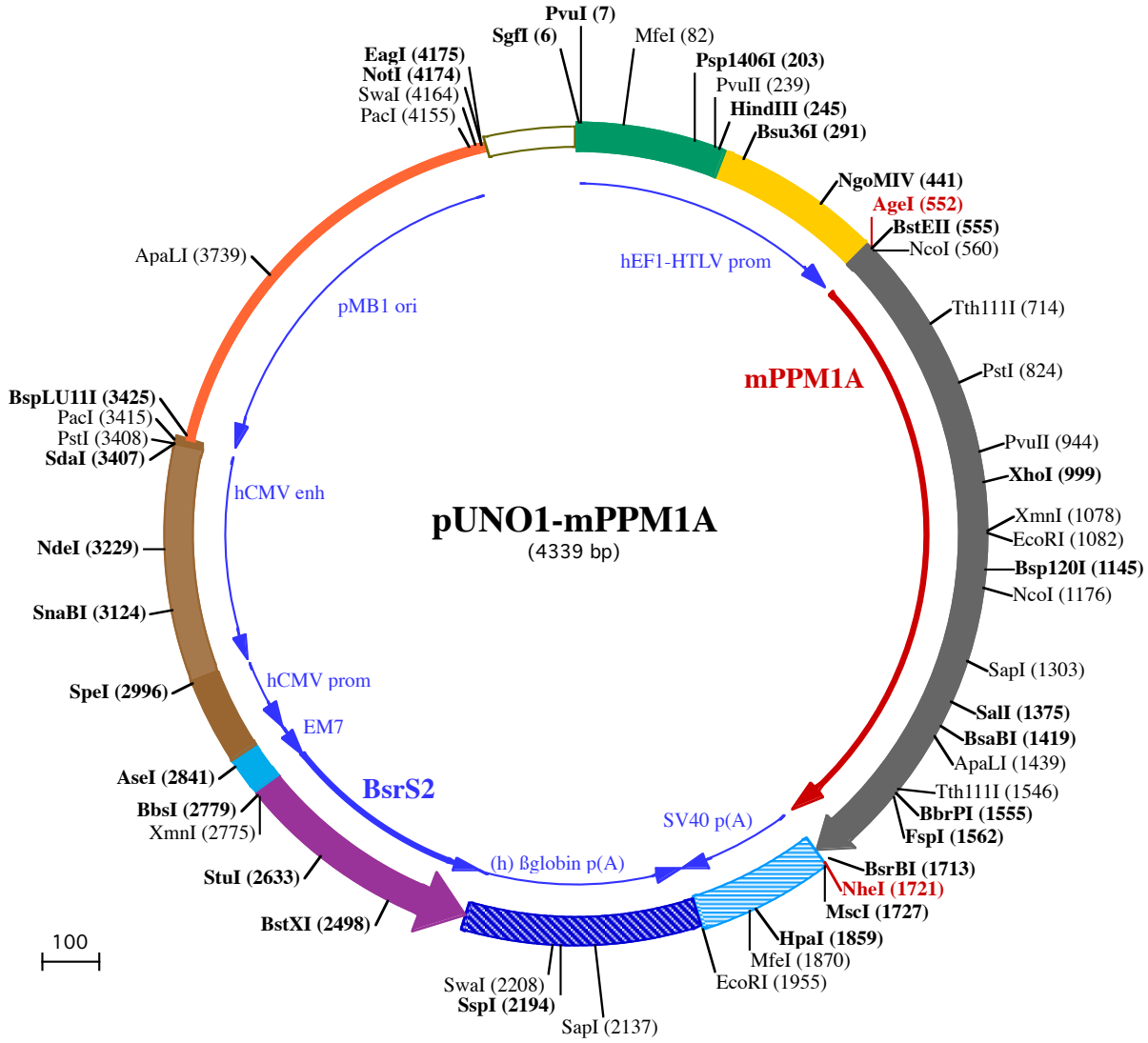
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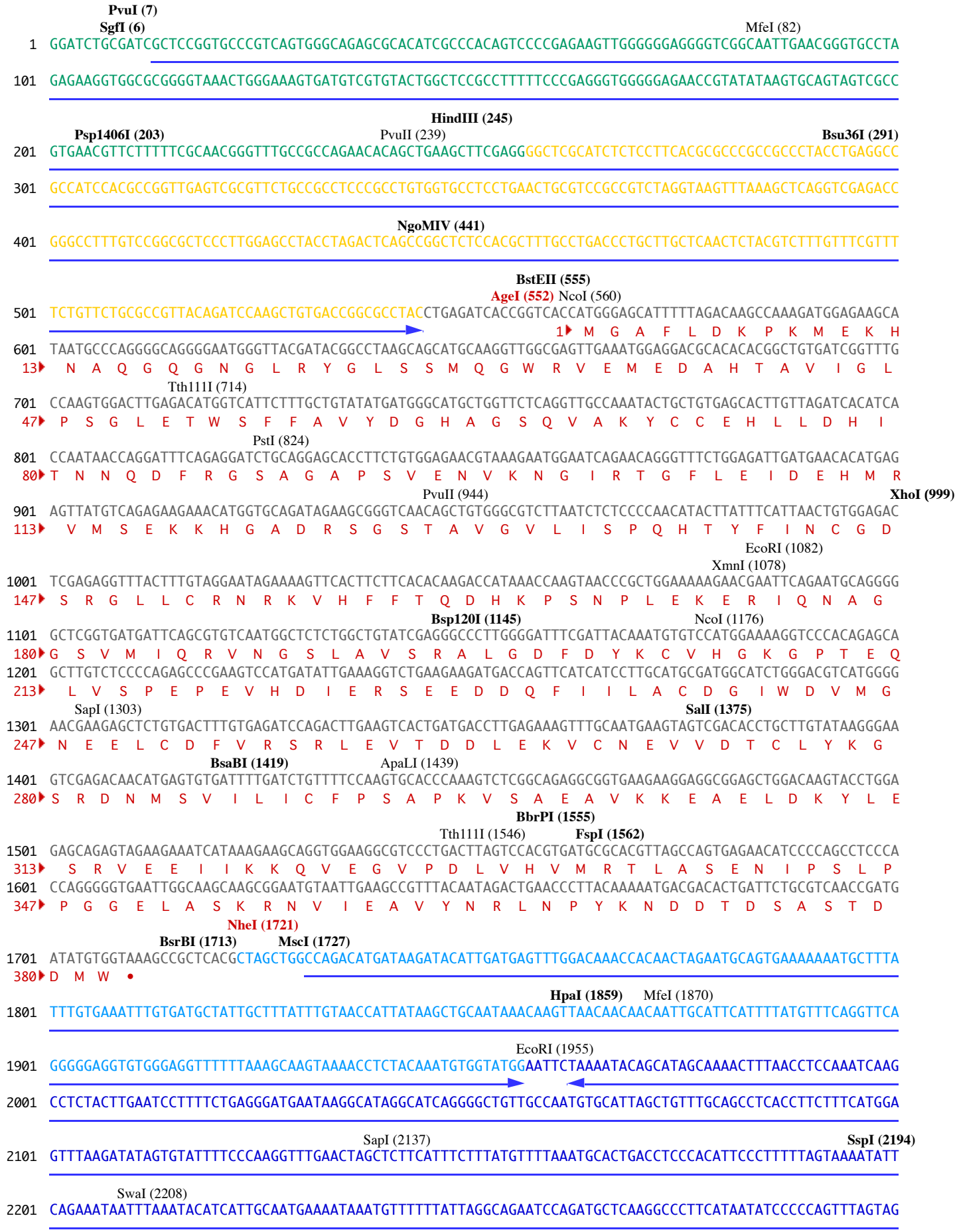
(4339 bp)
mPPM1A
BsrS2
hEF1-HTLV prom
pMB1 ori
hCMV enh
hCMV prom
EM7
SV40 p(A)
(h) ßglobin p(A)
PvuI (7)
SgfI (6)
MfeI (82)
Psp1406I (203)
PvuII (239)
HindIII (245)
Bsu36I (291)
NgoMIV (441)
AgeI (552)
BstEII (555)
NcoI (560)
Tth111I (714)
PstI (824)
PvuII (944)
XhoI (999)
XmnI (1078)
EcoRI (1082)
Bsp120I (1145)
NcoI (1176)
SapI (1303)
SalI (1375)
BsaBI (1419)
ApaLI (1439)
Tth111I (1546)
BbrPI (1555)
FspI (1562)
BsrBI (1713)
NheI (1721)
MscI (1727)
HpaI (1859)
MfeI (1870)
EcoRI (1955)
SapI (2137)
SwaI (2208)
SspI (2194)
BstXI (2498)
StuI (2633)
BbsI (2779)
XmnI (2775)
AseI (2841)
SpeI (2996)
SnaBI (3124)
NdeI (3229)
BspLU11I (3425)
PacI (3415)
PstI (3408)
SdaI (3407)
ApaLI (3739)
EagI (4175)
NotI (4174)
SwaI (4164)
PacI (4155)
100


PvuI (7)
SgfI (6)
MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
HindIII (245)
Psp1406I (203)
PvuII (239)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
BstEII (555)
AgeI (552) NcoI (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCACCATGGGAGCATTTTTAGACAAGCCAAAGATGGAGAAGCA
1 M G A F L D K P K M E K H
601 TAATGCCCAGGGGCAGGGGAATGGGTTACGATACGGCCTAAGCAGCATGCAAGGTTGGCGAGTTGAAATGGAGGACGCACACACGGCTGTGATCGGTTTG
13 N A Q G Q G N G L R Y G L S S M Q G W R V E M E D A H T A V I G L
Tth111I (714)
701 CCAAGTGGACTTGAGACATGGTCATTCTTTGCTGTATATGATGGGCATGCTGGTTCTCAGGTTGCCAAATACTGCTGTGAGCACTTGTTAGATCACATCA
47 P S G L E T W S F F A V Y D G H A G S Q V A K Y C C E H L L D H I
PstI (824)
801 CCAATAACCAGGATTTCAGAGGATCTGCAGGAGCACCTTCTGTGGAGAACGTAAAGAATGGAATCAGAACAGGGTTTCTGGAGATTGATGAACACATGAG
80 T N N Q D F R G S A G A P S V E N V K N G I R T G F L E I D E H M R
PvuII (944)
XhoI (999)
901 AGTTATGTCAGAGAAGAAACATGGTGCAGATAGAAGCGGGTCAACAGCTGTGGGCGTCTTAATCTCTCCCCAACATACTTATTTCATTAACTGTGGAGAC
113 V M S E K K H G A D R S G S T A V G V L I S P Q H T Y F I N C G D
EcoRI (1082)
XmnI (1078)
1001 TCGAGAGGTTTACTTTGTAGGAATAGAAAAGTTCACTTCTTCACACAAGACCATAAACCAAGTAACCCGCTGGAAAAAGAACGAATTCAGAATGCAGGGG
147 S R G L L C R N R K V H F F T Q D H K P S N P L E K E R I Q N A G
Bsp120I (1145)
NcoI (1176)
1101 GCTCGGTGATGATTCAGCGTGTCAATGGCTCTCTGGCTGTATCGAGGGCCCTTGGGGATTTCGATTACAAATGTGTCCATGGAAAAGGTCCCACAGAGCA
180 G S V M I Q R V N G S L A V S R A L G D F D Y K C V H G K G P T E Q
1201 GCTTGTCTCCCCAGAGCCCGAAGTCCATGATATTGAAAGGTCTGAAGAAGATGACCAGTTCATCATCCTTGCATGCGATGGCATCTGGGACGTCATGGGG
213 L V S P E P E V H D I E R S E E D D Q F I I L A C D G I W D V M G
SapI (1303)
SalI (1375)
1301 AACGAAGAGCTCTGTGACTTTGTGAGATCCAGACTTGAAGTCACTGATGACCTTGAGAAAGTTTGCAATGAAGTAGTCGACACCTGCTTGTATAAGGGAA
247 N E E L C D F V R S R L E V T D D L E K V C N E V V D T C L Y K G
BsaBI (1419)
ApaLI (1439)
1401 GTCGAGACAACATGAGTGTGATTTTGATCTGTTTTCCAAGTGCACCCAAAGTCTCGGCAGAGGCGGTGAAGAAGGAGGCGGAGCTGGACAAGTACCTGGA
280 S R D N M S V I L I C F P S A P K V S A E A V K K E A E L D K Y L E
BbrPI (1555)
Tth111I (1546)
FspI (1562)
1501 GAGCAGAGTAGAAGAAATCATAAAGAAGCAGGTGGAAGGCGTCCCTGACTTAGTCCACGTGATGCGCACGTTAGCCAGTGAGAACATCCCCAGCCTCCCA
313 S R V E E I I K K Q V E G V P D L V H V M R T L A S E N I P S L P
1601 CCAGGGGGTGAATTGGCAAGCAAGCGGAATGTAATTGAAGCCGTTTACAATAGACTGAACCCTTACAAAAATGACGACACTGATTCTGCGTCAACCGATG
347 P G G E L A S K R N V I E A V Y N R L N P Y K N D D T D S A S T D
NheI (1721)
BsrBI (1713)
MscI (1727)
1701 ATATGTGGTAAAGCCGCTCACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTA
380 D M W •
HpaI (1859)
MfeI (1870)
1801 TTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCA
EcoRI (1955)
1901 GGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTTTAACCTCCAAATCAAG
2001 CCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGA
SapI (2137)
SspI (2194)
2101 GTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAATATT
SwaI (2208)
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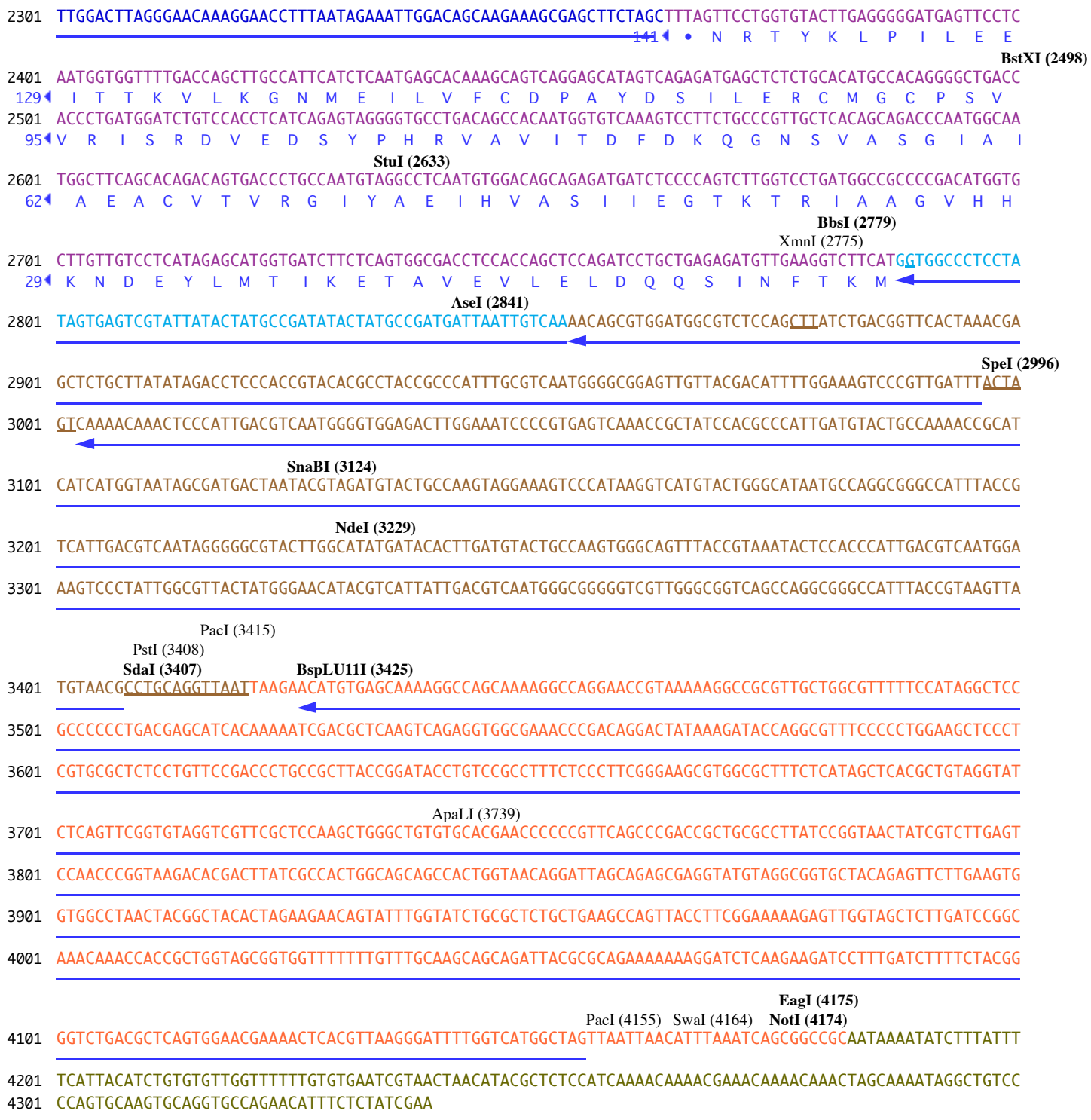
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141 • N R T Y K L P I L E E
BstXI (2498)
2401 AATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACC
129 I T T K V L K G N M E I L V F C D P A Y D S I L E R C M G C P S V
2501 ACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAA
95 V R I S R D V E D S Y P H R V A V I T D F D K Q G N S V A S G I A I
StuI (2633)
2601 TGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCCGACATGGTG
62 A E A C V T V R G I Y A E I H V A S I I E G T K T R I A A G V H H
BbsI (2779)
XmnI (2775)
2701 CTTGTTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTA
29 K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M
AseI (2841)
2801 TAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGA
SpeI (2996)
2901 GCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTA
3001 GTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCATTGATGTACTGCCAAAACCGCAT
SnaBI (3124)
3101 CATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCG
NdeI (3229)
3201 TCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGA
3301 AAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTA
PacI (3415)
PstI (3408)
SdaI (3407)
BspLU11I (3425)
3401 TGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCC
3501 GCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCT
3601 CGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT
ApaLI (3739)
3701 CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGT
3801 CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG
3901 GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC
4001 AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG
EagI (4175)
PacI (4155) SwaI (4164) NotI (4174)
4101 GGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTT
4201 TCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCC
4301 CCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA