



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

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**AgeI (552)**
**SphI (560)**
**XcmI (569)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTGAGCATGCAGGCCATCAAGTGTGGTGGTGGGAGACGGAGC

1▶ M Q A I K C V V V G D G A

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**NsiI (638)**
**BstXI (686)**

601 TGTGGTAAAACCTGCCTGCTCATCAGTTACACGACCAATGCATTTCTGGAGAGTACATCCCCACCGTCTTTGACAACTATTCTGCAATGTTATGGTA

13▶ V G K T C L L I S Y T T N A F P G E Y I P T V F D N Y S A N V M V

701 GATGAAAACAGTGAATCTGGCCTATGGGACACAGCTGGACAAGAAGATTATGACAGATTGCGTCCCTCTCTACCCGACAGACAGCTGTTCTTAA

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

801 TTTGCTTTCCCTGTGAGTCTGCATCATTGAAAATGTCGGTGCAAAGTGGTATCCTGAACTGCGACACCACTGTCCCAATACTCCTATCATCCTCGT

80▶ I C F S L V S P A S F E N V R A K W Y P E V R H H C P N T P I I L V

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**HindIII (907)**
**NcoI (992)**

901 GGGGACGAAGCTTGATCTTAGGGATGATAAGGACACCATTGAGAAGCTGAAGGAGAAGAAGCTGACTCCCATCACCTACCCGACGGGCTGGCCATGGCG

113▶ G T K L D L R D D K D T I E K L K E K K L T P I T Y P Q G L A M A

1001 AAAGAGATCGGTGCTGCAAAATACCTGGAGTGTCTCAGCTCTCACACAGCGAGGACTCAAGACAGTGTGTTGACGAAGCTATCCGAGCGGTTCTGTGCC

147▶ K E I G A V K Y L E C S A L T Q R G L K T V F D E A I R A V L C P

MscI (1161)

1101 CTCCTGTCAAGAAGAGGAAGAGAAAATGCCTGCTGTTGTAATGTCGGAGCCCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAA

180▶ P P V K K R K R K C L L L •

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**HpaI (1293)**

1201 ACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGTGCAATAAACAAAGTTAA

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**MfeI (1304)**
**EcoRI (1389)**

1301 ACAACAATTGCATTATTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGGTATGGAATTCTAAAA

1401 TACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGC

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**SapI (1571)**

1501 ATTAGCTGTTGACGCTCACCTCTTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCA

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**SspI (1628)**
**SwaI (1642)**

1601 CTGACCTCCACATTCCCTTTTATGATAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGC

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**EcoO109I (1703)**

1701 TCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTT

141▶ •

1801 AGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGA

140▶ 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 Y D S

**SacI (1903)**
**BstXI (1932)**

1901 GATGAGCTCTCTGCATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCC

107▶ 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 D F D

**StuI (2067)**

2001 TTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCC

73▶ 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 I I E G

2101 CAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACAGCTCCAGATCCCTGCTG

40▶ 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 V E V L E L D Q Q

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**BbsI (2213)**
**AseI (2275)**

2201 AGAGATGTTGAAGGTCTTCATGTTGGCCCTCTATAGTGTGATCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATG

7▶ S I N F T K M

2301 GCGTCTCCAGCTTATCTGACGGTTCACATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTG  
 SacI (2332)

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2401 TTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCT  
 SpeI (2430)

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2501 ATCCACGCCCATTTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGTCAT  
 SnaBI (2558)

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2601 GTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGTACTGCCAAGTGGGCAGTT  
 NdeI (2663)

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2701 TACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGG

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2801 GCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAA  
 PacI (2849)  
 PstI (2842)  
 SdaI (2841) BspLU11I (2859)

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2901 AAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT

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3001 AAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAG

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3101 CGTGGCGCTTTTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCCGAC  
 ApaLI (3173)

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3201 CGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGA

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3301 GGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC

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3401 CTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAA

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3501 GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACAT  
 PacI (3589) SwaI (3598)

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3601 TTAATCAGCGGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACATAACGCTCTCCATCAAACAAA  
 EagI (3609)  
 NotI (3608)

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3701 ACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAAGTGCCAGAGTCCAGAACATTTCTCTATCGAA