



100

PvuI (7)  
 SgfI (6) MfeI (82)  
 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)  
 Psp1406I (203) PvuII (239) Bsu36I (291)  
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC  
 301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
 NgoMI (441)  
 NaeI (441)  
 401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)  
 BstEII (555) AgeI (552) KasI (535) BsrGI (573) XbaI (586)  
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGGTCCCATGGCACATTTTGTACAGGGCACATCTAGAATGATTGC  
 601 CGCAGAAAGTTCTACGGAGCATAAAGAGTGTGCTGAACCATCAACAAGAAAGAACTTGTGAATTCCTTTGAACAAAAGATAAGGTGTTTGGAAAAACAA  
 13▶ A E S S T E H K E C A E P S T R K N L M N S L E Q K I R C L E K Q  
 701 AGAAAAGAGCTCTGGAAGTTAACAGCAATGGGATCAGCAATTTAGAAGTATGAAAGAGTTATATGAAAGAAAGGTAGCAGAGCTGAAGACGAAACTGG  
 47▶ R K E L L E V N Q Q W D Q Q F R S M K E L Y E R K V A E L K T K L

HpaI (718)  
 BsiBI (835)  
 BsaBI (835)  
 BamHI (834) XmaI (899)  
 SmaI (899)  
 801 ACGCCGCGAAAGATTCTCAGCACGGGAGAAAGGATCCGCATCAGAGGCAGAGAAAGGACGACAGGCAGAGAGAGGACGACAGGCAGCGCGACCTGAC  
 80▶ D A A E R F L S T R E K D P H Q R Q R K D D R Q R E D D R Q R D L T  
 901 CCGGGACCGGCTGCAGCGGAGGAGAAGGAAAAGAACGCCTAAATGAAGAATTACATGAATTGAAAGAGAGAATAAACTTTTAAAGGGAAAAAATACT  
 113▶ R D R L Q R E E K E K E R L N E E L H E L K E E N K L L K G K N T  
 1001 CTTGCGAACAAGGAAAAGAACATTACGAATGTGAAATAAAACGCCTCAATAAGGCTCTTCAGGATGCCTTGAATATCAAGTGTTCATTTCCGAGGACT  
 147▶ L A N K E K E H Y E C E I K R L N K A L Q D A L N I K C S F S E D

XhoI (1112)  
 1101 GTTTGAGGAAGTCTCGAGTGAATTTCTGCCATGAGGAGATGAGAACAGAAATGGAAGTTCTGAAGCAGCAGGTGCAAAATATACGAAGAAGACTTCAAAAA  
 180▶ C L R K S R V E F C H E E M R T E M E V L K Q Q V Q I Y E E D F K K

PvuI (1204)  
 VspI (1252)  
 AseI (1252)  
 1201 GGAACGATCGGATCGAGAGAGACTTAATCAAGAGAAAGAGGAGCTACAGCAAAATTAAGAACTCCCAATCCAGTTGAACAGGCTGAATTCAGATA  
 213▶ E R S D R E R L N Q E K E E L Q Q I N E T S Q S Q L N R L N S Q I

HindIII (1301)  
 NcoI (1396)  
 1301 AAAGCTTGTGAGTGGAGAAAGAAAACTAGAAAAGCAATTAAGACAGATGTATTGCCACCCTGTAAGTGGGCTTGGTTTTCCACCTGCAAGATCCAT  
 247▶ K A C Q M E K E K L E K Q L K Q M Y C P P C N C G L V F H L Q D P

EcoO109I (1410)  
 Asp718I (1401) XcmI (1447) BsrGI (1488)  
 1401 GGGTACCAACAGGCGCTGGAGCTGTGCAGAAGCAACGGGAGCACCACAGACTATCAGTGGTATGCTCTTGACCAGCTTCCGCCAGATGTACAACACAA  
 280▶ W V P T G P G A V Q K Q R E H P P D Y Q W Y A L D Q L P P D V Q H K

MscI (1555)  
 BclI (1555)  
 NheI (1549)  
 1501 GGCAATGGTTTATCCTCAGTAAAGAAAGTCCATCCGTAGAAAGTACACAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACA  
 313▶ A N G L S S V K K V H P •

HpaI (1687) MfeI (1698)  
 1601 ACTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACA  
 1701 ATTGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGC  
 1801 ATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGC  
 1901 TGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCTTTTATGTTTTAAATGCACTGACC

SspI (2022) SmaI (2036) EcoO109I (2097)  
 2001 TCCCACATCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGG  
 2101 CCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCC  
 2201 TGGTGAAGTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAG  
 138▶ 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 P A Y D S I L  
 BstXI (2326)  
 2301 CTCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGTCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCCTCTGC  
 105▶ 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 I T D F D K Q

**StuI (2461)**  
**Eco147I (2461)**  
 2401 CCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCT  
 71 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 S I I E G T K  
 2501 TGGTCCTGATGGCCGCCCGACATGGTCTTGTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGAT  
 38 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 E L D Q Q S I

**BspHI (2611)** **VspI (2669)**  
**XmnI (2603)** **AseI (2669)**  
 2601 GTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCT  
 5 N F T K M  
 2701 CCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACG

**SpeI (2824)**  
 2800 ACATTTTGGAAAGTCCCCTTGTATTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCTGAGTCAAACCGCTATCC

**SnaBI (2952)**  
**Eco105I (2952)**  
 2899 ACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTAC

**NdeI (3057)**  
 2999 TGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACC  
 3099 GTAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGTCTTGGGCGG

**PstI (3236)**  
**SdaI (3235)** **PacI (3243)** **BspLU11I (3253)**  
 3199 TCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTG C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G C A A A A G G C C A G G A A C C G T A A A A A  
 3297 GGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA  
 3397 AGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCTGTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCG

**ApaLI (3567)**  
 3497 TGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCG  
 3597 CTGCGCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG  
 3697 TATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT  
 3797 TCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGG

**PacI (3983)** **SwaI (3992)**  
 3897 ATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTT

**EagI (4003)**  
**NotI (4002)**  
 3997 AAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAAC  
 4097 GAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAAGTGCCAGAACATTTCTCTATCGAA