



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


---

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC  


---

**HindIII (245)**  
**Psp1406I (203)** **PvuII (239)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC  


---

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  


---

**NgoMIV (441)**  
401 GGGCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT  


---

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


---

1▶ M S T N T D L S L S S Y D  
**BstXI (653)** **BsrGI (695)**  
601 TGAAGTCAAGGGTCTAAGTTTATTCGAAAGCTAAGGAGACACCGTTTGTCCCATTTGGAATGGCGGGCTTGCAGCGATTGTTGCCTATGGGTTGTAC  
13▶ E G Q G S K F I R K A K E T P F V P I G M A G F A A I V A Y G L Y  


---

**SapI (705)**  
701 AAGCTGAAGAGCAGAGAAATACAAAGATGTCCATTCACTTGTACCATGCGTGTAGCAGCCAGGGCTTGTGTGGGGCCATGACTCTTGGTATGG  
47▶ K L K S R G N T K M S I H L I H M R V A A Q G F V V G A M T L G M  


---

**NheI (850)**  
801 GCTACTCCATGTATCAAGAAATTCTGGCCAACCTAAGCCTAAGCCTTAGGCTAGTGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCAC  
80▶ G Y S M Y Q E F W A N P K P K P •  


---

**EcoRI (817)** **Bsu36I (844)** **MscI (856)**  
901 AACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA  


---

**HpaI (988)** **MfeI (999)**  
1001 AATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAG  


---

EcoRI (1084)  
1101 CATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAG  


---

**SapI (1266)**  
1201 CTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCAAGTTTGAAGTCTCTTCATTCTTTATGTTTTAAATGCAGTAC  


---

**SspI (1323)** **Swal (1337)** **EcoO109I (1398)**  
1301 CTCCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAG  


---

1401 GCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTAAATAGAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTC  
141▶ • N  


---

**SacI (1598)**  
1501 CTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTCGCAATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGA  
138▶ 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 L  


---

**BstXI (1627)**  
1601 GCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTG  
105▶ 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 Q  


---

**StuI (1762)**  
1701 CCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCATGAGGACAGCAGAGATGATCTCCCAGTC  
72▶ 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 T  
1801 TTGGTCTGATGGCCGCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTAGTGGCAGCTCCACCAGCTCCAGATCCTGCTGAGAGA  
38▶ 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 I  


---

**BbsI (1908)**  
**XmnI (1904)** **AseI (1970)**  
1901 TGTTGAAGGCTTCATGGTGGCCCTCTATAGTGTGATCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTC  
5▶ N F T K M  


---

**SacI (2027)**  
2001 TCCAGCTTATCTGACGGTTCACATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACG  


---

**SpeI (2125)**  
2101 ACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCCTGAGTCAAACCGCTATCCA  


---

**SnaBI (2253)**  
2201 CGCCATTGATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAAGTCCATAAGGTCATGACT  


---

