



**PvuI (7)**  
**SgfI (6)**
**MfeI (82)** **EcoNI (96)**

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)**
**HindIII (245)** **Bsu36I (291)**

201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC  
 301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTGTTTCGTTT

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**NcoI (560)** **BstEII (555)** **AgeI (552)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCACCATGGACCCAGGGCTGCAGCAAGCACTCAACGGAATGGC  
1▶ M D P G L Q Q A L N G M A

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**NsiI (619)**
**NgoMIV (627)** **XcmI (686)**

601 CCTCCTGGAGACACAGCCATGCATGTGCCGGCGGGCTCCGTGCCAGCCACCTGGGACCACGAGCCGAGCTATTTCTATTTGACCACAGCCACTCTG  
 13▶ P P G D T A M H V P A G S V A S H L G T T S R S Y F Y L T T A T L

**Tth111I (778)**

701 GCTCTGTGCCCTGTCTTACGGTGGCCACTATTATGGTGTGGCTGTTAGAGGACGGACTCCATTCCCAACTCACCTGACAACGTCCTCCCTCAAAGGAG  
 47▶ A L C L V F T V A T I M V L V V Q R T D S I P N S P D N V P L K G

801 GAAATTGCTCAGAAGACCTTTATGTATCCTGAAAAGGCTCCATTCAAGAAATCATGGGCTACCTCAAGTGGCAAAGCATCTAAACAAAACCAAGTT  
 80▶ G N C S E D L L C I L K R A P F K K S W A Y L Q V A K H L N K T K L

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**NcoI (924)** **EcoRV (935)**
**BsaBI (943)**

901 GTCTTGAACAAAGATGGCATTCTCCATGGAGTCAGATATCAGGATGGGAATCTGGTGTATCCAATTCCCTGGTTTGTACTTCATCATTGGCCAACTGCAG  
 113▶ S W N K D G I L H G V R Y Q D G N L V I Q F P G L Y F I I C Q L Q

**BsrGI (1005)**
**EcoO109I (1073)**

1001 TTTCTTGTACAATGCCAAATAATTCTGTGCATCTGAAGTTGGAGCTTCTCATCAACAAGCATATCAAAAAACAGGCCCTGGTGACAGTGTGTGAGTCTG  
 147▶ F L V Q C P N N S V D L K L E L L I N K H I K K Q A L V T V C E S

**Bst1107I (1117)**
**SdaI (1152)**

1101 GAATGCAACGAAACAGTATACAGAATCTCTCAATTCTTGTGGATTACCTGCAGGTCACACCACCATATCAGTCAATGTGGATACATTCCAGTA  
 180▶ G M Q T K H V Y Q N L S Q F L R D Y L Q V N T T I S V N V D T F Q Y

**XmnI (1265)** **NheI (1290)**

1201 CATAGATAAAGCACCTTCTCTTGTGAAATGTGTTGTCCATCTTCTTATACAGTAATTCAGACTGAACAGTTTCTTGGCCTTCAGGAGCTAGCTGGC  
 213▶ I D T S T F P L E N V L S I F L Y S N S D •

1301 CAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATT

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**HpaI (1428)** **MfeI (1439)**

1401 TGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAG

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**EcoRI (1524)**

1501 TAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAA  
 1601 TAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTCCCAAGGTTT

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**SapI (1706)**
**SspI (1763)** **SwaI (1777)**

1701 GAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGA

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**EcoO109I (1838)**

1801 AAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATA

1901 GAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATC  
141▶ • N R T Y K L P I L E E I T T K V L K G N M

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**SacI (2038)**

2001 TCAATGAGCAAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACTGATGGATCTGTCCACTCATCAGAGT  
 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

2101 AGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAAT  
 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 (2202)**

2201 GTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTC  
 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 (2344)**

2301 TCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATAC  
 18▶ E T A V E V L E L D Q Q S I N F T K M

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**AseI (2410)**
**SacI (2467)**

2401 TATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACAC

2501 GCCTACCGCCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTACTAGTCAAAAACAACTCCCATTGACGTCAATGGG  
SpeI (2565)  
←

2601 GTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAG  
SnaBI (2693)

2701 ATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTACCCTCATTGACGTCAATAGGGGGCGTACTTGGCA  
NdeI (2798)

2801 TATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATA

2901 CGTCATTATTGACGTCAATGGGGCGGGTCTGTTGGGCGGTCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGT  
SdaI (2976) PacI (2984) BspLU111 (2994)  
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3001 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGAGC

3101 CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTT

3201 ACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTCCGCTCCAAGC

ApaLI (3308)

3301 TGGGCTGTGTGCACGAACCCCCGTTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAGACTTATCGCCACT

3401 GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACA

3501 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTT

3601 TTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACTCACG

EagI (3744)  
PacI (3724) SwaI (3733) NotI (3743)

3701 TTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTG

3801 AATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCT

3901 CTATCGAA