



**PvuI (7)**  
**SgfI (6)** MfeI (82) EcoNI (96)  
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

---

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
EcoNI (287)  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

---

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

---

**AgeI (552)** **BspLU11I (560)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCAACATGTGGTTCTTGACAACCTGCTCCTTTGGGTTCCAGT  
1 M W F L T T L L L W V P V

---

**NcoI (646)**  
601 TGATGGGCAAGTGGACACCAAAAGGCAGTGATCACTTTGAGCCTCCATGGGTGAGCGTGTTCGAAGAGGAAACCGTAACTTGCACGTGTGAGGTGCTC  
13 D G Q V D T T K A V I T L Q P P W V S V F Q E E T V T L H C E V L  
701 CATCTGCCTGGGAGCAGCTCTACACAGTGGTTTCTCAATGGCACAGCCACTCAGACCTCGACCCAGCTACAGAATCACCTCTGCCAGTGTCAATGACA  
47 H L P G S S S T Q W F L N G T A T Q T S T P S Y R I T S A S V N D  
801 GTGGTGAATACAGGTGCCAGAGAGGTCTCTCAGGGCGAAGTGACCCATACAGCTGGAATCCACAGAGGCTGGCTACTACTGACGGTCTCCAGCAGAGT  
80 S G E Y R C Q R G L S G R S D P I Q L E I H R G W L L L Q V S S R V

---

**BsrGI (956)**  
901 CTTACGGAAGGAGAACCTCTGGCCTTGAGGTGTCATGCGTGGAAAGGATAAGTTGGTGTACAATGTGCTTTACTATCGAAATGGCAAAGCCTTTAAGTTT  
113 F T E G E P L A L R C H A W K D K L V Y N V L Y Y R N G K A F K F

---

**EcoRI (1008)**  
1001 TTCCACTGGAATTCTAACCTCACCACTTCTGAAAACCAACATAAGTCACAATGGCACCTACCATTGCTCAGGCATGGGAAAGCATCGCTACACATCAGCAG  
147 F H W N S N L T I L K T N I S H N G T Y H C S G M G K H R Y T S A

---

**NsiI (1145)** **BstEII (1182)**  
1101 GAATATCTGTCAGTGTGAAAGAGCTATTTCCAGCTCCAGTGTGAATGCATCTGTGACATCCCACTCCTGGAGGGGAATCTGGTCACCTGAGCTGTGA  
180 G I S V T V K E L F P A P V L N A S V T S P L L E G N L V T L S C E

---

**StuI (1219)**  
1201 AACAAAGTTGCTCTTGACAGAGCCTGGTTTGCAGCTTTACTTCTCCTTCTACATGGGCGAGCAAGACCCTGCGAGGCGAGGAACACATCCTCTGAATACCAA  
213 T K L L L Q R P G L Q L Y F S F Y M G S K T L R G R N T S S E Y Q  
1301 ATACTAAGTCTAGAAAGAGAAGACTCTGGGTTACTGGTGGCAGGCTGCCACAGAGGATGGAATGTCTTAAGCGCAGCCCTGAGTTGGAGCTTCAAG  
247 I L T A R R E D S G L Y W C E A A T E D G N V L K R S P E L E L Q

---

**XcmI (1417)** **SnaBI (1499)**  
1401 TGCTTGGCCTCCAGTTACCAACTCCTGTCTGGTTTCATGTCCTTTTCTATCTGGCAGTGGGAATAATGTTTTAGTGAACACTGTTCTCTGGGTGACAAT  
280 V L G L Q L P T P V W F H V L F Y L A V G I M F L V N T V L W V T I

---

**BspHI (1557)**  
1501 ACGTAAAGAACTGAAAAGAAAAGAAAAGTGGGATTTAGAAATCTCTTTGGATTCTGGTTCATGAGAAGAAAGTAATTTCCAGCCTTCAAGAAGACAGACAT  
313 R K E L K R K K K W D L E I S L D S G H E K K V I S S L Q E D R H

---

**SapI (1606)** **ApaLI (1654)** **NheI (1699)**  
1601 TTAGAAGAAGAGCTGAAATGTCAGGAACAAAAAGAAAGACAGCTGCAGGAAGGGTGCACCGGAAGGACCCAGGGGGCCACGTAGCAGCGGCTCAGTG  
347 L E E L K C Q E Q K E E Q L Q E G V H R K E P Q G A T •

---

**MscI (1705)**  
1701 CTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAAGTGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGCTAT

---

**HpaI (1837)** **MfeI (1848)**  
1801 TGCTTTATTTGTAACATTATAAGCTGCAATAAACAAGTTAAACAACAATTCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTT

---

**EcoRI (1933)**  
1901 TAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTG  
2001 AGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGTATTTTC

---

**SapI (2115)** **SspI (2172)** **SwaI (2186)**  
2101 CCAAGGTTTGAAGTACTCTTTCATTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGATAAAATATTCAGAAATAATTTAAATACATCA

---

**EcoO109I (2247)**  
2201 TTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTATGAGTTGGACTTAGGGAACAAAGGAA  
2301 CCTTTAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTGATTCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTG  
141 • N R T Y K L P I L E E I T T K V L K

---

**SacI (2447)**  
2401 CCATTCTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCT  
121 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 V R I S R D V E  
2501 CATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGCTTCTGCCCCTTGTCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGC  
88 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 I A E A C V T V

2601 <sup>StuI (2611)</sup> CCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATG  
55 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 H K N D E Y L M

2701 <sup>XmnI (2753)</sup> GTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATG  
21 T I K E T A V E V L E L D Q Q S I N F T K M

2801 <sup>AseI (2819)</sup> CCGATATACTATCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCC  
<sup>SacI (2876)</sup>

2901 <sup>SpeI (2974)</sup> ACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGAC  
3001 GTC AATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACT

3101 <sup>SnaBI (3102)</sup> AATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTACTGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCG

3201 <sup>NdeI (3207)</sup> TACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTAT

3301 <sup>PacI (3393)</sup> GGG AACATACGT CATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAITTA  
<sup>SdaI (3385)</sup>

3401 <sup>BspLUIII (3403)</sup> AGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAA  
3501 AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACC  
3601 CTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT

3701 <sup>ApaLI (3717)</sup> GTC CCAAGCTGGGCTGTGTGCACGAACCCCGTT CAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTT  
3801 ATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACT  
3901 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGATTGGTAGCTTTGATCCGGCAAACAAACCCGCTGGTAGCG  
4001 GTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGA

4101 <sup>EagI (4153)</sup> <sup>PacI (4133)</sup> <sup>Swal (4142)</sup> <sup>NotI (4152)</sup> AAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGTGGTT  
4201 TTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAG  
4301 AACATTTCTCTATCGAA