



**PvuI (7)**  
**SgfI (6)** **MfeI (82)**  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

---

**Psp1406I (203)**
**HindIII (245)**  
**PvuII (239)**
**Bsu36I (291)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

---

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

---

**BspLU11I (560)**  
**AgeI (552)**
**SspI (568)**
**BstXI (580)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCAACATGTCAAATATTACAGATCCACAGATGTGGGATTTTGA  
1▶ M S N I T D P Q M W D F D

---

**SphI (617)**
**PstI (626)**  
601 TGATCTAAATTTACTGGCATGCCACTGCAGATGAAGATTACAGCCCTGTATGCTAGAAAAGTGCAGACTCAACAAGTATGTTGTGATCATCGCCTAC  
13▶ D L N F T G M P P A D E D Y S P C M L E T E T L N K Y V V I I A Y

---

**BsrBI (771)**  
701 GCCCTAGTGTTCCTGCTGAGCCTGCTGGGAAACTCCCTGGTGATGCTGGTTCATCTTATACAGCAGGGTCCGCCGCTCCGCTCACTGATGCTACCTGCTGA  
47▶ A L V F L L S L L G N S L L V M L V I L Y S R V G R S V T D V Y L L  
801 ACCTGGCCTTGCCGACCTACTCTTGCCTGACCTGGCCATCTGGGCCCTCCAAGTGAATGGCTGGATTGGCACATTCCTGTGCAAGGTGGT  
80▶ N L A L A D L L F A L T L P I W A A S K V N G W I F G T F L C K V V

---

**MscI (971)**  
901 CTCACCTCTGAAGGAAGTCAACTTCTACAGTGGCATCCTGCTGTTGGCCTGCATCAGTGTGGACCGTTACCTGGCCATTGTCCATGCCACACGCACACTG  
113▶ S L L K E V N F Y S G I L L L A C I S V D R Y L A I V H A T R T L  
1001 ACCCAGAAGCGTCACTTGGTCAAGTTTGTCTTGGCTGCTGGGACTGTCTATGAATCTGCTCCCTGCCCTTCTTCCCTTCCGCCAGGCTTACCATC  
147▶ T Q K R H L V K F V C L G C W G L S M N L S L P F F L F R Q A Y H

---

**BamHI (1169)**  
1101 CAACAATTCCAGTCCAGTTTGTATGAGGTCCTGGGAAATGACACAGCAAATGGCGGATGGTGTTCGGATCCTGCCTCACACCTTTGGCTTCATCGT  
180▶ P N N S S P V C Y E V L G N D T A K W R M V L R I L P H T F G F I V  
1201 GCCGCTGTTTGTGATGCTGTTCTGCTATGGATTACCCTGCGTACACTGTTTAAAGCCACATGGGGCAGAAGCACCGAGCCATGAGGGTTCATCTTGTCT  
213▶ P L F V M L F C Y G F T L R T L F K A H M G Q K H R A M R V I F A

---

**BspHI (1361)**  
1301 GTCGCTCATCTTCTGCTTGTGGCTGCCCTACAACCTGGTCTGCTGGCAGACACCCTCATGAGGACCCAGGTGATCCAGGAGAGCTGTGAGCGCC  
247▶ V V L I F L L C W L P Y N L V L L A D T L M R T Q V I Q E S C E R

---

**XcmI (1427)**  
**Bsp120I (1415)**  
1401 GCAACAACATCGGCCGGCCCTGGATGCCACTGAGATTCTGGGATTTCTCCATAGCTGCCTCAACCCCATCATCTACGCCTTCATCGGCCAAAATTTTCG  
280▶ R N N I G R A L D A T E I L G F L H S C L N P I I Y A F I G Q N F R

---

**NcoI (1500)**
**NsiI (1525)**  
1501 CCATGGATTCTCAAGATCTGGCTATGCATGGCCTGGTCAAGAGGAGTTCTTGGCAGTGCATCGTGTACCTCCTACACTTCTTCTGCTGCAATGTC  
313▶ H G F L K I L A M H G L V S K E F L A R H R V T S Y T S S S V N V

---

**MscI (1629)**  
**NheI (1623)**  
1601 TCTTCAACCTCTGAAAACCATCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCAACTAGAATGCAGTGAAAAAATGCTT  
347▶ S S N L •

---

**HpaI (1761)**
**MfeI (1772)**  
1701 TATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACAATTGCATTTTATGTTTCAGGTT

---

**EcoRI (1857)**  
1801 CAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGAATTTAAAATACAGCATAGCAAACTTTAACCTCCAAATCA  
1901 AGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACCTTCTTTCATG

---

**SapI (2039)**
**SspI (2096)**  
2001 GAGTTTAAGATATAGTGATTTTTCCCAAGGTTTGAAGTCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGAAAAATA

---

**SwaI (2110)**  
2101 TTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGT  
2201 AGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGAGTTCC  
141▶ • N R T Y K L P I L E

---

**SacI (2371)**  
2301 TCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTCTGCACATGCCACAGGGGCTGA  
129▶ 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 S V  
**BstXI (2400)**  
2401 CCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGC  
96▶ 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 A

2501 AATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGG  
63 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 H  
StuI (2535) BbsI (2681)  
2601 TGCTTGTTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCC  
29 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  
XmnI (2677) AseI (2743)  
2701 TATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACAAAC  
SacI (2800) SpeI (2898)  
2801 GAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTAC  
2901 TAGTCAAACAAACTCCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGC  
SnaBI (3026)  
3001 ATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTGGGCATAATGCCAGGGGGCCATTAC  
NdeI (3131)  
3101 CGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATG  
3201 GAAAGTCCCTATTGGCGTACTATGGAAACATACGTCAATTATTGACGTCAATGGGCAGGGGTCGTTGGCGGTGAGCCAGGGGGCCATTACCGTAAGT  
PacI (3317) PstI (3310) SdaI (3309) BspLU11I (3327)  
3301 TATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCT  
3401 CCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCC  
3501 CTCGTGGCTCTCCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGT  
ApaLI (3641)  
3601 ATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGA  
3701 GTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAG  
3801 TGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCG  
3901 GCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTAC  
PacI (4057) SmaI (4066) NotI (4076)  
4001 GGGGCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTAT  
4101 TTTCATTACATCTGTGTGGTTTTTTGTTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGT  
4201 CCCAGTGCAGGTGCCAGAACATTTCTCTATCGAA