



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTCGCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
**KasI (535)** **AgeI (552)** **ApaLI (568)**  
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCT  
1▶ M G V H E C P A W L W L L

601 CCTGTCCCTCTGTGCTCCCTCTGGGCTCCAGTCTGGGCGCCACCACGCTCATCTGTGACAGCCGAGTCTGGAGAGGTACCTTTGGAGGCC **Acc65I (683)** **SfiI (696)**  
13▶ L S L L S L P L G L P V L G A P P R L I C D S R V L E R Y L L E A

701 AAGGAGCCGAGAATATCAGCAGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGA  
47▶ K E A E N I T T G C A E H C S L N E N I T V P D T K V N F Y A W K

801 GGATGGAGGTGGGAGCAGGCGGTAGAAGTCTGGCAGGGCTGGCCTGTCTGCGAAGTGTCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCCA  
80▶ R M E V G Q Q A V E V W Q G L A L L S E A V L R G Q A L L V N S S Q

901 GCCGTGGGAGCCCTGCAGCTGCATGTGATAAAGCCGTCAGTGGCCTTCGACGCTCACCCTCTGCTTCCGGCTCTGGGAGCCAGAAGGAAGCCATC  
113▶ P W E P L Q L H V D K A V S G L R S L T T L L R A L G A Q K E A I

1001 TCCCCTCAGATCGGCCCTCAGCTGCTCCACTCCGAACATCACTGCTGACACTTTCCGAAACTCTCCGAGTCTACTCCAATTTCTCCGGGGAAAGC  
147▶ S P P D A A S A A P L R T I T A D T F R K L F R V Y S N F L R G K

**SdaI (1121)** **BsrGI (1106)** **StuI (1118)** **NheI (1170)** **MscI (1176)**  
1101 TGAAGCTGTACACAGGGGAGGCCTGCAGGACAGGGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCGCTAGCTGGCCAGACATGATAAGATACATT  
180▶ L K L Y T G E A C R T G D R •

1201 GATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCA

**HpaI (1308)** **MfeI (1319)**  
1301 ATAAACAAGTTAAACAACAACAATTGCATTATTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACTCTACAAATGTGG

**EcoRI (1404)**  
1401 TATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGG

**SapI (1586)**  
1501 CTGTTGCCAATGTGATTAGCTGTTTGAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTATTTCCTCAAGGTTTGAAGTACTGCTTTCATTCTT

**SspI (1643)** **SwaI (1657)**  
1601 TATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAG

1701 GCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGAACCTTTAATAGAAATGGACAGCAAGAAAG

1801 CGAGCTTCTAGCTTGTAGTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTC  
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 (1918)** **BstXI (1947)**  
1901 AGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACA  
112▶ 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

**StuI (2082)**  
2001 ATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAG  
78▶ I 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 CAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCGACATGGTCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCG  
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 (2228)** **XmnI (2224)** **AseI (2290)**  
2201 CTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTC  
12▶ E L D Q Q S I N F T K M

**SacI (2347)**  
2301 AAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTC

**SpeI (2445)**  
2401 AATGGGGCGAGTGTACGACATTTTGAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCC

**SnaBI (2573)**  
2501 GTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAA

2601 GTCCATAAGGTCATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGACT  
2701 GCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATG

SdaI (2856) PacI (2864) **BspLU11I (2874)**

2801 GGCGGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCC**TGCAGGTTAA**TTAAGAA**CA**TGTGAGCAAAAGGCCAGCAAAAG  
2901 GCCAGGAACCGTAAAAAGGCCGCGTTGTGCGCTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA  
3001 ACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGGACCCTGCCGCTTACCGGATACCTGTCCGCCTT

ApaLI (3188)

3101 TCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC  
3201 CCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA  
3301 GGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCT  
3401 GCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATT  
3501 ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGG

EagI (3624)  
PacI (3604) SwaI (3613) **NotI (3623)**

3601 CTAGTTAATTAACATTTAAATC **AGCGGCCG**CAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCT  
3701 CTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA