



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82) EcoNI (96)

101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) 201 **Psp1406I (203)** GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC EcoNI (287) Bsu36I (291)

301 GCCATCCACGCGGTTGAGTTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTTCTTTGTTTCGTTT

501 **SphI (560)** TCTGTTTGTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAGCATGCCAGCCTCATCTCCTTTCTTGTAGCCCCAAAGG AgeI (552) NheI (585)

601 GCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGCCGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGACAGCTCTGGGGCCGTGGCTTGTGCCATG NcoI (695)

13▶ P P G N M G G P V R E P A L S V A L W L S W G A A L G A V A C A M

701 GCTCTGCTGACCCAAACAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCAGGGGACAGGAGCCCTCCAGAATGGGGAAGGGTATCCCT Bsu36I (732)

47▶ A L L T Q Q T E L Q S L R R E V S R L Q G T G G P S Q N G E G Y P

801 GGCAGAGTCTCCCGAGCAGAGTCCGATGCCCTGGAAGCCTGGGAGAGTGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTCACCCAAAAACAGAAGAA

80▶ W Q S L P E Q S S D A L E A W E S G E R S R K R R A V L T Q K Q K K

901 GCAGACTCTGCTCTGCACCTGGTTCCCATTAACGCCACTCCAAGGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGA StuI (999)

113▶ Q H S V L H L V P I N A T S K D D S D V T E V M W Q P A L R R G R

1001 GGCCTACAGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGCTCTGTTTCAAGACGTGACTTTACCATGGGTC XcmI (1091)

147▶ G L Q A Q G Y G V R I Q D A G V Y L L Y S Q V L F Q D V T F T M G NcoI (1091)

1101 AGTGGTGTCTCGAGAAGGCAAGGAGCAGGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCGGACCGGGCTACAACAGCTGCTATAG RsrII (1172) PvuII (1188)

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

1201 CGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTGATAATCCCGGGCAAGGGGAAACTTAACCTCTCTCCACATGGAACCTTCTGGGG BbsI (1207) XmaI (1250)

213▶ A G V F H L H Q G D I L S V I I P R A R A K L N L S P H G T F L G

1301 TTTGTAAACTGTGATTGTGTTATAAAAAGTGGCTCCAGAAATTCGCTAGCTCGACATGATAAGATACATTGATGAGTTTGGACAAAACCAACTAGAAT NheI (1345)

247▶ F V K L • EcoRI (1339)

1401 GCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCA

1501 **HpaI (1508)** AATAACAAGTTAAACAACAATAATTCATTTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTTACAAATGTGG MfeI (1519)

1601 **EcoRI (1604)** TATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGG

1701 **SapI (1786)** CTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTATTTTCCCAAGTTTGAAGTACTAGCTTTCATTTCTT

1801 **SspI (1843)** TATGTTTTAAATGCAGTACCTCCACATTCCCTTTTATAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAG SwaI (1857)

1901 GCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACAAAGGAACCTTAAATAGAATTGGACAGCAAGAAAG

2001 CGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTC

141▶ 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

2101 AGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACA SacI (2118)

112▶ 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 H R V A V

2201 ATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAG StuI (2282)

78▶ 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 A E I H V A

2301 CAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAG

45▶ 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 T A V E V L

2401 **XmnI (2424)** CTCCAGATCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTC BbsI (2428) AseI (2490)

12▶ E L D Q Q S I N F T K M

2501 AAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTC
SacI (2547)

2601 AATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTTGACGTCAATGGGGTGGAGACTTGGAAATCCCC
SpeI (2645)

2701 GTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAA
SnaBI (2773)

2801 GTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACT
NdeI (2878)

2901 GCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATG

3001 GCGGGGGTCTGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCGTCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAG
PacI (3064) SdaI (3056) BspLU11I (3074)

3101 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAA
BspLU11I (3074)

3201 ACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTT

3301 TCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC
ApaLI (3388)

3401 CCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA

3501 GGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCT

3601 GCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGGTGAAGCAGCAGATT

3701 ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGG

3801 CTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCT
PacI (3804) SnaI (3813) EagI (3824) NotI (3823)

3901 CTCCATCAAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA