



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

MfeI (82)  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

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

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

**BstEII (555)**  
**AgeI (552)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCCGAGGATCTGGGACTGAGCTTTGGGAAACAGC

**NcoI (560)** 1 M A E D L G L S F G E T A

**PstI (630)**  
**PvuII (627)** 601 CAGTGTGGAAATGCTGCCAGAGCACGGCAGCTGCAGGCCAAGGCCAGGAGCAGCAGCGCACGCTGGGCTCTCACCTGCTGCCTGGTGTGCTCCCTTC

13 S V E M L P E H G S C R P K A R S S S A R W A L T C C L V L L P F

**Bsp120I (740)**  
701 CTTGCAGGACTCACCACATACCTGCTTGTGACGACGCTCCGGGCCAGGGAGAGGCCCTGTGTGACGTTCCAGGCTCTAAAAGGACAGGAGTTGCACCTT

47 L A G L T T Y L L V S Q L R A Q G E A C V Q F Q A L K G Q E F A P

801 CACATCAGCAAGTTTATGCACCTTAGAGCAGACGGAGATAAGCCAAGGCCACACCTGACAGTTGTGAGACAACTCCCACACAGCACTTTAAAAATCA

80 S H Q Q V Y A P L R A D G D K P R A H L T V V R Q T P T Q H F K N Q

**XcmI (904)**  
901 GTTCCCAGCTCTGCACTGGGAACATGAACTAGGCTGCGCTTACCAAGAACCGAATGAACTATACCAACAAATTCCTGCTGATCCCAGAGTCGGGAGAC

113 F P A L H W E H E L G L A F T K N R M N Y T N K F L L I P E S G D

**BstXI (1088)**  
1001 TACTTCATTTACTCCCAGTACATTCCGTGGGATGACCTCTGAGTGCAGTGAATCAGACAAGCAGGCCACAAACAAGCCAGACTCCATCACTGTGG

147 Y F I Y S Q V T F R G M T S E C S E I R Q A G R P N K P D S I T V

**Tth111I (1152)**  
1101 TCATCACCAAGGTAACAGACAGTACCCTGAGCCAACCCAGCTCCTCATGGGGACCAAGTCTGTGTGAAGTAGGTAGCAACTGGTTCAGCCCATCTA

180 V I T K V T D S Y P E P T Q L L M G T A K T S V C E V G S N W F Q P I Y

1201 CCTCGAGCCATGTTCTCCTTGAAGAAGGGGACAAGTAATGGTGAACGTCAGTGCATCTCTTTGGTGGATTACACAAAAGAAGATAAAACCTTCTTT

213 L G A M F S L Q E G D K L M V N V S D I S L V D Y T K E D K T F F

**MscI (1333)**  
**NheI (1327)**  
**Eco47III (1324)** 1301 GGAGCCTTCTACTATAGGAGGAGCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAAACCACAACCTAGAATGCAGTGAACAAAAAT

247 G A F L L •

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

**EcoRI (1561)**  
1501 GGTTCAAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAA

1601 ATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTT

**SapI (1743)**  
1701 CATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACAGTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCCACATCCCTTTTATAGTAA

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

1901 TAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAG

141 • N R T Y K L P I L

**SacI (2075)**  
2001 TTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGG

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 CTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCAGCAGACCCAA

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

2201 TGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCCGAC

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

**BbsI (2385)**  
**XmnI (2381)**  
 2301 ATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCC  
 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 CTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACT

**SacI (2504)**  
 2501 AAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTGAT

**SpeI (2602)**  
 2601 TTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAA

**SnaBI (2730)**  
 2701 CCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGTCAATGTACTGGGCATAATGCCAGGCGGGCCAT

**NdeI (2835)**  
 2801 TTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTC  
 2901 AATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGT

**Pacl (3021)**  
**PstI (3014)**  
**SdaI (3013)**  
**BspLU11I (3031)**  
 3001 AAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATA  
 3101 GGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAG  
 3201 CTCCCTCGTGGCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGT

**ApaLI (3345)**  
 3301 AGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTC  
 3401 TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTT  
 3501 GAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGA  
 3601 TCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTT

**EagI (3781)**  
**Pacl (3761)** **SwaI (3770)** **NotI (3780)**  
 3701 CTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCT

3801 TTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGG  
 3901 CTGTCACCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA