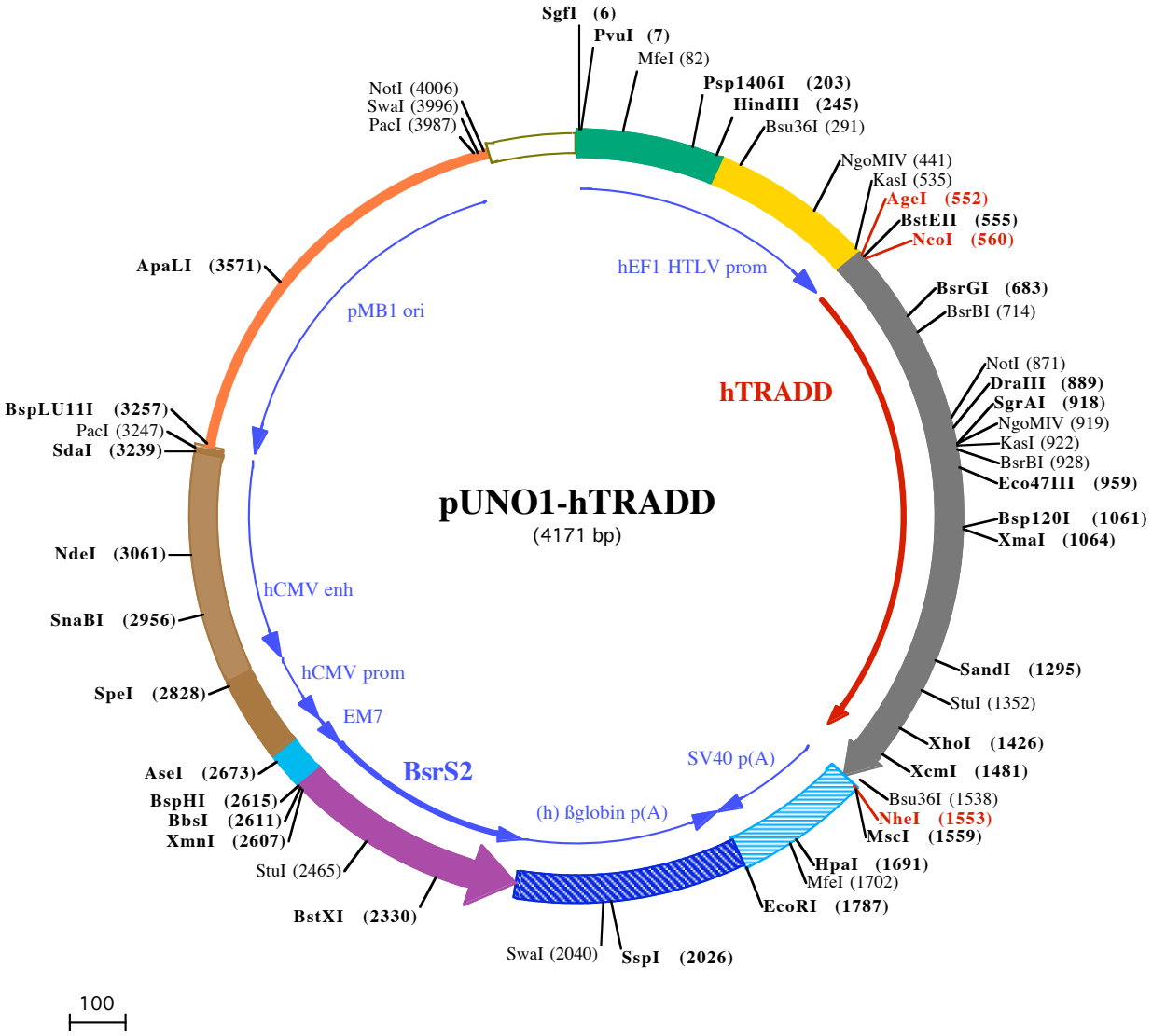
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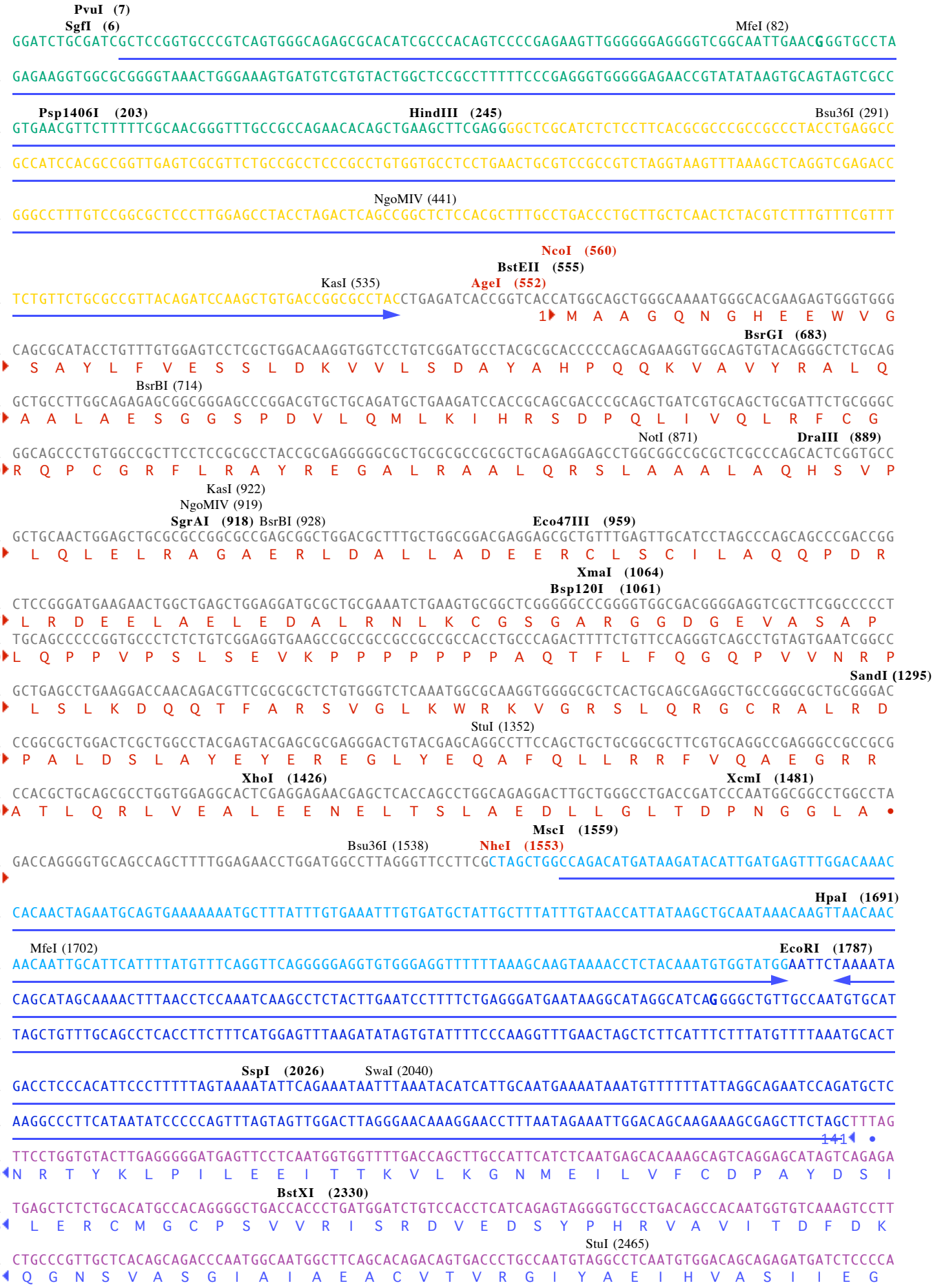
(4171 bp)
SgfI (6)
PvuI (7)
MfeI (82)
Psp1406I (203)
HindIII (245)
Bsu36I (291)
NgoMIV (441)
KasI (535)
AgeI (552)
BstEII (555)
NcoI (560)
BsrGI (683)
BsrBI (714)
NotI (871)
DraIII (889)
SgrAI (918)
NgoMIV (919)
KasI (922)
BsrBI (928)
Eco47III (959)
Bsp120I (1061)
XmaI (1064)
SandI (1295)
StuI (1352)
XhoI (1426)
XcmI (1481)
Bsu36I (1538)
NheI (1553)
MscI (1559)
HpaI (1691)
MfeI (1702)
EcoRI (1787)
SspI (2026)
SwaI (2040)
BstXI (2330)
StuI (2465)
XmnI (2607)
BbsI (2611)
BspHI (2615)
AseI (2673)
SpeI (2828)
SnaBI (2956)
NdeI (3061)
SdaI (3239)
PacI (3247)
BspLU11I (3257)
ApaLI (3571)
NotI (4006)
SwaI (3996)
PacI (3987)
hEF1-HTLV prom
hTRADD
pMB1 ori
hCMV enh
hCMV prom
EM7
BsrS2
SV40 p(A)
(h) ßglobin p(A)
100


PvuI (7)
SgfI (6)
MfeI (82)
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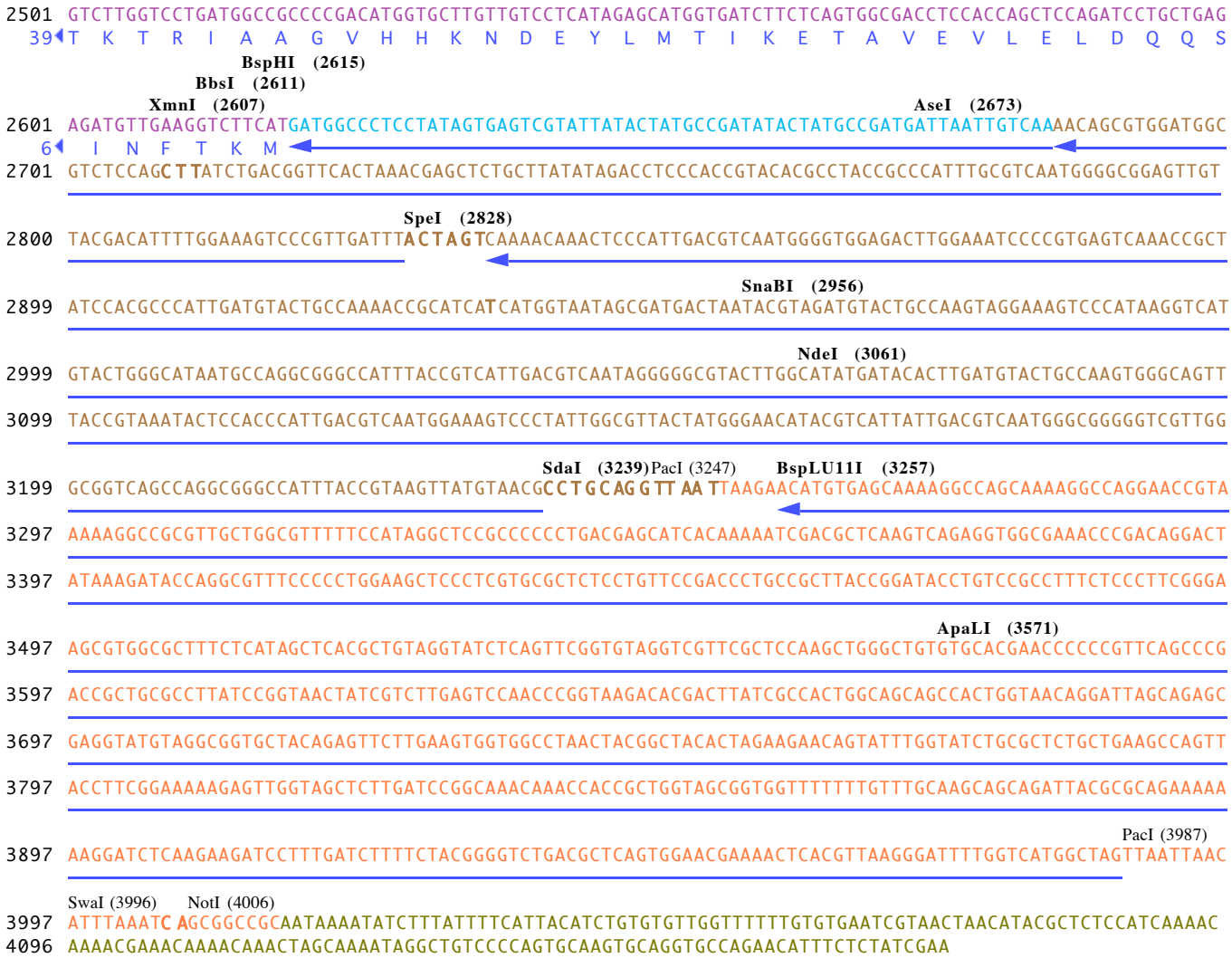
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
Psp1406I (203)
HindIII (245)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTT
NcoI (560)
BstEII (555)
KasI (535)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCACCATGGCAGCTGGGCAAAATGGGCACGAAGAGTGGGTGGG
1 M A A G Q N G H E E W V G
BsrGI (683)
601 CAGCGCATACCTGTTTGTGGAGTCCTCGCTGGACAAGGTGGTCCTGTCGGATGCCTACGCGCACCCCCAGCAGAAGGTGGCAGTGTACAGGGCTCTGCAG
13 S A Y L F V E S S L D K V V L S D A Y A H P Q Q K V A V Y R A L Q
BsrBI (714)
701 GCTGCCTTGGCAGAGAGCGGCGGGAGCCCGGACGTGCTGCAGATGCTGAAGATCCACCGCAGCGACCCGCAGCTGATCGTGCAGCTGCGATTCTGCGGGC
47 A A L A E S G G S P D V L Q M L K I H R S D P Q L I V Q L R F C G
NotI (871)
DraIII (889)
801 GGCAGCCCTGTGGCCGCTTCCTCCGCGCCTACCGCGAGGGGGCGCTGCGCGCCGCGCTGCAGAGGAGCCTGGCGGCCGCGCTCGCCCAGCACTCGGTGCC
80 R Q P C G R F L R A Y R E G A L R A A L Q R S L A A A L A Q H S V P
KasI (922)
NgoMIV (919)
SgrAI (918)
BsrBI (928)
Eco47III (959)
901 GCTGCAACTGGAGCTGCGCGCCGGCGCCGAGCGGCTGGACGCTTTGCTGGCGGACGAGGAGCGCTGTTTGAGTTGCATCCTAGCCCAGCAGCCCGACCGG
113 L Q L E L R A G A E R L D A L L A D E E R C L S C I L A Q Q P D R
XmaI (1064)
Bsp120I (1061)
1001 CTCCGGGATGAAGAACTGGCTGAGCTGGAGGATGCGCTGCGAAATCTGAAGTGCGGCTCGGGGGCCCGGGGTGGCGACGGGGAGGTCGCTTCGGCCCCCT
147 L R D E E L A E L E D A L R N L K C G S G A R G G D G E V A S A P
1101 TGCAGCCCCCGGTGCCCTCTCTGTCGGAGGTGAAGCCGCCGCCGCCGCCGCCACCTGCCCAGACTTTTCTGTTCCAGGGTCAGCCTGTAGTGAATCGGCC
180 L Q P P V P S L S E V K P P P P P P P A Q T F L F Q G Q P V V N R P
SandI (1295)
1201 GCTGAGCCTGAAGGACCAACAGACGTTCGCGCGCTCTGTGGGTCTCAAATGGCGCAAGGTGGGGCGCTCACTGCAGCGAGGCTGCCGGGCGCTGCGGGAC
213 L S L K D Q Q T F A R S V G L K W R K V G R S L Q R G C R A L R D
StuI (1352)
1301 CCGGCGCTGGACTCGCTGGCCTACGAGTACGAGCGCGAGGGACTGTACGAGCAGGCCTTCCAGCTGCTGCGGCGCTTCGTGCAGGCCGAGGGCCGCCGCG
247 P A L D S L A Y E Y E R E G L Y E Q A F Q L L R R F V Q A E G R R
XhoI (1426)
XcmI (1481)
1401 CCACGCTGCAGCGCCTGGTGGAGGCACTCGAGGAGAACGAGCTCACCAGCCTGGCAGAGGACTTGCTGGGCCTGACCGATCCCAATGGCGGCCTGGCCTA
280 A T L Q R L V E A L E E N E L T S L A E D L L G L T D P N G G L A •
MscI (1559)
Bsu36I (1538)
NheI (1553)
1501 GACCAGGGGTGCAGCCAGCTTTTGGAGAACCTGGATGGCCTTAGGGTTCCTTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAAC
313
HpaI (1691)
1601 CACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAC
MfeI (1702)
EcoRI (1787)
1701 AACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATA
1801 CAGCATAGCAAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCAT
1901 TAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACT
SspI (2026)
SwaI (2040)
2001 GACCTCCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTC
2101 AAGGCCCTTCATAATATCCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAG
141 •
2201 TTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGA
139 N R T Y K L P I L E E I T T K V L K G N M E I L V F C D P A Y D S I
BstXI (2330)
2301 TGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTT
106 L E R C M G C P S V V R I S R D V E D S Y P H R V A V I T D F D K
StuI (2465)
2401 CTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCA
73 Q G N S V A S G I A I A E A C V T V R G I Y A E I H V A S I I E G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39 T K T R I A A G V H H K N D E Y L M T I K E T A V E V L E L D Q Q S
BspHI (2615)
BbsI (2611)
XmnI (2607)
AseI (2673)
2601 AGATGTTGAAGGTCTTCATGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGC
6 I N F T K M
2701 GTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGT
SpeI (2828)
2800 TACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCT
SnaBI (2956)
2899 ATCCACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCAT
NdeI (3061)
2999 GTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTT
3099 TACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCGTTGG
SdaI (3239) PacI (3247) BspLU11I (3257)
3199 GCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA
3297 AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT
3397 ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA
ApaLI (3571)
3497 AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCG
3597 ACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC
3697 GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT
3797 ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAA
PacI (3987)
3897 AAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAAC
SwaI (3996) NotI (4006)
3997 ATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAC
4096 AAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA