



100

PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTATGTCGTGACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NgoMIV (441)

501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTACCATGGCGCTCCTCAGCTGCTCCTCTTTGCCATGCTGGC

BstEII (555) **AgeI (552)** **NcoI (560)** 1▶ M A L L Q L L L F A M L A

601 TGCCTGTGGCTTCTCAGAGGAGCAGACAGAAGGCATCACCATTGCCTACAAAGTACTGGAAGTTTATCCCAAAGCCGGAGGGTGTATAACCTGCGAT

13▶ A C G F S E E Q T E G I T I A Y K V L E V Y P Q S R R V L I T C D

Scal (651)

701 GCCCTGAGGCGTCCAGCCCATCACATACTCTCCTGCTAGCCAGGTATCCTGGTGGCAAAAAAGTTGTGCATGACTCCGTGCCGCTCCTTCA

47▶ A P E A S Q P I T Y S L L A S R G I L V A K K V V H D S V P A S F

NheI (739) **NgoMIV (786)**

801 ACATCAATATCACCATCAAGTCCAGCCAGACCTGCTCACCTACTCCTGCCAGGCAACCTCGAACTCTGGCACCTATGGACCCAGCAGCAGGCTCCAGAT

80▶ N I N I T I K S S P D L L T Y S C Q A T S N S G T Y G P S S R L Q M

901 GTACCAGAACTGTGGGCTAAGCCAGTGTCTCAGTGCAGGCTGACTTCGTCTACGCCATGGGGACTCGGGCCCACTGTGGAGCTGCTCCTGCCTGGCA

113▶ Y Q E L W A K P V S Q L Q A D F V L R H G D S G P T V E L S C L A

PstI (934) **Tth111I (943)** **NcoI (957)** **EcoO109I (969)**

1001 TCCTCAGGAGCCCGCCATCACCTACCCTGGTGGGGAATGDTGGGCGTGTCTTGACAGCAAAGGCCACTTCATGAAAAACAGCCAATTCTCCC

147▶ S S G S P P I T Y R L V G N G G R V L A Q Q R P L H G K P A N F S

1101 TCCCGCTGTCCCAGACCACTGGTTGGTTCAGTGCGAAGCTGAAAACGATGTGGTGTGGACAGCAGTGCCCGCATCCCGTCCCGGAGCAGAGGCCGG

180▶ L P L S Q T T G W F Q C E A E N D V G V D S S A R I P L P R A E A R

BstXI (1110)

1201 AGCCAAGCTGGTGACCACCTCGCAGGGGAGCTGCCCTGACACCCACCTGTATTCTGGCTGGCAGCCTCGTCTCCATAGCCGTTATTGCTTCCAGGATG

213▶ A K L V T T L A G E L P L T P T C I L A G S L V S I A V I A S R M

BstEII (1209) **XcmI (1244)**

1301 CTGAGCTCGACCGGTTGTGACCGGAAGACAGGCCATGCCTAGGACTAGTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC

247▶ L S S T G L •

BbsI (1324) **AvrII (1339)** **MscI (1351)**

1401 GAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTG

HpaI (1483) **MfeI (1494)**

1501 CATTCAATTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAG

EcoRI (1579)

1601 CAAAACTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTT

1701 TGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTACTGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCC

SapI (1761)

1801 ACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCT

SspI (1818) **SwaI (1832)** **EcoO109I (1893)**

1901 TCATAATATCCCCAGTTTAGTGTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGT

141▶ • N R T

2001 GACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCT

137▶ 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 L E

BstXI (2122)

2101 CTGCATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGT

103▶ 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 Q G N

StuI (2257)

2201 TGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTGGT

70▶ 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 T K T

XmnI (2399)

2301 CCTGATGGCCGCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTCTAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTG

37▶ 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 I N

BbsI (2403) AseI (2465)
 2401 AAGGTCCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAG
 3 F T K M
 2501 CTTATCTGACGGTTCACATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATT

SpeI (2620)
 2601 TTGAAAGTCCCCTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCC

SnaBI (2748)
 2701 ATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAAGTCATGTACTGGGCA

NdeI (2853)
 2801 TAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAAT
 2901 ACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGGCGGTGACGC

PacI (3039)
 PstI (3032) SdaI (3031) BspLU11I (3049)
 3001 AGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGT
 TGCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCA
 3101
 3201 GCGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTT

ApaLI (3363)
 3301 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCCACCGCTGCGCCT
 3401 TATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGG
 3501 CGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAA
 3601 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAG

EagI (3799)
 3701 AAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGC
PacI (3779) SnaI (3788) NotI (3798)

3801 GGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAA
 3901 ACAAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA