



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82)  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCC

PvuII (239) **Bsu36I (291)**  
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAATGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
401 GGGCCTTTGTCCGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

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**AgeI (552)** **NcoI (560)** **BspEI (578)**  
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTACCATGGCTTGTCTTGGACTCCGGAGGTACAAAGCTCAACT

PvuII (601) **BbsI (658)**  
601 GCAGCTGCCTTAGGACTTGGCCTTTGTAGCCTGCTCACTTTCTTTTCCATCCAGTCTTCTCTGAAGCCATACAGGTGACCCAACTTCAGTGGTG

**NheI (703)** **NcoI (711)** **SspI (737)**  
701 TTGGTAGCAGCATGGTGTCCGAGCTTTCCATGTGAATATTCACCGTCACACAACACTGATGAGGTCCGGGTGACTGTGCTGCGGCAGACAAATGACC

**PshAI (804)** **Acc65I (874)**  
801 AAATGACTGAGGTCTGTGCCACGACATTACAGAGAAGAATACAGTGGGCTTCTAGATTACCCCTTCTGCGAGTTAGCTTGGGGTGTTTTTTACAGTTTCC

**BamHI (1055)**  
80▶ Q M T E V C A T T F T E K N T V G F L D Y P F C S G T F N E S R V N  
901 CCTCACCATCCAAGACTGAGAGCTGTTGACACGGGACTGTACCTCTGCAAGGTGAAACTCATGTACCACCGCCATACTTTGTGGGCATGGGCAACGGG

113▶ L T I Q G L R A V D T G L Y L C K V E L M Y P P P Y F V G M G N G  
1001 ACGCAGATTTATGTCATTGATCCAGAACCATGCCCGATTCTGACTTCTCCTTTGGATCCTTGTGCGAGTTAGCTTGGGGTGTTTTTTACAGTTTCC

147▶ T Q I Y V I D P E P C P D S D F L L W I L V A V S L G L F F Y S F  
1101 TGGTCACTGCTGTTTCTTTGAGCAAGATGCTAAAGAAAAGAAGTCTTACAACAGGGGTCTATGTGAAAATGCCCCAACAGAGCCAGAATGTGAAAA

180▶ L V T A V S L S K M L K K R S P L T T G V Y V K M P P T E P E C E K  
NheI (1250)  
1201 GCAATTTGAGCCTTATTTTATCCCATCAACTGAAAGCGCTTGAATTCGTAGCTCGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC

**EcoRI (1244)**  
213▶ Q F Q P Y F I P I N •

1301 AGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAG

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**HpaI (1413)** **MfeI (1424)**  
1401 CTGCAATAAACAGTTAAACAACAACATTCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAA

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**EcoRI (1509)**  
1501 TGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATC

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**SapI (1691)**  
1601 AGGGGCTGTTGCAATGTGATTAGCTGTTGAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTACTAGCTTCTCAT

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**SspI (1748)** **SwaI (1762)**  
1701 TTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTT

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**EcoO109I (1823)**  
1801 ATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAA

1901 GAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAG

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

**SacI (2023)** **BstXI (2052)**  
2001 CAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAG

113◀ 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 P H R V A

**StuI (2187)**  
2101 CCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCCTCAATGTG

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  
2201 GACAGCAGAGATGATCTCCCGTCTGGTCTGATGGCCGCCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCC

47◀ 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

**BbsI (2333)** **XmnI (2329)** **AseI (2395)**  
2301 ACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAAGTCTTATACTATGCCGATATACTATGCCGATGATTA

13◀ V L E L D Q Q S I N F T K M

2401 **SacI (2452)**  
TTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACGTACACGCCTACCGCCATT

2501 **SpeI (2550)**  
GCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGAGACTTGAAAA

2601 **SnaBI (2678)**  
TCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTA

2701 **NdeI (2783)**  
GGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTACCCTGATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGAT

2801  
GTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGT

2901 **SdaI (2961)** **PacI (2969)** **BspLU11I (2979)**  
CAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTACCCTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGC

3001  
AAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTG

3101  
GCGAAACCGACAGGACTATAAAGATACCAGGCTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCC

3201 **ApaLI (3293)**  
GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCAGC

3301  
AACCCCCGTTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGG

3401  
TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGC

3501  
GCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGC

3601  
AGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACACTCACGTTAAGGGATTTTGGT

3701 **EagI (3729)** **PacI (3709)** **Swal (3718)** **NotI (3728)**  
CATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACAT

3801  
ACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA