



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

**HindIII (245)**  
Psp1406I (203) PvuII (239) **Bsu36I (291)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

**KasI (535)** **AgeI (552)** **BspHI (560)**  
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCATCATGATAGAAACATACAGCCAACCTTCCCCAGATCCGT  
601 GGCAACTGGACTTCAGCGAGCATGAAGATTTTATGTATTTACTTACTGTTTTCTTATCACCCAAATGATTGGATCTGTGCTTTTTGCTGTGTATCTT  
137▶ A T G L P A S M K I F M Y L L T V F L I T Q M I G S V L F A V Y L 1▶ M I E T Y S Q P S P R S V

**BspHI (738)** **BsaBI (791)**  
701 CATAGAAGATTGGATAAGGTCGAAGAGGAAGTAAACCTTCATGAAGATTTGTATTCAAAAAAGCTAAAGAGATGCAACAAAGGAGAAGGATCTTTAT  
47▶ H R R L D K V E E E V N L H E D F V F I K K L K R C N K G E G S L

**Tth11I (838)** **BbsI (835)** **Psp1406I (855)**  
801 CCTTGCTGAAGTGTGAGGAGATGAGAAGCAATTTGAAGACCTGTCAAGGATATAACGTTAAACAAAGAAGAGAAAAAGAAAAACAGCTTTGAAATGCA  
80▶ S L L N C E E M R R Q F E D L V K D I T L N K E E K K E N S F E M Q

**BamHI (912)** **BsaBI (907)**  
901 AAGAGGTGATGAGGATCCTCAAATTCAGCACACGTTGTAAGCGAAGCCAACAGTAATGCAGCATCCGTTCTACAGTGGGCCAAGAAAGGATATTATACC  
113▶ R G D E D P Q I A A H V V S E A N S N A A S V L Q W A K K G Y Y T

**PvuII (1036)**  
1001 ATGAAAAGCAACTTGGTAATGCTTGAAAATGGGAAACAGCTGACGGTTAAAAGAGAAGGACTCTATTATGTCTACACTCAAGTACCTTCTGCTCTAATC  
147▶ M K S N L V M L E N G K Q L T V K R E G L Y Y V Y T Q V T F C S N  
1101 GGGAGCCTTCGAGTCAACGCCATTTCATCGTGGCCTCTGGCTGAAGCCAGCAGTGGATCTGAGAGAATCTTACTCAAGGGCGCAAATACCCACAGTTC  
180▶ R E P S S Q R P F I V G L W L K P S S G S E R I L L K A A N T H S S  
1201 CTCCAGCTTTGCGAGCAGCAGTCTGTTCACTTGGCGGAGTGTGTAATTACAAGCTGGTGCTTCTGTGTTGTCAACGTGACTGAAGCAAGCCAAGTG  
213▶ S Q L C E Q Q S V H L G G V F E L Q A G A S V F V N V T E A S Q V

**MscI (1353)** **NheI (1347)**  
1301 ATCCACAGAGTTGGCTTCTCATCTTTGGCTTACTCAAACCTCTGAACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC  
247▶ I H R V G F S S F G L L K L •

**HpaI (1485)** **MfeI (1496)**  
1401 TAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAAACAACAAT

**EcoRI (1581)**  
1501 TGCATTCAATTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCAT  
1601 AGCAAACTTTAACTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTG

**SapI (1763)**  
1701 TTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTACGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTC

**SspI (1820)** **SwaI (1834)** **EcoO109I (1895)**  
1801 CCACATCCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCC  
1901 CTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTG  
141▶ • N R

**SacI (2095)**  
2001 GTGTAAGTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCT  
137▶ 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 E  
2101 CTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCC  
104▶ 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 G

**StuI (2259)**  
2201 GTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGCCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTG  
71▶ 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  
2301 GTCCTGATGGCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGT  
37▶ 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 N

**BbsI (2405)** **XmnI (2401)** **AseI (2467)**  
2401 TGAAGTCTTCATGGTGGCCCTCTATAGTGTGATGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCC  
4▶ F T K M

2501 **SacI (2524)**  
 AGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACA

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2601 **SpeI (2622)**  
 TTTTGAAAGTCCCCTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGC

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2701 **SnaBI (2750)**  
 CCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAAGGCATGTACTGGG

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2801 **NdeI (2855)**  
 CATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAA

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2901  
 ATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGCGGTCAG

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3001 **PacI (3041)**  
**PstI (3034)**  
**SdaI (3033)** **BspLU11I (3051)**  
 CCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGC

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3101  
 GTTGCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC

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3201  
 CAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGCCGC

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3301 **ApaLI (3365)**  
 TTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCCG

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3401  
 CTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA

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3501  
 GGGGTGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA

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3601  
 AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCA

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3701 **PacI (3781)** **SwaI (3790)**  
 AGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC A

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3801 **EagI (3801)**  
**NotI (3800)**  
 GCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACA

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3901  
 AAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA