



**PvuI (7)**  
**SgfI (6)** **MfeI (82)** **EcoNI (96)**  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

---

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
**PvuII (239)** **EcoNI (287)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

---

**NgoMIV (441)**  
**NaeI (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

---

*NcoI (560)*  
**BstEII (555)**  
**KasI (535)** **AgeI (552)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGCAGCGTCTGCGTGGCGCTGCTGGTTCTGGCGCT  
1 M A A S C V A L L V L A L

---

**Bsp120I (653)**  
601 GCTGTTGCTGGTGTCTGCTGCTGGGCTTGTGGAAGCTGGGCGGCAAACGGGACGGGCCCGGCACATGGTGTCTGCTGGTGTGGGCGACGTGGGCCGACG  
13 L L L V L L L G L W K R G R Q T G R A R H M V V V V L G D V G R S

---

**SphI (704)** **XhoI (779)**  
701 CCCCGCATGCAGTACCACGCGCTGTATTGGCCAGAGCGGCTTTTGGTGTGCTGCTGGGTTCTACAACCTCAAACCTCGAGATGAAGTCTTGCAGA  
47 P R M Q Y H A L S L A Q S G F S V T L L G F Y N S K P R D E L L Q

---

**BglII (828)** **Bsp120I (850)**  
801 ATGATAGGATTCCGATTGTGAAGTTGACAGATCTGCGGGCCTGGGAGCTGGGCCCGAATTCTCCAGTATGGAGTCAAGTTGTATTTCAGGCAAGTGA  
80 N D R I R I V K L T D L R G L G A G P R I L Q Y G V K V V F Q A V Y

---

**FspI (917)**  
901 CTTGCTGTGGAAGATGATGCGCATGGACCCTGCAGCCTACATCTTCTCCAGAACCCTCCAGGTCTGCCTGCTATTGCCGTCTGCTGGTTTGTGGGCTGC  
113 L L W K M M R M D P A A Y I F L Q N P P G L P A I A V C W F V G C

---

*NcoI (1062)*  
1001 ATTTGTGGGAGCAAATTTGGTTCATCGACTGGCACAACCTATGGTACTCCATCATGGGCTTGGTCCATGGCCCCGCCACCCATTGTGCTGCTGGCCAAAT  
147 I C G S K L V I D W H N Y G Y S I M G L V H G P R H P I V L L A K

---

**XmnI (1107)** **KasI (1118)**  
1101 GGTATGAGAAGTTCTTCGGGCGCCTGTCCACCTGAACCTGTGTGTGACCAATGCTATGCGGGAGGACCTGGCAGAGAAGTGGTGTGTCAGGGCTGTGAC  
180 W Y E K F F G R L S H L N L C V T N A M R E D L A E N W C V R A V T

---

1201 GCTCTACGACAAGCCAGCATCTTTCTTTAAGGAGACACCCTGGACCTGCAGCATGAAGTCTTTATGAAGCTGAGCCACACGTAAGTCTCTCTTTCCAGAGC  
213 L Y D K P A S F F K E T P L D L Q H E L F M K L S H T Y S P F Q S

---

1301 TGCTCAGATCCCTACATCCTGACACAGAGAGGTCGGCCTTCTACTGAGAGGATTGTGAGGGGTTGTGAGGCGTCTGCATGGGCGGCGCAGCACTGC  
247 C S D P S H P D T E R S A F T E R D C Q S G V V R R L H G R P A L

---

1401 TCGTGAGCAGCACAAGCTGGACAGAGGACGAGGACTTCTCCATCTGCTTCGAGCATTAGAAAAGTTTGGCAACAAGCACTACTGGAGACAGCCTCCC  
280 L V S S T S W T E D E D F S I L L R A L E K F E Q Q A L T G D S L P

---

*NcoI (1597)*  
1501 TTCCCTGCTGTGTGATAACAGGGAAGGGACCGTCCAGAGACTACCGCCACCTCATCAGCCAGAAGCACCTTCAGCAGTCCGGTTCTGCACCCCA  
313 S L V C V I T G K G P L R E H Y R H L I S Q K H L Q H V R F C T P

---

1601 TGGCTGGAAGCCGAGGACTACCCACTGCTTCTAGGGTCCAGCGGATCTGGGTGTCTGTCTACACATGCTCTCCAGTGGTCTGGACCTGCCCATGAAGGTGG  
347 W L E A E D Y P L L L G S A D L G V C L H M S S S G L D L P M K V

---

1701 TGGACATGTTTGGGTGCCACTTGCCTGTGTGCGCGTGAACCTCAAGTGTCTGCACGAGCTAGTAAGACATGGAGAGAATGGTCTGGTCTTCAAGGATGC  
380 V D M F G C H L P V C A V N F K C L H E L V R H G E N G L V F K D A

---

**PvuII (1816)** **BspEI (1871)**  
1801 TGAGGAGCTGGCAGCTCAGCTGCAGATGCTTTTCTCAAAGTCCAGACCTGCTGAAAAGCTAAGCCAGTCCGGAAGAAATGCAGGAGTCGGGGCAG  
413 E E L A A Q L Q M L F S K F P D P A G K L S Q F R K K L Q E S G Q

---

**DraIII (1924)** **DraIII (1976)**  
1901 CAACGCTGGGATGAGAGCTGGCAGCACACTGTGCTCCCTGCTCGCTCACTCACAGATGACCCCGAGCCCCATCCACCTGTGGCCACCCCTTCTGCCC  
447 Q R W D E S W Q H T V L P L L A H S Q M T P R P H P P C G H P S C

---

**Bsu36I (2032)** **NheI (2049)**  
2001 GGGGCTTTTGTAGTGGCCCTAGTGGTCATAAGCCTGAGGACAGCAGTGGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACA  
480 R G F •

---

**HpaI (2187)** **MfeI (2198)**  
2101 ACTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGTGCATAAACAAGTTAACACAACA

---

**EcoRI (2283)**  
2201 ATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGGAATCTAAATAACAGC  
2301 ATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGC  
2401 TGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTGCTTTCATTTCTTTATGTTTAAATGCACTGACC

---

**SspI (2522)** **SwaI (2536)**  
2501 TCCCACATTCCTTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGG

2601 CCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCC  
141 • N R

2701 TGGTGACTTGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAG  
SacI (2797)

138 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

2801 CTCTCTGCACATGCCACAGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGC  
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 (2961)**

2901 CCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCT  
71 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 K

3001 TGGTCTGATGGCCGCCCGACATGGTGTCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGAT  
38 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

**BspHI (3111)**

3101 GTTGAAGGCTTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCT  
5 N F T K M

**XmnI (3103)** **AseI (3169)**

3201 CCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGA  
SacI (3226)

**SpeI (3324)**

3301 CATTGAAAGTCCCGTTGATTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCA

**SnaBI (3452)**

3400 CGCCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGACT

**NdeI (3557)**

3500 GGGCATAATGCCAGGCGGGCATTACCCTGATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCGAGTTACCG  
3600 TAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTTGGGGCGT

**SdaI (3735)** **PacI (3743)**

3700 CAGCCAGGCGGGCATTACCCTGAAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAG  
3798 GCCGCGTTGCTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAA  
3898 GATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCGCCCTTCTCCCTTCGGGAAGCGT

**ApaLI (4067)**

3998 GGGCCTTTCATAGCTCAGCTGATAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGC  
4098 TGGCCTTATCCGGTAACTATCGTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT  
4198 ATGTAGGGCGGTGCTACAGAGTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT  
4298 CGGAAAAAGAGTTGGTAGCTCTTATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACGGCAGAAAAAAGGA

PacI (4483) SmaI (4492)

4398 TCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTA

**EagI (4503)**  
**NotI (4502)**

4498 AATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACG  
4598 AAACAAAACAAACTAGCAAAATAGGCTGTCCCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA