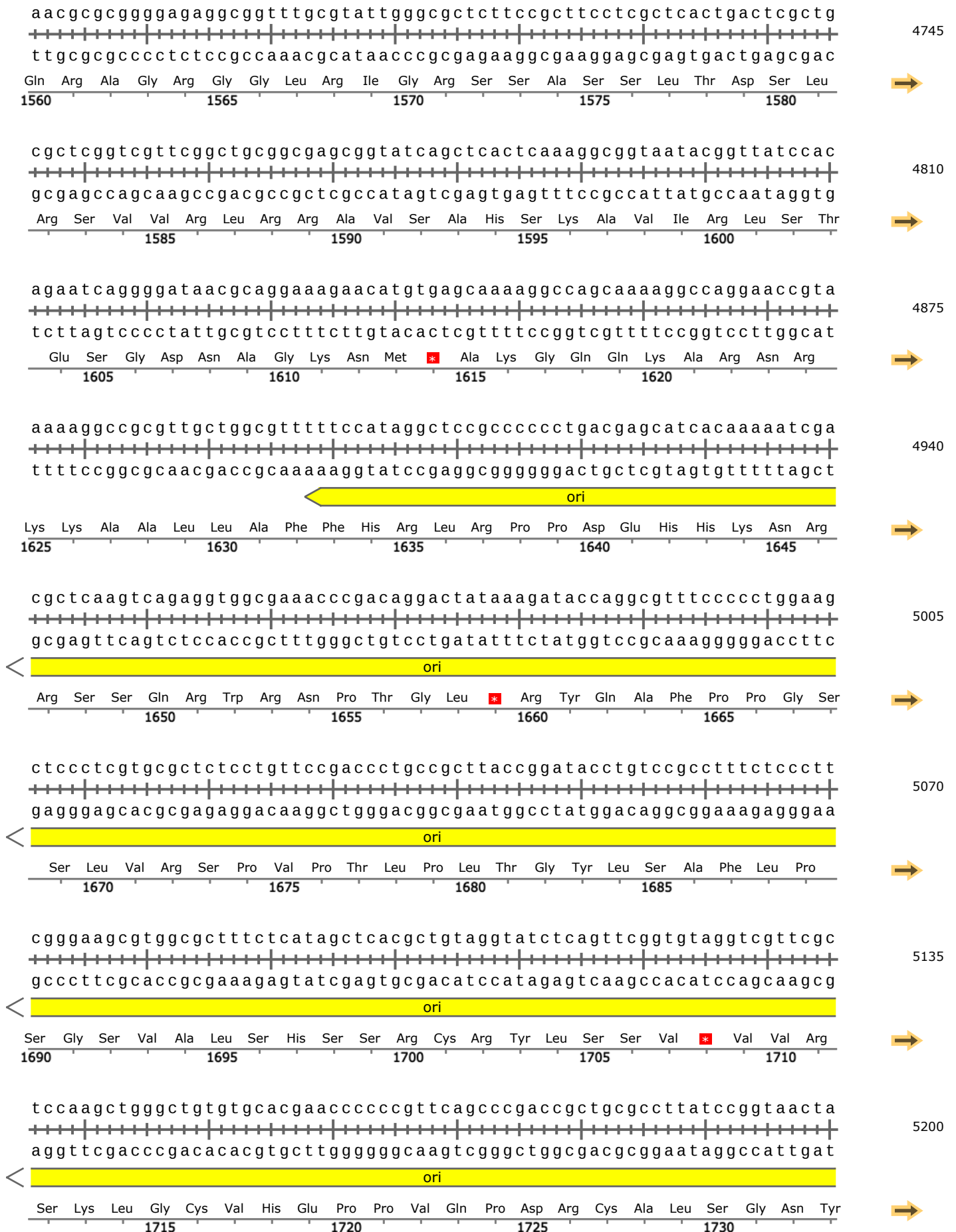
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 T7 terminator

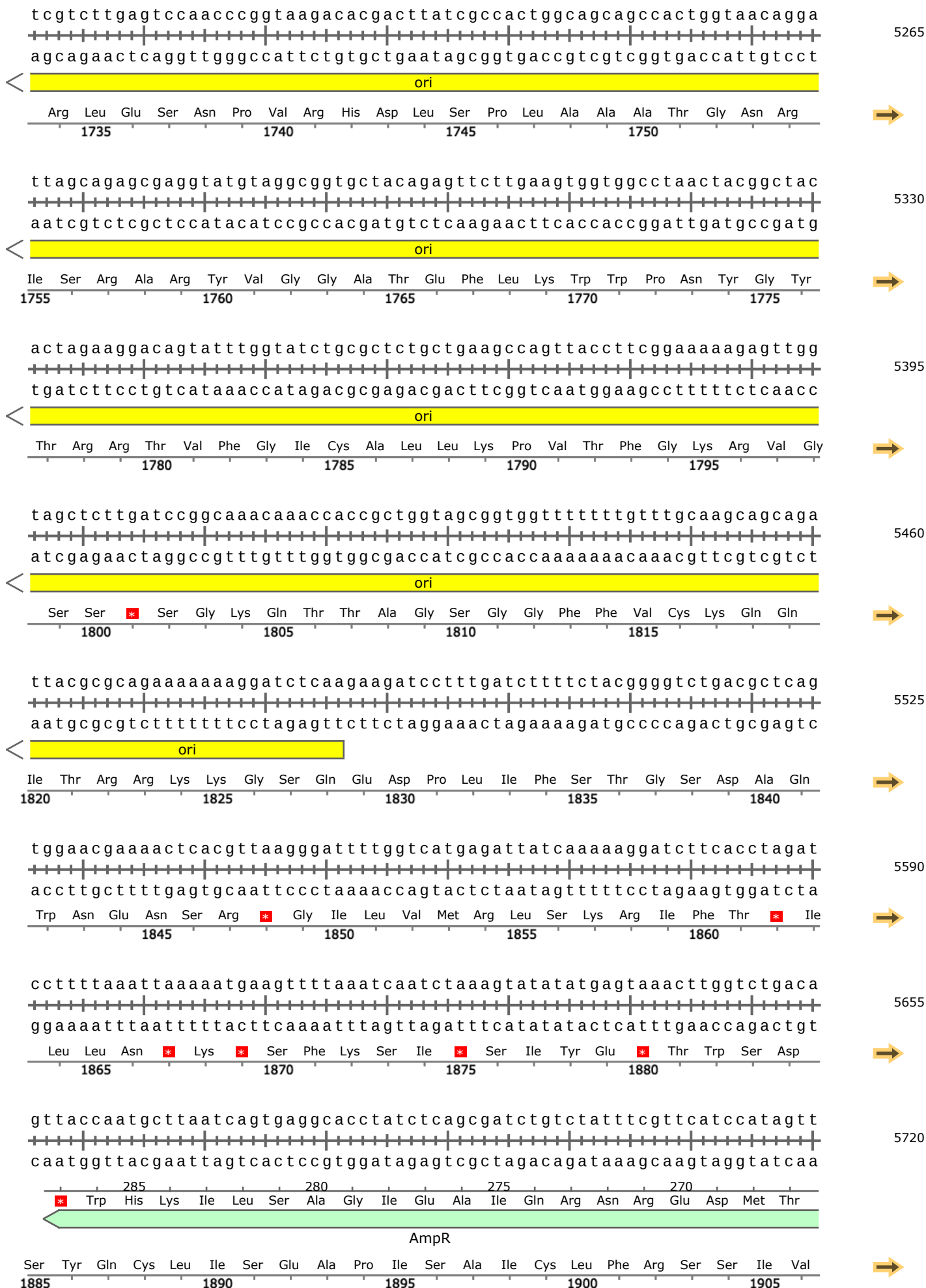
Asn * His Asn Pro Leu Gly Pro Leu Asn Gly Ser * Gly Val Phe Cys * Lys Glu Glu
 1345 1350 1355 1360

- MroI
- Kpn2I
- BseAI
- BspEI
- AccIII
- Bsp13I
- Aor13HI

tatatccggatatccacaggacgggtgtggtcgccatgatcgcgtagtcgatagtggtccaagt
 atataggcctatagggtgtcctgcccacaccagcggtagcgcgatcagctatcaccgaggttca
 Leu Tyr Pro Asp Ile His Arg Thr Gly Val Val Ala Met Ile Ala * Ser Ile Val Ala Pro Ser
 1365 1370 1375 1380 1385







DriI
AhdI
AspEI
BmeRI
Eam1105I

g c c t g a c t c c c c g t c g t g t a g a t a a c t a c g a t a c g g g a g g g c t t a c c a t c t g g c c c c a g t g c t g c
 c g g a c t g a g g g g c a g c a c a t c t a t t g a t g c t a t g c c c t c c c g a a t g g t a g a c c g g g g t c a c g a c g

5785

265 260 255 250 245
 Ala Gln Ser Gly Thr Thr Tyr Ile Val Val Ile Arg Ser Pro Lys Gly Asp Pro Gly Leu Ala Ala



AmpR

Ala Leu Pro Val Val Ile Thr Thr Ile Arg Glu Gly Leu Pro Ser Gly Pro Ser Ala Ala
 1910 1915 1920 1925



a a t g a t a c c g c g a g a c c c a c g c t c a c c g g c t c c a g a t t t a t c a g c a a t a a a c c a g c c a g c c g g a a
 t t a c t a t g g c g c t c t g g g t g c g a g t g g c c g a g g t c t a a a t a g t c g t t a t t g g t c g g t c g g c c t t

5850

240 235 230 225
 Ile Ile Gly Arg Ser Gly Arg Glu Gly Ala Gly Ser Lys Asp Ala Ile Phe Trp Gly Ala Pro Leu



AmpR

Met Ile Pro Arg Asp Pro Arg Ser Pro Ala Pro Asp Leu Ser Ala Ile Asn Gln Pro Ala Gly
 1930 1935 1940 1945



g g g c c g a g c g c a g a a g t g g t c c t g c a a c t t t a t c c g c c t c c a t c c a g t c t a t t a a t t g t t g c c g g
 c c c g g c t c g c g t c t t c a c c a g g a c g t t g a a a t a g g c g g a g g t a g g t c a g a t a a t t a a c a a c g g c c

5915

220 215 210 205
 Ala Ser Arg Leu Leu Pro Gly Ala Val Lys Asp Ala Glu Met Trp Asp Ile Leu Gln Gln Arg



AmpR

Arg Ala Glu Arg Arg Ser Gly Pro Ala Thr Leu Ser Ala Ser Ile Gln Ser Ile Asn Cys Cys Arg
 1950 1955 1960 1965 1970



g a a g c t a g a g t a a g t a g t t c g c c a g t t a a t a g t t t g c g c a a c g t t g t t g c c a t t g c t a c a g g c a t
 c t t c g a t c t c a t t c a t c a a g c g g t c a a t t a t c a a a c g c g t t g c a a c a a c g g t a a c g a t g t c c g t a

5980

200 195 190 185 180
 Ser Ala Leu Thr Leu Leu Glu Gly Thr Leu Leu Lys Arg Leu Thr Thr Ala Met Ala Val Pro Met



AmpR

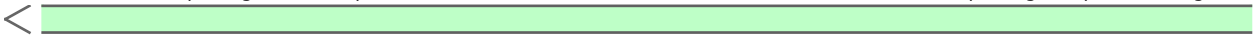
Glu Ala Arg Val Ser Ser Ser Pro Val Asn Ser Leu Arg Asn Val Val Ala Ile Ala Thr Gly Ile
 1975 1980 1985 1990



c g t g g t g t c a c g c t c g t c g t t t g g t a t g g c t t c a t t c a g c t c c g g t t c c c a a c g a t c a a g g c g a g
 g c a c c a c a g t g c g a g c a g c a a a c c a t a c c g a a g t a a g t c g a g g c c a a g g t t g c t a g t t c c g c t c

6045

175 170 165 160
 Thr Thr Asp Arg Glu Asp Asn Pro Ile Ala Glu Asn Leu Glu Pro Glu Trp Arg Asp Leu Arg Thr



AmpR

Val Val Ser Arg Ser Ser Phe Gly Met Ala Ser Phe Ser Ser Gly Ser Gln Arg Ser Arg Arg
 1995 2000 2005 2010



