



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGCTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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**AgeI (552)** **BspHI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTATCATGACAACCTCCAAAAGCACCGAGACTTCGTGGCAGA

1▶ M T T S Q K H R D F V A E

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**NcoI (602)**
**MscI (699)**

601 GCCCATGGGGGAAAAGCCAGTGGGGAGCCTGGCCGGGATTGGTGACGTCTGAGCAAGAGGCTGGAGGAAAGGGGCTTGACAAGGCTTATGTGGTCCTT

13▶ P M G E K P V G S L A G I G D V L S K R L E E R G F D K A Y V V L

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**BbsI (727)**
**BspLU11I (757)** **XmaI (782)**

701 GGCCAGTTTCTGGTGCTAAAGAAAGTGAAGACCTCTCCGAGAATGGCTGAAGGATACATGTGGTGCCAATGCCAAGCAGTCCCGGACTGCTTTGGGT

47▶ G Q F L V L K K D E D L F R E W L K D T C G A N A K Q S R D C F G

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**NheI (850)**

801 GCCTTCGAGAATGGTGTGATGCCTTCTGTAGTGTCTCTGGGATCCCTGCTAGTGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCAC

80▶ C L R E W C D A F L •

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**HpaI (988)** **MfeI (999)**

901 AACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACA

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**EcoRI (1084)**

1001 AATTGCATTCATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAG

1101 CATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAG

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**SapI (1266)**

1201 CTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAAGTTTGAAGTACTGCTTTCATTTCTTTATGTTTTAAATGCAGTAC

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**SspI (1323)** **Swal (1337)**
**EcoO109I**

1301 CTCCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAG

1401 GCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTAAATAGAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTC

141▶ • N

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**SacI (1598)**

1501 CTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGA

138▶ 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 Y D S I L

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**BstXI (1627)**

1601 GCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTG

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

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**StuI (1762)**

1701 CCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTC

72▶ 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

1801 TTGGTCTGATGGCCGCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTAGTGGCAGCTCCACCAGCTCCAGATCCTGCTGAGAGA

38▶ 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 D Q Q S I

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**XmnI (1904)**
**AseI (1970)**

1901 TGTTGAAGGCTTCATGGTGGCCCTCTATAGTGTGATCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTC

5▶ N F T K M

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**SacI (2027)**

2001 TCCAGCTTATCTGACGGTTCACATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACG

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**SpeI (2125)**

2101 ACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGGAGTCAAACCGCTATCCA

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**SnaBI (2253)**

2201 CGCCATTGATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGACT

**NdeI (2358)**

2301 GGGCATAATGCCAGGCGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCG

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2401 TAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGT

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PacI (2544)

**PstI (2537)**  
**SdaI (2536)**      BspLU11I (2554)

2501 CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGAAAGCCAGGAACCGTAAAAAGGC

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2601 CGCGTTGCTGGCGTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA

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2701 TACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTCGGGAAGCGTGG

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**ApaI (2868)**

2801 CGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTG

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2901 CGCCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTAT

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3001 GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG

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3101 GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATC

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PacI (3284)    SmaI (3293)

3201 TCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAA

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**EagI (3304)**  
**NotI (3303)**

3301 TCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAA

3401 ACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA