



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

---

**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC  
**HindIII (245)**  
**Bsu36I (291)**  
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

---

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

---

**BstEII (555)**  
**AgeI (552)** 501 TCTGTTCTGCCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATTGGGGTGGCGCTTTGAGCGGGTAGTCCGGAGAGTGGT  
**BsrBI (577)** **BspEI (587)**  
1▶ M G S A F E R V V R R V V  
601 CCAGGAGCTGGACCATGGTGGGAGTTCATCCCTGTGACCAGCCTGCAGAGCTCCACTGGCTTCCAGCCCTACTGCCTGGTGGTTAGGAAGCCTCAAGC  
13▶ Q E L D H G G E F I P V T S L Q S S T G F Q P Y C L V V R K P S S  
701 TCATGGTCTGGAACCCCGTTATAAGTGTGCAACCTGTCTATCAAGGACATCCTGGAGCCGGATGCCGCGGAACAGAGCTGCAGCTGGCAGGAGCT  
47▶ S W F W K P R Y K C V N L S I K D I L E P D A A E P D V Q R G R S  
801 TCCACTTCTACGATGCCATGGATGGGAGATACAGGGCAGCGTGGAGCTGGCAGCCCCAGGACAGGCAAGATCGCAGGGCGGGCCGGTGTCTGACAG  
80▶ F H F Y D A M D G Q I Q G S V E L A A P G Q A K I A G G A A V S D S  
901 CTCCAGCACCTCAATGAATGTGACTCGCTGAGTGTGGACCCTAACACCTGGCAGACTCTGCTCCATGAGAGGCACCTGCCGAGCCAGAACAAGTGC  
113▶ S S T S M N V Y S L S V D P N T W Q T L L H E R H L R Q P E H K V

---

**FspI (1010)** 1001 CTGCGAGCTGCGCAGCCGCGGGGACAACGTGTACGTGGTACTGAGGTGCTGCAGACACAGAAGGAGTGGAACTCACGCGACCCACAAGCGGGAGG  
147▶ L Q Q L R S R G D N V Y V V T E V L Q T Q K E V E V T R T H K R E

---

**BbrPI (1128)** 1101 GCTCGGGCCGGTTTTCCCTGCCCGAGCCAGCTGCTTGCAGGGTGGAGGCCAGGGCCATCTGAGCCAGAAGAAGACGGTCCACATCCCCTCAGGACAGC  
**BstEII (1176)** **Bsu36I (1187)**  
180▶ G S G R F S L P G A T C L Q G E G Q G H L S Q K K T V T I P S G S T  
1201 CCTCGCATTCCGGGTGGCCAGCTGGTATTGACTCTGACTTGGAGCTCCTTCTTCCCGGATAAGAAGCAGAGGACCTTCCAGCCACCCGCGACAGGC  
213▶ L A F R V A Q L V I D S D L D V L L F P D K K Q R T F Q P P A T G

---

**MscI (1327)** 1301 CACAAGCGTCCACGAGCGAAGGCGCCTGGCCACAGCTGCCCTCTGGCCTCTCCATGATGAGGTGCCTCCACAACCTCCTGACAGATGGGGTCCCTGCGG  
**SmaI (1388)**  
247▶ H K R S T S E G A W P Q L P S G L S M M R C L H N F L T D G V P A  
1401 AGGGGCGTTCAGTGAAGACTTCCAGGGCCTACGGGAGAGTGGAGACCATCCAAGGAAGTGGAGCTTTGGACAGAGAGCTGTGCCAGCTGCTGTCT  
280▶ E G A F T E D F Q G L R A E V E T I S K E L E L L D R V T L C Q L L L  
1501 GGAGGGCCTGGAGGGGTGCTGCGGGACAGCTGGCCCTGCGAGCCTTGGAGGAGGCGCTGGAGCAGGGCCAGAGCCTTGGGCGGTGGAGCCCTGGAC  
313▶ E G L E G V L R D Q L A L R A L E E A L E Q G Q S L G P V E P L D

---

**BspEI (1639)** 1601 GGTCCAGCAGGTGCTGTCTGGAGTGCCTGGTGTGCTCCTCCGGAATGCTGGTGGCCGAACTCGTATCCCTGTTGTCTACCTGCTGGGGCACTGACCA  
347▶ G P A G A V L E C L V L S S G M L V P E L A I P V V Y L L G A L T

---

**XhoI (1765)**  
**BsrBI (1762)** 1701 TGCTGAGTAAACGCAGCACAAGCTGCTGGCGGAGGCGCTGGAGTGCAGACCCTGTTGGGCGGCTCGAGCTGGTGGGAGCCTCTTGGAGCAGAGTGC  
380▶ M L S E T Q H K L L A E A L E S Q T L L G P L E L V G S L L E Q S A

---

**XmaI (1834)** 1801 CCCGTGGCAGGAGCGCAGCACCATGTCCTGCCCGGGCTCCTGGGAACAGCTGGGGCAAGGAGCACCAGGCTGGTCTTGGTGGACGAGTGTGGC  
413▶ P W Q E R S T M S L P P G L L G N S W G E G A P A W V L L D E C G

---

**BbrPI (1924)** 1901 CTAGAGCTGGGGAGGACTCCCCACGTGTGCTGGGAGCCGAGGCCAGGGCCGATGTGTGACTCTACGCTCCCTGGCACTGCTATCAGGACTGA  
447▶ L E L G E D T P H V C W E P Q A Q G R M C A L Y A S L A L L S G L  
**MscI (2096)**

---

**BamHI (2014)** 2001 GCCAGGAGCCCCAGGATCCGATTACAAGGATCACGACGGCGACTATAAAGACCAGATATTGACTACAAAGACGACGACGACAAGTAAAGCTAGCTGGC  
480▶ S Q E P H G S D Y K D H D G D Y K D H D I D Y K D D D D K • -  
2101 CAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATT

---

**HpaI (2228)** **MfeI (2239)** 2201 TGTAACCATTATAAGCTGCAATAACAAGTTAAACAACAATTCATTTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAG

---

**EcoRI (2324)** 2301 TAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAA  
2401 TAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTCATGGAGTTAAGATATAGTATTTTCCAAGGTTT

**SapI (2506)** **SspI (2563)** **SwaI (2577)**  
 2501 GAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGA  
 2601 AAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATA  
 2701 GAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTATC  
 141 • N R T Y K L P I L E E I T T K V L K G N M  
 2801 TCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGT  
 118 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 D S Y  
 2901 AGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAAT  
 85 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 R G I  
**StuI (3002)**  
 3001 GTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTC  
 52 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 T I K  
**XmnI (3144)**  
 3101 TCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATAC  
 18 E T A V E V L E L D Q Q S I N F T K M  
**AseI (3210)**  
 3201 TATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACAC  
**SpeI (3365)**  
 3301 GCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGG  
**SnaBI (3493)**  
 3401 GTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAG  
**NdeI (3598)**  
 3501 ATGTAAGTCCAAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCA  
 3601 TATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATA  
**PacI (3784)** **SdaI (3776)** **BspLU11I (3794)**  
 3701 CGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCAGGTTAATTAAGAACAATGT  
 3801 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGAGC  
 3901 CCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTT  
 4001 ACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCCGCTCCAAGC  
**ApaLI (4108)**  
 4101 TGGGCTGTGTGCACGAACCCCCGTTACGCCCACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGTAAGACACGACTTATCGCCACT  
 4201 GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA  
 4301 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTATCCGGCAAACAAACCACCGCTGGTAGCGTGGTTTTT  
 4401 TTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCAGC  
**EagI (4544)** **PacI (4524)** **SwaI (4533)** **NotI (4543)**  
 4501 TTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTG  
 4601 AATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAATTTCT  
 4701 CTATCGAA