



PvuI (7)
SgfI (6)
MfeI (82)

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCC

301 GCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) **NcoI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGCGAAGACCTACGATTACCTGTTCAAGCTGCTGCT

1▶ M A K T Y D Y L F K L L L

PshAI (624)

601 GATCGGGGACTCGGGGTGGGGAAGACCTGTGTCTGTTCGCTTCTCCGAGGACGCCTTCAACTCCACTTTTATCTCCACCATAGGAATTGACTTTAAA

13▶ I G D S G V G K T C V L F R F S E D A F N S T F I S T I G I D F K

701 ATTAGGACCATAGAGCTCGATGGCAAGAGAATAAAGTGCAGATATGGGACACAGCCGTCAGGAACGGTTTCGGACGATCACAACGGCCTACTACAGGG

47▶ I R T I E L D G K R I K L Q I W D T A G Q E R F R T I T T A Y Y R

BspEI (857)

801 GTGCAATGGGCATCATGCTGGTCTACGACATCACCAACGAGAAGTCTTCGACAACATCCGGAACGGATTGCAACATTGAGGAGCAGCGCTCTGCAGA

80▶ G A M G I M L V Y D I T N E K S F D N I R N W I R N I E E H A S A D

901 CGTCGAAAAGATGATACTCGGGAACAAGTGTGATGTGAATGACAAGAGACAAGTTTCCAAGGAACGGGGAGAAAAGCTGGCCCTCGACTATGGAATCAAG

113▶ V E K M I L G N K C D V N D K R Q V S K E R G E K L A L D Y G I K

XcmI (1022) **NsiI (1040)** **EcoRV (1063)**

1001 TTCATGGAGACCAGCGCAAGGCCAACATCAATGTGAAAAATGCATTTTCTACTCTCGCCAGAGATATCAAAGCAAAAATGGACAAAAAATTGGAAGGCA

147▶ F M E T S A K A N I N V E N A F F T L A R D I K A K M D K K L E G

MscI (1193)

NheI (1187)

1101 ACAGCCCCAGGGGAGCAACCAGGGAGTCAAAATCACACCGGACCAGCAGAAGAGGAGCAGCTTTTTCCGATGTGTTCTTCTGTGAGGCTAGCTGGCCAG

180▶ N S P Q G S N Q G V K I T P D Q Q K R S S F F R C V L L •

1201 ACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGT

HpaI (1325) **MfeI (1336)**

1301 AACCAATTATAAGCTGCAATAAAACAAGTTAAACAACAACATTGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAA

EcoRI (1421)

1401 AACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAA

1501 GGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAA

SapI (1603)
SspI (1660)
SwaI (1674)

1601 CTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAA

EcoO109I (1735)

1701 TAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAA

1801 ATTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCATCTCA

141▶ • N R T Y K L P I L E E I T T K V L K G N M E

BstXI (1964)

1901 ATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGG

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 (2099)

2001 GGTGCCTGACAGCCAAATGGTGTCAAAGTCTTCTGCCGTTGCTCAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGCCTGCCAATGTA

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

2101 GGCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCGACATGGTGTCTGTTGTCCTCATAGAGCATGGTGTCTTCTCA

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

2201 GTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTAT

17▶ T A V E V L E L D Q Q S I N F T K M

AseI (2307)

2301 GCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCC

2401 TACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTG
SpeI (2462)
←

2501 GAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATG
SnaBI (2590)

2601 TACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATAT
NdeI (2695)

2701 GATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGT

2801 CATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAG
SdaI (2873) **PaeI (2881)** **BspLU11I (2891)**
←

2901 CAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAAATCGACGCTC

3001 AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGCTTACC

3101 GGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCCAAGCTGG

3201 **ApaLI (3205)**
GCTGTGTGCACGAACCCCGTTAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGC

3301 AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA

3401 TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG

3501 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTA

3601 **EagI (3641)**
PaeI (3621) **SwaI (3630)** **NotI (3640)**
AGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGTTTTTGTGTGAAT

3701 CGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGAAGTGACGGTGCCAGAACATTTCTCTA

3801 TCGAA