



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTATGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGGCTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

BstEII (555) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGGGTGGAGGGCTGCACCAAATGCATCAAATACCT

AgeI (552) **NcoI (560)** **NsiI (585)** **BstAPI (578)**
1 M G V E G C T K C I K Y L

AvrII (645) 601 GCTCTTCGTTCAATTCGTTCTTGCTGGCTGGAGGCGTGATCCTAGGTGTAGCTCTGTGGTTCGCTCATGATCCACAGACCACCAGCCTGCTGTAC

13 L F V F N F V F W L A G G V I L G V A L W L R H D P Q T T S L L Y
701 CTGGAACCTGGGAACAACCGGCACCCAACACCTTCTACGTGGGCATCATCTCATTGCTGTGGAGCTGTGATGATGTTGTAGGCTTCTGGGGT

47 L E L G N K P A P N T F Y V G I Y I L I A V G A V M M F V G F L G
801 GCTATGGGCCATCCAGGAGTCCAGTGTCTGTGGGACGTTCTCACCTGCCTTGTGATCCTGTTGCTGTGAGGTGGCTGCAGGCATCTGGGGCTT

80 C Y G A I Q E S Q C L L G T F F T C L V I L F A C E V A A G I W G F
901 CGTAAACAAGACAGATCGCCAAGGATGTGAAGCAGTTCATGACCAGGCCCTCAGCAAGCTGTGATGGATGATGATGCAACAATGCCAAGGCTGTG

113 V N K D Q I A K D V K Q F Y D Q A L Q Q A V M D D D A N N A K A V

Bsu36I (1088)
1001 GTGAAGACTTTCATGAGACGCTCAACTGTTGTGGCTCCAACGCCTGACCACACTGACTACCACCACTACTGAGGAACAGCCTGTGTCCTCAGGCGGCA

147 V K T F H E T L N C C G S N A L T T L T T T I L R N S L C P S G G

BsaBI (1126) 1101 ACATACTACCCCTTACTGCAGCAAGATTGCATCAGAAAATCGATGAGCTTCTCTGGGAAGCTGTACCTCATTGGAATTGCAGCATTGTGGTAGC

180 N I L T P L L Q Q D C H Q K I D E L F S G K L Y L I G I A A I V V A

ClaI (1141)
BspEI (1250) 1201 TGTCATTATGATCTTTGAGATGATTCTGAGCATGGTGTGTGCTGTGGCATCCGGAACAGCTCCGTGTACTGAGGCCCTTGCATTGCAGCTAGCTGGCC

213 V I M I F E M I L S M V L C C G I R N S S V Y •

1301 AGACATGATAAGATACATTGATGAGTTTGGACAACCACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTT

MscI (1295)
NheI (1289)
HpaI (1427) 1401 GTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCATTTATGTTTCAGGTTGAGGGGAGGTGTGGGAGTTTTTAAAGCAAGT

1438 MfeI (1438)
EcoRI (1523) 1501 AAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGAAAACCTTAACTCCAAATCAAGCCTCTACTGAACTCTTTTCTGAGGGATGAAT

1523
1601 AAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATATAGTATTTTCCCAAGGTTTG

SspI (1762) 1701 AACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAA

1762
SwaI (1776) 1801 AATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAG

1776
1901 AAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCT

1911 • N R T Y K L P I L E E I T T K V L K G N M E
2001 CAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTA

118 I L V F C D P A Y D S I L E R C M G C P S V V R I S R D V E D S Y
2101 GGGTGCTGACAGCCAAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATG

85 P H R V A V I T D F D K Q G N S V A S G I A I A E A C V T V R G I
StuI (2201) 2201 TAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTCT

51 Y A E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E
2301 CAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACT

18 T A V E V L E L D Q Q S I N F T K M
AseI (2409) 2401 ATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTGCTTATATAGACCTCCACCGTACAGC

2501 CCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGG
SpeI (2564)
←

2601 TGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGA
SnaBI (2692)

2701 TGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTACCCTGTCATTGACGTCAATAGGGGGCGTACTTGGCAT
NdeI (2797)

2801 ATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATAC

2901 GTCATTATTGACGTCAATGGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTACCCTAAGTTATGTAACGCCTGCAGGTTAAITAAAGAACATGTG
SdaI (2975) PacI (2983) BspLU11I (2993)
←

3001 AGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGC

3101 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTCCGACCCTGCCGCTTA

3201 CCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCT

3301 GGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTG
ApaLI (3307)

3401 GCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAG

3501 TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGTTTTTT

3601 TGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGT

3701 TAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGA
PacI (3723) SwaI (3732) EagI (3743) NotI (3742)

3801 ATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTCTC

3901 TATCGAA