



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

**MfeI (82)**  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

**PvuII (239)**  
**Bsu36I (291)** 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**AgeI (552)** **BspLU11I (560)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCAACATGTGGCAGCTACTACTACCAACAGCTCTGGTACTTAC

1 M W Q L L L P T A L V L T  
601 AGCTTTCTCTGGCATTCAAGCTGGTCTCCTCAAAAGGCTGTGGTGAACCTAGACCCCAAGTGGTTCAGGGTCTGAGGAAGACAGCGTACCCCTCAGATGC

13 A F S G I Q A G L Q K A V V N L D P K W V R V L E E D S V T L R C  
701 CAAGGCATTTTCCCCGAGGACAATTCTATCAAGTGTTCCATAACGAAAGCCTATCCACACAGGATGCCAACTATGTCTCAAAAGTCCAGAG

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

**BsrGI (815)** **NdeI (871)** **DraIII (897)**  
801 TTAAGGACAGTGAATGTACAGTGCCAGACAGCCCTCTCCACGATCAGTGACCCAGTGAACCTAGAGTCCATATGGGCTGGCTATTGCTTCAGACCAC

80 V K D S G M Y R C Q T A L S T I S D P V Q L E V H M G W L L L Q T T

**SmaI (920)** **EcoO109I (920)** **BstEII (972)**  
901 TAAGTGGCTGTTCCAGGAGGGGACCCCATCTGAGATGCCACAGTTGGCAAAACAGACCTGTACGGAAGGTCACCTATTTACAGAACGGCAAAGGC

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

**XmnI (1002)** **PstI (1071)**  
1001 AAGAAGTATTTCCATGAAAATTCTGAATTACTCATTCCAAAAGCTACACACAATGACAGTGGCTCCTACTTCTGAGAGGGCTCATTGGACACAACAACA

147 K K Y F H E N S E L L I P K A T H N D S G S Y F C R G G L I G H N N

**AvrII (1125)**  
1101 AATCTTCAGCATCCTTTTCGTATAAGCCTAGGCGATCCAGGGTCTCCATCCATGTTTCCACCGTGGCATCAAATCACATTCTGCCTGCTGATAGGACTCTT

180 K S S A S F R I S L G D P G S P S M F P P W H Q I T F C L L I G L L

**Bsu36I (1297)**  
1201 GTTTGCAATAGACACAGTGTCTGATTTCTGTGCGGAGGGTCTTCAAAGTCTGTGGCTGACTATGAGGAACCCAAGATTCAATGGAGCAAGGAACCT

213 F A I D T V L Y F S V R R G L Q S P V A D Y E E P K I Q W S K E P

**NheI (1327)** **SphI (1321)** **MscI (1333)**  
1301 CAGGACAAGTGAGCTCTTATCGCATGCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAAT

247 Q D K •

**HpaI (1465)** **MfeI (1476)**  
1401 GCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACACAACCAATTGCATTCATTTTATGTTTCA

**EcoRI (1561)**  
1501 GTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAA

1601 ATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTT

**SapI (1743)**  
1701 CATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATAGTAA

**SspI (1800)** **SwaI (1814)** **EcoO109I (1875)**  
1801 AATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTT

1901 TAGTAGTTGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTACTTGGAGGGGATGAG

141 • N R T Y K L P I L  
2001 TTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGG

131 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 R C M G C P

**BstXI (2104)**  
2101 CTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAA

97 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 S V A S G I

**StuI (2239)**  
2201 TGGCAATGGCTTCAGCACAGACAGTACCCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCCGAC

64 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 R I A A G V

**XmnI (2381)**  
2301 ATGGTGCTTGTGCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCC

31 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 F T K M

**AseI (2447)**

2401 CTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCT

2501 AAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGAT

**SpeI (2602)**

2601 TTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAA

**SnaBI (2730)**

2701 CCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCAT

**NdeI (2835)**

2801 TTACCGTCATTGACGTCAATAGGGGGCTACTTGCCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTC

2901 AATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGT

**PaeI (3021)**

**PstI (3014)**

**SdaI (3013)**

**BspLU11I (3031)**

3001 AAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTCCATA

3101 GGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCTGGAAG

3201 CTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCGTGT

**ApaLI (3345)**

3301 AGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC

3401 TTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTT

3501 GAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGA

3601 TCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTT

**EagI (3781)**

**Pacl (3761)** **Swal (3770)** **NotI (3780)**

3701 CTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCT

3801 TTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAACGAAACAACAACTAGCAAATAGG

3901 CTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA