



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACCGCCCGCCGCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTTCATCATGACATTTGCTGAGGACAAGACCTATAAGTATATCCG

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1▶ M T F A E D K T Y K Y I R

**BstAPI (611)**

601 AGACAACCACAGCAAGTTTTGCTGTGTTGACGTTCTGGAGATCCTGCCTTACCTGTCTCGCTCACAGCTAGTGACCAGGATCGACTGCGGGTCTCTAC

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

**XcmI (747)** **BglII (791)**

701 AGGCAGATCGGGAACCGGACACTCTGGGACTCTTCAATAATCTCCAGCGCCGGCTGGCTGGTGGAGGCTTTCATCCGGGCACTGCAGATCTGTG

47▶ R Q I G N R D T L W G L F N N L Q R R P G W V E V F I R A L Q I C

**XhoI (827)** **EcoO109I (856) BsrBI (867)**

801 AGCTGCCTGGGCTGGCTGATCAAGTACTCGAGTTTATCAGAGCTACCTGCCTCCGGGACCTCACTCCGCTCCCTAGAGCCACTGCAGTTACCAGACTT

80▶ E L P G L A D Q V T R V Y Q S Y L P P G T S L R S L E P L Q L P D F

**NcoI (954)**

901 TCCTGCTGCGGTTTCTGGACCCTCTGCATTTGCCCAGGTCAACATCCCTGACCATGGCTTACGAGAGACCAAGTTGCCCAAGCTGTCCAGGAC

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

**EcoRI (1026)** **NruI (1064)**

1001 ACCCAGCCACCAGAGTCCCAGTAGAGAATTCAGAGCAACTCTCCAGACCACTCCGGGGCCGTCGCGAGGATGTCTGGTGGCTCTTTGATACCCCTCTC

147▶ T Q P P E S P V E N S E Q L L Q T N S G A V A R M S G G S L I P S

**BstAPI (1177)**

1101 CTAACCAGCAGGCTCTCAGCCCTCAGCCCTCCAGAGAGCATCAAGAGCAAGAACCAGAAGTGGTGGCGCCACGCAGCAAATGTTGCCTCTGTTCCCAT

180▶ P N Q Q A L S P Q P S R E H Q E Q E P E L G G A H A A N V A S V P I

**PshAI (1211)** **Bsu36I (1257)**

1201 AGCAACCTATGGACCTGTGTCTCAACCGTTTCTTCCAGCCCTTCCAGTACTGCCCTGAGGACAAACCTTGTCTGGGGTACAGTATCAGCCCTA

213▶ A T Y G P V S P T V S F Q P L P R T A L R T N L L S G V T V S A L

**BstEII (1357)** **ScaI (1387)**

1301 TCTGCTGATACCTCTTTGCTCCTCGTCCACTGGATCAGCTTTTGC AAAGGAGCTGGTACCAGGCCAAAGCTGCCACCTGTTTCAGTACTACACTCA

247▶ S A D T S L S S S S T G S A F A K G A G D Q A K A A T C F S T T L

1401 CCAATTCTGTGACTACCAGCTCAGTGCCTTCTCCAGATTGGTCCCAGTAAAACCATGTCTTCCAAGTTGCCCTCAGTTCAAAGTCCACTGCTGCGAT

280▶ T N S V T T S S V P S P R L V P V K T M S S K L P L S S K S T A A M

**MscI (1592)**

1501 GACGTCTACTGTGCTACCAATACAGCGCCATCAAAATTACCCAGCAACTCAGTGTATGCGGGCACAGTGCCATCCAGAGTGCTGTAGTGTGGCCAAA

313▶ T S T V L T N T A P S K L P S N S V Y A G T V P S R V P A S V A K

1601 GCACCTGCCAACCAATACCACCTGAGAGGAACAGCAAGCAAGGAGACCCCGAGGGTCCAGCAACCAAGTCACTGGAGGCAACCCAGACTG

347▶ A P A N T I P P E R N S K Q A K E T P E G P A T K V T T G G N Q T

1701 GACCAATAGCAGTATCAGGAGCTTGCCTGACTCTGGACCAGAGTGAAGCCAGGTGTGCTGGTATCCAGTTGGACGAGCCATTCTCAGCCTGCTGT

380▶ G P N S S I R S L H S G P E M S K P G V L V S Q L D E P F S A C S V

**NcoI (1845)**

1801 GGACCTTGCCATTAGCCCTAGCAGCTCCTGGTCTCAGAACCACCATGGTCCAGAGGAGAATGAGTATTCGTCCTTTAGAATCCAGGTAGACGAAAGC

413▶ D L A I S P S S S L V S E P N H G P E E N E Y S S F R I Q V D E S

1901 CCCAGTGTGATCTATTAGGAAGCCCTGAGCCACTAGCCACCCAGCAGCCCAAGAAGAGGAAGAATTGTGCCAGTTCAATGCCCTGGGCTAAGTGGC

447▶ P S A D L L G S P E P L A T Q Q P Q E E E E H C A S S M P W A K W

**ApaLI (2012)** **MscI (2080)**

2001 TTGGGGCCACCAGTGCCTCTTGGCTGTATTCTGGCAGTGATGCTGTACCGTAGTAGCGCCTGGCCAGTGAAGTCTAGCTAGCCAGACATGATAAGATA

480▶ L G A T S A L L A V F L A V M L Y R S R R L A Q •

2101 CATTGATGAGTTTGGACAACCAACAATAAGTGCATTGCTTTTATTTGTAAGTTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGC

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**HpaI (2212) MfeI (2223)**

2201 TGCAATAAACAAGTTAAACAACAATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAAT

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**EcoRI (2308)**

2301 GTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCA

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2401 GGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGTTTGAAGTAGCTCTTCATT **SapI (2490)**

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2501 TCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTA **SspI (2547)** **SwaI (2561)**

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2601 TTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAG **EcoO109I (2622)**

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2701 AAAGCGAGCTTCTAGCTTTAGTTCTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGC  
 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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2801 AGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGC **SacI (2822)** **BstXI (2851)**  
 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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2901 CACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGG **StuI (2986)**  
 80 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

3001 ACAGCAGAGATGATCTCCCAGTCTTGGTCTGTAGGCCGCCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCA  
 46 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 E T A V E V

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3101 CCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAAT **XmnI (3128)** **AseI (3194)**  
 13 L E L D Q Q S I N F T K M

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3201 TGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTG **SacI (3251)**

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3301 CGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAAT **SpeI (3349)**

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3401 CCCCCTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAG **SnaBI (3477)**

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3501 GAAAGTCCATAAGGTCTACTGTTGGGCATAATGCCAGGCGGGCCATTTACCGTCAATGAGGCGTACTTGGCATATGATACACTTGTATG **NdeI (3582)**

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3601 TACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTC

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3701 AATGGGCGGGGTCGTTGGGCGGTCAGCCAGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCA **PacI (3768)** **SdaI (3760)** **BspLU11I (3778)**

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3801 AAAGGCCAGGAACCGTAAAAAGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG

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3901 CGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCG

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4001 CCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGA **ApaLI (4092)**

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4101 ACCCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT

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4201 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCG

---

4301 CTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCA

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4401 GATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTC

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4501 ATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATA **EagI (4528)** **PacI (4508)** **SwaI (4517)** **NotI (4527)**

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4601 CGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGACGGTGCCAGAACATTTCTCTATCGAA