



PvuI (7)
SgfI (6)

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) **NcoI (560)** **BspEI (581)** **XmnI (595)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGGTATATCTCAGAGGTCGGAAATTTCCAGGAAAC

601 TATCACCAGTTAGAGGGTGCCTTGTAAAGACAAGACCATCAATCCGGGAGCTGACTGCTAAATGGAACTCAGAGTATGTATGTAAGTGAGCTCAAA

13▶ I H Q L E G R L V R Q D H Q I R E L T A K M E T Q S M Y V S E L K

701 CGAACCATTGCAACCTTGAGGACAAAGTTGCTGAAATCGAAGCACAGCAGTGAATGGAATTTATATTTGGAAGATTGGCAACTTTGGAATGCATTTGA

47▶ R T I R T L E D K V A E I E A Q Q C N G I Y I W K I G N F G M H L

801 AATGTCAAGAAGAGGAGAAACCTGTTGTGATTCATAGCCCTGGATTCTACACTGGCAAACCCGGTACAACTGTGCATGCGCTTGCACCTTCAGTTACC

80▶ K C Q E E E K P V V I H S P G F Y T G K P G Y K L C M R L H L Q L P

901 GACTGCTCAGCGCTGTGCAAACTATATATCCCTTTTTGTCCACACAATGCAAGGAGAATATGACAGCCACCTCCCTTGGCCCTCCAGGGTACAATACGC

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

1001 CTTACAATTTCTGATCAGTCTGAAGCACCTGTAAGGCAAAACACGAAGAGATAATGGATGCCAAACAGAGCTGCTTCTTTCCAGCGACCCACAATCC

147▶ L T I L D Q S E A P V R Q N H E E I M D A K P E L L A F Q R P T I

1101 CACGGAACCCAAAAGTTTTGGCTATGTAACTTTTATGCATCTGGAAGCCCTAAGACAAGAAGCTTTTATTAAAGGATGACACATTATTAGTGCCTGTGA

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

1201 GGTCTCCACCCGCTTTGACATGGGTAGCCTTCGGAGGGAGGGTTTTACGACACGAAGTACTGATGCAGGGGTATAGCTTGCCTCACTTGTCAAAAAGC

213▶ V S T R F D M G S L R R E G F Q P R S T D A G V •

1301 TAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATT

HpaI (1436) **MfeI (1447)**

1401 GCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTT

EcoRI (1532)

1501 AAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGA

1601 GGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTCC

SapI (1714) **SspI (1771)** **SwaI (1785)**

1701 CAAGTTTGAAGTCTTCTTTCTTTATGTTTTAAATGACTGACCTCCACATTCCTTTTTTAGTAAATATTCAGAAATAATTTAAATACATCAT

EcoO109I (1846)

1801 TGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAAC

1901 CTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGC

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

2001 CATTCTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTC

121▶ N M E 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

2101 ATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTTCAGCAGACAGTACC

88▶ D S Y 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

2201 CTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGTCCTCATAGAGCATGG

54▶ R G I 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

2301 TGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCTCATGGTGGCCCTCTATAGTGAAGTCTATTATACTATGC

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

2401 **AseI (2418)**
CGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCA
2501 **SpeI (2573)**
CCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAAACAACTCCCATTGACG
2601 TCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTA
SnaBI (2701)
2701 ATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGT
NdeI (2806)
2801 ACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATG
PacI (2992)
PstI (2985)
SdaI (2984)
2901 GGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACCGCTGCAGGTTAATTAA
BspLU11I (3002)
3001 GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAA
3101 AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCGTGAAGCTCCCTCGTGCCTCTCTGTTCCGACCC
3201 TGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCG
ApaLI (3316)
3301 CTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTA
3401 TCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTA
3501 GAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGG
3601 TGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGAACGAA
EagI (3752)
PacI (3732) SwaI (3741) **NotI (3751)**
3701 AACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTT
3801 TTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAACGAAACAAACAACTAGCAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGA
3901 ACATTTCTCTATCGAA