



**PvuI (7)**  
**SgfI (6)** 1 **MfeI (82)**  
 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGTGCCTA  
 101 GAGAAGGTGGCGGGGTAAACTGGAAAGTGATGCTGCTACTGGTCCGCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

---

**HindIII (245)**  
**Psp1406I (203)** 201 **PvuII (239)** **Bsu36I (291)**  
 GTGAACGTTCTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC  
 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGCTCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC  
 401 GGGCCTTTGTCGGCGCTCCCTTGAGCGCTACCTAGACTACAGCGGCTCTCCACGCTTTGCTGACCTGCTTCTCACTCTACGTCTTTGTTTCGTTT

---

**BspHI (560)**  
**AgeI (552)** 501 **Bsp120I (571)**  
 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCTACCTGAGATCACCGGTCATGAGGCGAGGGCCCCGGAGCCTGCGGGGCAGGGACGC  
 1▶ M R R G P R S L R G R D A  
**SacII (682)**  
 601 **DraIII (652)** **FspI (674)**  
 GCCAGCCCCACGCCCTGCTCCCGCCGAGTGTTCGACTGCTGGTCCGCCACTGGCTGCGGGCTCCTGCGACGCGCGCGAAACCGGCC  
 13▶ P A P T P C V P A E C F D L L V R H C V A C G L L R T P R P K P A

---

**PstI (730)** 701 **XmaI (784)** **SrfI (783)**  
 GGGGCCAGCAGCCCTGCGCCAGGACGGCGTGCAGCCGAGGAGTCGGTGGGCGCGGGGGCCGGGCGAGCGGGCCTGCCCTGCCGGTCTGCTCTTTG  
 47▶ G A S S P A P R T A L Q P Q E S V G A G A G E A A L P L P G L L F  
 801 GCGCCCCCCGCTGCTGGCCTGGCACTGGCTCCTGGCGTGGTCTGGTGGGTCGGTGGGTCGGTGGGTCGGAGCGGGCAGCGGGCCTCGCGCGCTCTC  
 80▶ G A P A L L G L A L V L A L V L V L V G L V S W R R R Q R R L R G A S S

---

**Tth111I (943)** 901  
 CGCAGAGCCCCGACGGAGACAAGGAGCCCCAGAGCCCTGGACAAGGTCACTATTGTCTCCGGAATCTCTGATGCCACAGCTCTGCCTGGCCT  
 113▶ A E A P D G D K D A P E P L D K V I I L S P G I S D A T A P A W P

---

**BbsI (1009)** 1001 **MscI (1032)** **BstEII (1080)**  
 CCTCCTGGGGAAGACCCAGGAACCCACCTGGCCACAGTGTCCCTGTGCCAGCCACAGAGCTGGGCTCCACTGAACTGGTACCACCAAGACGGCCG  
 147▶ P P G E D P G T T P P G H S V P V P A T E L G S T E L V T T K T A  
**MscI (1139)**  
 1101 **NheI (1133)**  
 GCCCTGAGCAACAATAGCAGGGAGCCGGCAGGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAGTGAATGCAGTGAA  
 180▶ G P E Q Q •

---

**HpaI (1271)** 1201 **MfeI (1282)**  
 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAACAAACAACAAATTGCATTATTTTAT

---

**EcoRI (1367)** 1301  
 GTTTCAGTTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATTTAAAATACAGCATAGCAAACTTTAAC  
 1401 CTCCAATCAAGCCTCTACTTGAATCTTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACC

---

**SapI (1549)** 1501  
 TTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTACTGCTTCATTCTTTATGTTTTAAATGACTGACCTCCACATTCCTTTTT

---

**SspI (1606)** 1601 **SwaI (1620)**  
 TAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCC  
 1701 CCAGTTTAGTAGTTGAGCTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGG  
 141▶ • N R T Y K L P  
**SacI (1881)**  
 1801 **SacI (1881)**  
 GATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCA  
 133▶ 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 E R C M G  
 1901 CAGGGGCTGACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGGTCTCACAGCAG  
 99▶ 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 G N S V A S

---

**StuI (2045)** 2001  
 ACCCAATGGCAATGGCTTACGACAGACAGTACCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTTGGTCTGATGGCCGC  
 66▶ 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 K T R I A A  
**BbsI (2191)** 2101 **XmnI (2187)**  
 CCCGACATGGTGGTTGTTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCTATG  
 33▶ 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 N F T K M

---

**AseI (2253)** 2201  
 GTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGG  
 2301 TTTCACTAACGAGCTCTGTTATATAGACTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCC  
**SacI (2310)**  
 2401 **SpeI (2408)**  
 GTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCCTATCCACGCCATTTGATGACTG

2501 CAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCATGACTGGGCATAATGCCAGGCG  
**SnaBI (2536)**

2601 GGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATT  
**NdeI (2641)**

2701 GACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATT

2801 TACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTT  
**PstI (2820)** **SdaI (2819)** **BspLU11I (2837)** **PacI (2827)**

2901 TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGGAAACCCGACAGGACTATAAAGATACCAGGCGTTCCCCC  
←

3001 TGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCA

3101 CGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCCTGCGCTTATCCGGTAACT  
**ApaLI (3151)**

3201 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGA

3301 GTTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC

3401 TCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGA

3501 TCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAA  
**PacI (3567)** **SwaI (3576)** **NotI (3586)**

3601 ATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAA

3701 AATAGGCTGTCCCAGTGCAGGTGCCAGAACATTTCTCTATCGAA