



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

MfeI (82)  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

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

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**AgeI (552)** **BspHI (560)** **BbsI (589)**  
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTATCATGAAGCCGTACTTCTGCCGTGCTTTGTCTTCTGCTT

EagI (635) **BsrGI (672)**  
601 CCTAATCAGACTTTTAAACAGGAGAAATCAATGGCTCGGCCGATCATAGGATGTTTTCAATTCACAATGGAGGTGTACAGATTTCTGTAAATACCCTGAG

13▶ L I R L L T G E I N G S A D H R M F S F H N G G V Q I S C K Y P E  
701 ACTGTCCAGCAGTAAAAATGCGATTGTTGAGAGAGAGAAGTCTCTGCGAACTACCAAGACCAAGGAAAGCGGAAATGCGGTGTCCATCAAGAATC

47▶ T V Q Q L K M R L F R E R E V L C E L T K T K G S G N A V S I K N  
**PstI (885)**  
801 CAATGCTCTGTCTATATCATCTGTCAAACAACAGCGTCTCTTTTTTCTAAACAACCCAGACAGCTCCAGGGAAGCTATTACTTCTGAGCCTGTCCAT

80▶ P M L C L Y H L S N N S V S F F L N N P D S S Q G S Y Y F C S L S I  
**PvuII (976)**  
901 TTTTGACCCACCTCTTTTTCAAGAAAGGAACCTTAGTGGAGGATATTTGCATATTTATGAATCCCAGCTCTGCTGCCAGCTGAAGCTCTGGCTACCCGTA

113▶ F D P P P F Q E R N L S G G Y L H I Y E S Q L C C Q L K L W L P V  
**NsiI (1035)** **BamHI (1072)**  
1001 GGGTGTGAGCTTTCTGTTGTTGTTACTCCTTTTTGGATGCATCTATCATCTGGTTTTCAAAAAAGAAATACGGATCCAGTGTGCATGACCCATAAGTG

147▶ G C A A F V V V L L F G C I L I I W F S K K K Y G S S V H D P N S  
**MscI (1175)**  
1101 AATACATGTTTCATGGCGCAGTCAACACAAACAAAAGTCTAGACTTCGAGGTGTGACCTCATAAGCTGGCTAGCTGGCCAGACATGATAAGATACATTG

180▶ E Y M F M A A V N T N K K S R L A G V T S •  
1201 ATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTTATTGTAACCATTATAAGCTGCAA

**HpaI (1307)** **MfeI (1318)**  
1301 TAAACAAGTTAAACAACAATTGCATTCATTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGT

**EcoRI (1403)**  
1401 ATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGC

**SapI (1585)**  
1501 TGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTCTCTTCTTTCTTT

**SspI (1642)** **SwaI (1656)**  
1601 ATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGG

**EcoO109I (1717)**  
1701 CAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGC

1801 GAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCA

141▶ • 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  
**SacI (1917)** **BstXI (1946)**  
1901 GGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAA

111▶ P A Y D S I 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  
**StuI (2081)**  
2001 TGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGC

78▶ T D F D K 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  
2101 AGAGATGATCTCCCAGTCTTGGTCTGATGCCGCCCCGACATGGTGCTTGTGCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGC

45▶ S I I E G 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  
**BbsI (2227)** **XmnI (2223)** **AseI (2289)**  
2201 TCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCA

11▶ E L D Q Q S I N F T K M

2301 AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCA  
SacI (2346)

2401 ATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCG  
SpeI (2444)

2501 TGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAG  
SnaBI (2572)

2601 TCCATAAGGTCACTGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTG  
NdeI (2677)

2701 CCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGG

2801 GCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGG  
PacI (2863)  
PstI (2856)  
SdaI (2855) BspLU11I (2873)

2901 CCAGGAACCGTAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAA  
BspLU11I (2873)

3001 CCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTT

3101 CTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC  
ApaLI (3187)

3201 CCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAG

3301 GATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTG

3401 CTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTA

3501 CGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGC

3601 TAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTC  
EagI (3623)  
PacI (3603) SmaI (3612) NotI (3622)

3701 TCCATCAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA