



125

**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC  
**PvuII (239)**  
**Bsu36I (291)**  
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMI (441)**  
**NaeI (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

**KasI (535)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTACCATGGTGAAGTGGTTTACCGAGACCTCAGTGGGCTGGA  
**AgeI (552)** 1 M V R W F H R D L S G L D  
601 TGCAGAGACCCTGCTCAAGGGCCGAGGTGTCCACGGTAGCTTCTGGCTCGGCCAGTCGCAAGAACCAGGGTACTTTCGCTCCGTCAGGGTGGG  
13 A E T L L K G R G V H G S F L A R P S R K N Q G D F S L S V R V G

**BamHI (719)** 701 GATCAGGTGACCCATATTCGGATCCAGAACTCAGGGGATTTCTATGACCTGTATGGAGGGGAGAAGTTTGCAGCTCTGACAGAGCTGGTGGAGTACTACA  
**ScaI (791)** 47 D Q V T H I R I Q N S G D F Y D L Y G G E K F A T L T E L V E Y Y

**NcoI (894)** 801 CTCAGCAGCAGGGTGTCTGCAGGACCGGACGCACCATCATCCACCTCAAGTACCCGCTGAACTGCTCCGATCCCCTAGTGAAGGTTGGTACCATGG  
**SpeI (877)** 80 T Q Q Q G V L Q D R D G T I I H L K Y P L N C S D P T S E R W Y H G  
**Asp718I (890)**  
901 CCACATGTCTGGCGGGCAGGAGAGAGCTGCTGCAGGCCAAGGGCGAGCCCTGGACGTTTCTGTGCGTGAGAGCCTCAGCCAGCCTGGAGACTTCGTG  
113 H M S G G Q A E T L L Q A K G E P W T F L V R E S L S Q P G D F V

**BsrBI (1042)** 1001 CTTTCTGTGCTCAGTGACCAGCCAAAGGCTGGCCAGGCTCCCGCTCAGGGTCAACCACATCAAGGTCATGTGCGAGGGTGGACGCTACACAGTGGGTG  
147 L S V L S D Q P K A G P G S P L R V T H I K V M C E G G R Y T V G

**KasI (1171)** 1101 GTTTGGAGACCTTCGACAGCCTCACGGACCTGGTGGAGCATTCAAGAAGACGGGATTGAGGAGCCCTCAGGCGCCTTTGTCTACCTGCGGCAGCCGTA  
**Bsu36I (1166)** 180 G L E T F D S L T D L V E H F K K T G I E E A S G A F V Y L R Q P Y  
1201 CTATGCCACGAGGGTGAATGCGGCTGACATTGAGAACCAGTGTGGAAGTGAACAAGAAGCAGGAGTCCGAGGATACAGCCAAGGCTGGCTTCTGGGAG  
213 Y A T R V N A A D I E N R V L E L N K K Q E S E D T A K A G F W E  
1301 GAGTTTGAAGTGTGAGAAAGCAGGAGGTGAAGAACTGCACCAGCGTCTGAAAGGGCAGCGCCAGAGAACAAGGGCAAGAACCCTACAAGAACATTC  
247 E F E S L Q K Q E V K N L H Q R L E G Q R P E N K G K N R Y K N I

**XmaI (1450)** 1401 TCCCCTTTGACCACAGCCGAGTGATCCTGCAGGACGGGACAGTAACATCCCCGGTCCGACTACATCAATGCCAACTACATCAAGAACCAGCTGCTAGG  
**SmaI (1450)** 280 L P F D H S R V I L Q G R D S N I P G S D Y I N A N Y I K N Q L L G  
**PvuII (1489)** 1501 CCCTGATGAGAAGCTAAGACTATCCAGCCAGGCTGTCTGGAGCCACGGTCAATGACTTCTGGCAGATGGCTGGCAGGAGAACAGCCGCTGTC  
313 P D E N A K T Y I A S Q G C L E A T V N D F W Q M A W Q E N S R V

**BspHI (1604)** 1601 ATCGTCATGACCACCCGAGAGGTGGAGAAAGGCCGGAACAATGCGTCCATACTGGCCCGAGGTGGGCATGCAGCGTCTTATGGGCCCTACTCTGTGA  
**SphI (1667)** 347 I V M T T R E V E K G R N K C V P Y W P E V G M Q R A Y G P Y S V  
**Bsp120I (1684)**

**BglIII (1784)** 1701 CCAACTGCGGGGAGCATGACACAACCGAATAACAACTCCGTACCTTACAGGTCTCCCCGCTGGACAATGGAGACCTGATTCGGGAGATCTGGCATTACCA  
380 T N C G E H D T T E Y K L R T L Q V S P L D N G D L I R E I W H Y Q

**SandI (1823)** 1801 GTACCTGAGCTGGCCGACCATGGGGTCCCCAGTGAGCCTGGGGGTGCTCAGCTTCTGGACCAGATCAACCAGCGGCAGGAAAGTCTGCCTCAGCCA  
**NcoI (1818)** 413 Y L S W P D H G V P S E P G G V L S F L D Q I N Q R Q E S L P H A

**NgoMI (1924)** 1901 GGGCCATCATCGTGCATGACGCGCCGCGCATCGCCGCGACAGGACCATCATTGTCATCGACATGCTCATGGAGAACATCTCCACCAAGGGCCTGGACT  
**ApaLI (1912)** 447 G P I I V H C S A G I G R T G T I I V I D M L M E N I S T K G L D  
**EagI (1932)**

**Eco47III (2042)** 2001 GTGACATTGACATCCAGAAGACCATCCAGATGGTGGGGCGCAGCGCTCGGACATGGTGCAGACGGAGGCGCAGTACAAGTTCATCTACGTGGCCATCGC  
480 C D I D I Q K T I Q M V R A Q R S G M V Q T E A Q Y K F I Y V A I A  
2101 CCAGTTTATTGAAACCTAAGAAGAAGCTGGAGGCTGTCAGTGCAGAGAGGGCCAGGAGTCCGAGTACGGGAACATCACCTATCCCCAGCCATGAAG  
513 Q F I E T T K K K L E V L Q S Q K G Q E S E Y G N I T Y P P A M K  
2201 AATGCCATGCAAGGCTCCCGCACCTCGTCCAAACACAAGGAGGATGTGTATGAGAACCCTGCACACTAAGAACAAGAGGGAGGAGAAAGTGAAGAAGC  
547 N A H A K A S R T S S K H K E D V Y E N L H T K N K R E E K V K K

**BsrBI (2348)** 2301 AGCGGTCAGCAGACAAGGAGAAGAGCAAGGTTCCCTCAAGAGGAAGTGAAGGCTGCTGCTCAGCTAGCTGGCCAGACATGATAAGATACATTGATGA  
**NheI (2365)** 580 Q R S A D K E K S K G S L K R K •

2401 GTTTGGACAAACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAA

**HpaI (2503)** MfeI (2514) **EcoRI**  
 2501 CAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGG  
 2601 AATTCTAAAAACAGCATAGCAAAACTTTAACCTCAAATCAAGCCTCTACTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTT  
 2701 GCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTGATTTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGT  


---

**SspI (2838)** SwaI (2852)  
 2801 TTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGA  
 2901 ATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGC  
 3001 TTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAGCAGTCAGGAG  
 141 • N R 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  
**SacI (3113)**  
 3101 CATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGT  
 110 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 P H R V A V I T  
 3201 GTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAG  
 77 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 Y A E I H V A S  
 3301 ATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGCTCCA  
 43 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 E T A V E V L E L  
**BspHI (3427)** **VspI (3485)**  
**XmnI (3419)** **AseI (3485)**  
 3401 GATCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAC  
 10 D Q Q S I N F T K M  
**SacI (3542)**  
 3501 AGCGTGGATGGCGTCTCCAGCTATCTGACGGTTCATAAACGAGCTCTGTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATG  
**SpeI (3640)**  
 3600 GGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTG  
**SnaBI (3768)**  
**Eco105I (3768)**  
 3699 AGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTC  
**NdeI (3873)**  
 3799 CCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCCTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCC  
 3899 AAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGAAACATACGTCATTATTGACGTCAATGGGC  
**PacI (4059)** **BspLU11I (4069)**  
 3999 GGGGGTCTTTGGGCGGTGAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTG C A G G T T A A T T A A G A A C A T G T G A G C A A A A G C C A G C A A A A G G  
 4097 CCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAA  
 4197 CCCGACAGGACTATAAAGATACCAGCGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCTTT  
**ApaLI (4383)**  
 4297 CTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCC  
 4397 CCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAG  
 4497 GATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTG  
 4597 CTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTA  
 4697 CGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGC  
**EagI (4819)**  
**PacI (4799)** **SwaI (4808)** **NotI (4818)**  
 4797 TAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTGGTTTTTTGTGTGAATCGTAACTAACATACGCT  
 4896 CTCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA