



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**
301 GCCATCCACGCGGTTGAGTGCCTGTTGCGCCCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTGTTTCGTTT

NcoI (560)
BstEII (555) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTCCACCTGGGAGTGGAGGGCTGCACCAAGTGCATCAAGTACCT **DraIII (579)**
AgeI (552) **BstAPI (578)** 1 M G V E G C T K C I K Y L

SapI (600)
601 GCTCTTCGTCTTCAATTTCTGCTTCTGGCTGGTGGAGGCGTGATCCTGGGTGTGGCCCTGTGGCTCCGCCATGACCCGACAGACCACCAACCTCCTGTAT
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 N L L Y
701 CTGGAGCTGGGAGACAAGCCCGCGCCCAACACCTTCTATGTAGGCATCTACATCCTCATCGTGTGGGCGCTGCATGATGTTCTGGCTTCTCTGGGCT
47 L E L G D 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
BspHI (773)
801 GCTACGGGGCCATCCAGGAATCCAGTGCCTGTGGGACGTTCTTACCTGCCTGGTGCATCCTGTTTGCCTGTGAGGTGGCCGCCGATCTGGGGCTT
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 TGTCAACAAGGACAGATCGCCAAGGATGTGAAGCAGTTCTATGACCAGGCCCTACAGCAGGCGTGGTGGATGATGACGCCAACAACGCAAGGCTGTG
113 V N K D Q I A K D V K Q F Y D Q A L Q Q A V V D D D A N N A K A V
1001 GTGAAGACCTTCCACGAGACGCTTGACTGCTGTGGCTCCAGCACACTGACTGCTTTGACCACCTCAGTGCCTCAAGAACAATTTGTGCTCCCTCGGGCAGCA
147 V K T F H E T L D C C G S S T L T A L T T S V L K N N L C P S G S
NgoMIV (883)

ClaI (1141)
1101 ACATCATCAGCAACCTCTTCAAGGAGGACTGCCACCAGAAGATCGATGACCTTCTCCGGGAAGCTGTACCTCATCGGCATTGCTGCCATCGTGGTCCG
180 N I I S N L F K E D C H Q K I D D L F S G K L Y L I G I A A I V V A

BspHI [m] (1205) 1201 TGTGATCATGATCTTCGAGATGATCCTGAGCATGGTGTGCTGTGGCTGGCAGCAGCTCCGTGACTGAGGCCCGCAGCTCTGCTAGCTGGCCAG **BsaBI (1203)** **BspEI (1250)** **NheI (1287)**
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 ACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTGTGAAATTTGTGATGCTATTGCTTTATTGT

HpaI (1425) 1401 AACCATATAAGCTGCAATAAACAGTTAAACAACAACATTCATTTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAA **MfeI (1436)**

EcoRI (1521)
1501 AACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAA
1601 GGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCCTCACCTTTTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGTTTTGAA

SapI (1703) 1701 CTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAAA **SspI (1760)** **SwaI (1774)**
1801 TAAATGTTTTTTATTAGGAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAA
1901 ATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCA
141 • N R T Y K L P I L E E I T T K V L K G N M E

SacI (2035)
2001 ATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGG
117 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 P
StuI (2199)
2101 GGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTA
84 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 Y
2201 GGCCTCAATGTGGACAGCAGAGATGATCTCCCGCTTGGTCTGATGGCCGCCGACATGGTGTGTTGCTCCTCATAGAGCATGGTGTCTTCTCA
51 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 GTGGGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTAT
17 T A V E V L E L D Q Q S I N F T K M

AseI (2407) 2401 GCCGATGATTAATGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCC **SacI (2464)**

SpeI (2562)
2501 TACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAGTCCCGTTGATTTACTAGTCAAACAACCTCCATTGACGTCAATGGGGT

2601 GAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATG **SnaBI (2690)**

 2701 TACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATAT **NdeI (2795)**

 2801 GATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGT

PstI (2974)
SdaI (2973)

PacI (2981)
BspLU11I (2991)

 2901 CATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAG

 3001 CAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTC

 3101 AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACC

 3201 GGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGG

ApaLI (3305)

 3301 GCTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGC

 3401 AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA

 3501 TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTG

 3601 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTA

EagI (3741)

PacI (3721) **SwaI (3730)** **NotI (3740)**

 3701 AGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAAT

 3801 CGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTA
 3901 TCGAA