



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

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

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101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**

**Psp1406I (203)**
**PvuII (239)**
**Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCC

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301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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**BstEII (555)**

**AgeI (552)** **NcoI (560)**
**EcoO109I (576)**

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCCTCTCACTCAGGCCCTCGACGTCTGTGCTCTT

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**BsrGI (672)**

601 TCTGTTCTGCTGCTGGGAGGCTGGCTGGCCTCCACACGTTGCCCGTCCGTTTACTACGACCAAGTATGATGTACAGAAAATAGTCGAGGAATTACAG

13▶ L F C C L G G W L A S H T L P V R L L R P S D D V Q K I V E E L Q

701 TCCCTCTGAAGATGCTTTGAAAGATGTGGAGGAAGAGAGGGCGTGTCTGTCCAGAATTACACGCTGCCGTGTCTCAGCCCTGACGCCAGCCGC

47▶ S L S K M L L K D V E E K G V L V S Q N Y T L P C L S P D A Q P

801 CAAACAACATCCACAGCCAGCCATCCGGGCATATCTCAAGACAATCAGACAGCTAGACAACAACTGTTATTGATGAGATCATAGACACCTCGACAA

80▶ P N N I H S P A I R A Y L K T I R Q L D N K S V I D E I I E H L D K

901 ACTCATATTTCAAGATGCACCAGAAAACAACATTTCTGTGCCAACAGACCCATGAATGAAACGTTTCATCTGACTATTTCTCAACAGTTTTAGAG

113▶ L I F Q D A P E T N I S V P T D T H E C K R F I L T I S Q Q F S E

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**MscI (1079)**

**NheI (1073)**

1001 TGCATGGACCTCGCACTAAAATCATTGACCTCTGGAGCCCAACAGGCCACCACTTAAGCCATCTCTTCTTTGCTAGCTGGCCAGACATGATAAGATAC

147▶ C M D L A L K S L T S G A Q Q A T T •

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1101 ATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCT

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**HpaI (1211)** **MfeI (1222)**

1201 GCAATAACAAGTTAACAACAACAATTGCATTCAATTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATG

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**EcoRI (1307)**

1301 TGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCTCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAG

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**SapI (1489)**

1401 GGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTTCTTCAAT

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**SspI (1546)** **SwaI (1560)**

1501 CTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTAT

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**EcoO109I (1621)**

1601 TAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGA

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1701 AAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCA

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

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**SacI (1821)** **BstXI (1850)**

1801 GTCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTCCCTGACAGCC

113◀ 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 P H R V A

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**StuI (1985)**

1901 ACAATGGTGTCAAAGCTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCTCAATGTGGA

79◀ 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 Y A E I H V

2001 CAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCGACATGGTGTCTGTTGCTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCAC

46◀ 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 E T A V E V

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**BbsI (2131)**

**XmnI (2127)**
**AseI (2193)**

2101 CAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAAT

13◀ L E L D Q Q S I N F T K M

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**SacI (2250)**

2201 GTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGGC

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**SpeI (2348)**

2301 GTCAAATGGGGCGAGTTGTTACGACATTTTGGAAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATC

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2401 CCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGG **SnaBI (2476)**

2501 AAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGT **NdeI (2581)**

2601 ACTGCCAAGTGGGCGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCA

2701 ATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACG **PacI (2767)**  
**PstI (2760)** **SdaI (2759)** **BspLU11I (2777)**  
CCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAA

2801 AAGGCCAGGAACCGTAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGC

2901 GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGC

3001 CTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAA **ApaLI (3091)**

3101 CCCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA

3201 ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGC

3301 TCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAG

3401 ATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGTCA

3501 **EagI (3527)**  
**PacI (3507)** **SwaI (3516)** **NotI (3526)**  
TGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATAC

3601 GCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA