



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**Psp1406I (203)**
**HindIII (245)** **EcoNI (287)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGCC  
 301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

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**BspLU11I (560)**

501 TCTGTTTGTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTGGCAGCTGCTCCTCCAACTGCTCTGCTACTTCT  
**AgeI (552)**

601 AGTTTCAGCTGGCATGCGGACTGAAGATCTCCCAAAGGCTGTGGTGTCTGGAGCCTCAATGGTACAGCGTGTGAGAAGGACAGTGTGACTCTGAAG  
 13▶ V S A G M R T E D L P K A V V F L E P Q W Y S V L E K D S V T L K  
**XhoI (774)**

701 TGCCAGGGAGCCTACTCCCTGAGGACAATCCACACAGTGGTTTACAAATGAGAGCCTCATCTCAAGCCAGGCTCAGCTACTTCATTGACGCTGCCA  
 47▶ C Q G A Y S P E D N S T Q W F H N E S L I S S Q A S S Y F I D A A  
**StuI (770)**

801 CAGTCAACGACAGTGGAGAGTACAGGTGCCAGACAAACCTCTCCACCCTCAGTGACCCGGTGCAGCTAGAAGTCCATATCGGTGGCTGTTGCTCCAGGC  
 80▶ T V N D S G E Y R C Q T N L S T L S D P V Q L E V H I G W L L L Q A  
 901 CCCTCGGTGGGTGTTCAAGGAGGAAGACCTATTACCTGAGGTGTACAGCTGGAAGAACACTGCTCTGCATAAGGTACATATTTACAGAATGGCAAA  
 113▶ P R W V F K E E D P I H L R C H S W K N T A L H K V T Y L Q N G K  
**EcoO109I (896)**

1001 GACAGGAAGTATTTTCATCATAATTCTGACTTCCACATTCAAAAGCCACACTCAAAGATAGCGGCTCCTACTTCTGCAGGGGCTTGTGGGAGTAAA  
 147▶ D R K Y F H H N S D F H I P K A T L K D S G S Y F C R G L V G S K  
**Acc65I (1178)**

1101 ATGTGCTTCAGAGACTGTGAACATCACCATCACTCAAGGTTTGGCAGTGTCAACCATCTCATATTCTCACCCTGGGTACCAAGTCTCTTTCTGCTT  
 180▶ N V S S E T V N I T I T Q G L A V S T I S S F S P P G Y Q V S F C L  
**NheI (1290)**

1201 GGTGATGGTACTCCTTTTTGCGAGTGACACAGGACTATATTTCTCTGTGAAGACAAACATTTGAAGCTCAACAAGAGACTGGAAGGACCAGCTAGCTGGC  
 213▶ V M V L L F A V D T G L Y F S V K T N I •  
**BstXI (1287)** **MseI (1296)**

1301 CAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATT

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**HpaI (1428)** **MfeI (1439)**

1401 TGTAACCATTATAAGCTGCAATAACAAGTTAAACAACAACATTGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAG

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**EcoRI (1524)**

1501 TAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAA  
 1601 TAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTTATGAGTAAAGATATAGTATTTTCCCAAGGTTT

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**SapI (1706)** **SspI (1763)** **SwaI (1777)**

1701 GAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAAAATTTAAATACATCATTGCAATGA

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**EcoO109I (1838)**

1801 AAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATA  
 1901 GAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTTCAT  
**SacI (2038)** **BstXI (2067)**

2001 TCAATGAGCACAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTGACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGT  
 118▶ E I L V F 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  
 2101 AGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGCTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCTTGCCAAT  
 85▶ P H R V A 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  
**StuI (2202)**

2201 GTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGTCTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTC  
 52▶ Y A E I H 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  
**BspHI (2352)**

2301 TCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAAGTCTATTATACTATGCCGATATAC  
 18▶ E T A V E V L E L D Q Q S I N F T K M  
**XmnI (2344)**

2401 TATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATAGACCTCCACCGTACAC  
**AseI (2410)** **SacI (2467)**

2501 GCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCC GTT GATT **SpeI (2565)** **ACTAGTCAAACAAACTCCATTGACGTCAATGGG**  
 2601 GTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAG **SnaBI (2693)**  
 2701 ATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCA **NdeI (2798)**  
 2801 TATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATA  
 2901 CGTCATTATTGACGTCAATGGGGCGGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAAC **PstI (2977)** **PacI (2984)** **SdaI (2976)** **BspLU11I (2994)** **GCC TGCAGGTTAATTAAGAACATGT**  
 3001 **GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGAGC**  
 3101 **CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTCCGACCCTGCCGCTT**  
 3201 **ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGGTGTAGGTCGTTGCTCCAAGC**  
 3301 **TGGGCTGTGTGCACGAACCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACT** **ApaLI (3308)**  
 3401 **GCGAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA**  
 3501 **GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTT**  
 3601 **TTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACG**  
 3701 **TTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC** **PacI (3724)** **Swal (3733)** **EagI (3744)** **NotI (3743)** **AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTG**  
 3801 AATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCT  
 3901 CTATCGAA