



**PvuI (7)**  
**SgfI (6)**
**MfeI (82)** **EcoNI (96)**

1 GGATCTGGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**
**Bsu36I (291)**

**Psp1406I (203)**
**PvuII (239)**
**EcoNI (287)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGGCC

301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**
**NaeI (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**PvuII (559)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTTCAAGTGCAGTGGAGGGCACAACATGTCACCGCTGCTGCTATGGCT

601 GGGGTGATGCTCTGTGTCTCGGACTCCAAGCTGGAGATGAGGAAGAACAACAAGTGTCTTCTGGAGGGCAGAACTGACCCCTGACTTGCCTTACAAC

8▶ G L M L C V S G L Q A G D E E E H K C F L E G E N L T L T C P Y N

**KasI (535)**
**AgeI (552)**
**BspLU11I (575)**

**StuI (725)**

701 ATCATGCTATACTCACTGAGCCTGAAGGCTGGCAGCGGGTCAGAAGCCACGGTTCTCCAGAGACTCTGGTGTCAACAAACACAGAAAGGCAGACTTCA

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

**MscI (803)**
**ScaI (818)**
**PstI (874)**

801 ACGTGGCCAGGGCTGGGAAGTACTTGTGGAGGATTATCCACCGAATCTGTCGTCGAAGTCAAGTGCAGGGTCAAGATGTGGGGCTGTA

75▶ N V A R A G K Y L L E D Y P T E S V V K V T V T G L Q R Q D V G L Y

**BsaBI (984)**

901 CCAGTGTGTGGTCTACCTCTCTCTGACAATGTTATCATTCTCGCTCAACGGATACGGTGGCATGGTGTCAAGGAAGCCAGTGATGGTGTGATCGTTCTG

108▶ Q C V V Y L S P D N V I I L R Q R I R L A W C Q G K P V M V I V L

**EcoO109I (1022)**
**Bsu36I (1069)**

1001 ACGTGTGGCTTCACTAAACAAGGGCCTGGTCTTCTCAGTCCTGTTTGTCTTCTCTGCAAAGCTGGGCTAAGGTGTTACAGCCTTCAAGACATCCA

142▶ T C G F I L N K G L V F S V L F V F L C K A G P K V L Q P S K T S

**MscI (1159)**

**NheI (1153)**

1101 AAGTACAGGGAGTCTCTGAGAAACAGTAGCCTTCTGCTACAAGCTGTGAGCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAAC

175▶ K V Q G V S E K Q •

**HpaI (1291)**

1201 CACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAAC

**MfeI (1302)**
**EcoRI (1387)**

1301 AACAAATTCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATTTAAAATA

1401 CAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCAT

1501 TAGCTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCTTCTTATGTTTAAATGCACT

**SspI (1626)**
**SwaI (1640)**

1601 GACCTCCACATTCCTTTTATGAAAAATTCAGAAAATATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTC

1701 AAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAGAACCTTTAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAG

**EcoO109I (1701)**

1801 TTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAGAGA

139▶ 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 P A Y D S I

**SacI (1901)**
**BstXI (1930)**

1901 TGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTT

106▶ 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 I T D F D K

**StuI (2065)**

2001 CTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCA

73▶ 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 S I I E G

2101 GTCTTGGTCTGATGGCCCGCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAG

39▶ 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 E L D Q Q S

**XmnI (2207)**
**AseI (2273)**

2201 AGATGTTGAAGGTTCTCATGATGGCCCTCTATAGTGAAGTCTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGC

6▶ I N F T K M

**SacI (2330)**

2301 GTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTT

**SpeI (2428)**

2401 ACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAACCTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAAGTCAAACCGCTA

2500 TCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCATG **SnaBI (2556)**

2600 TACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGCCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTT **NdeI (2661)**

2700 ACCGTAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGG

2800 CGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAA **PstI (2840)**  
**SdaI (2839)** **PacI (2847)** **BspLU11I (2857)**

2898 AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTA

2998 TAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAA

3098 GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGA **ApaLI (3171)**

3198 CCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG

3298 AGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA

3398 CCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAA

3498 AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACA **PacI (3587)** **SwaI (3596)**

3598 TTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAA **EagI (3607)**  
**NotI (3606)**

3698 AACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA