



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCAGCGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGCTCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

**KasI (535)** **AgeI (552)** **NeoS (575)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCTACCTGAGATCACCGGTCAACATGTGTTCCCTCCCATGGCAAGATACTACATAATTA M C S L P M A R Y Y I I K

**MscI (633)** **BglII (683)**  
601 ATATGCAGACCAGAAGGCTCTATACACAAGAGATGGCCAGTCTGCTGGTGGGAGATCCTGTTGCAGACAAGTCTGTGCAGAGAAGATCTGCACACTTCTCT 13▶ Y A D Q K A L Y T R D G Q L L V G D P V A D N C C A E K I C T L P

**BstXI (728)** **BamHI (740)**  
701 AACAGAGGCTTGGACCGCACCAAGGTCCCATTCTTCTGGGATCCAGGGAGGGAGCCGCTGCTGGCATGTGTGGAGACAGAAGAGGGGCTTCCCTAC 47▶ N R G L D R T K V P I F L G I Q G G S R C L A C V E T E E G P S L

**BsrGI (827)**  
801 AGCTGGAGGATGTGAACATTGAGGAAGTGTACAAAGTGGTGAAGAGGCCACACGCTTACCTTCTTCCAGAGCAGCTCAGGCTCCGCTTACAGGCTTGA 80▶ Q L E D V N I E E L Y K G G E E A T R F T F F Q S S S G S A F R L E

901 GGCTGCTGCTGGCTGGCTGGTCTGCTGTGGCCCGCAGAGCCCAGCAGCCAGTACAGCTACCAAGGAGAGTGAGCCCTCAGCCGTACCAAGTTT 113▶ A A A W P G W F L C G P A E P Q Q P V Q L T K E S E P S A R T K F

**MscI (1037)** **NheI (1031)**  
1001 TACTTTGAACAGAGCTGGTAGGGAGACAGGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAACCACAAGTGAATGCAGTGAAAA 147▶ Y F E Q S W •

**HpaI (1169)** **MfeI (1180)**  
1101 AAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCATTTATGT

**EcoRI (1265)**  
1201 TTCAGGTTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCT

1301 CCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCT

**SapI (1447)**  
1401 CTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTACTCTTCTTATTTGTTTTAAATGCACTGACCTCCACATTCCCTTTTAA

**SspI (1504)** **Swal (1518)**  
1501 GTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCC

1601 AGTTTAGTAGTTGGACTTAGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGA 141▶ • N R T Y K L P I

**SacI (1779)**  
1701 TGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACA 132▶ 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 I L E R C M G C

**BstXI (1808)**  
1801 GGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGAC 99▶ 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 K Q G N S V A S

**StuI (1943)**  
1901 CCAATGGCAATGGCTTCAAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCC 65▶ 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 T K T R I A A G

**BbsI (2089)** **XmnI (2085)**  
2001 CGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGT 32▶ V H H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M

**AseI (2151)**  
2101 GGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTT

**SacI (2208)**  
2201 CACTAAACGAGCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGGCTCAATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGT

**SpeI (2306)**  
2301 TGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCC

**SnaBI (2434)**  
2401 AAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTATGACTGGGCATAATGCCAGGCGGG

**NdeI (2539)**

2501 CCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGA  
2601 CGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTGACGCCAGCGGGCCATTTA

**PacI (2725)**

**PstI (2718)**

**SdaI (2717)**

**BspLU11I (2735)**

2701 CCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTC  
2801 CATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTG  
2901 GAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACG

**ApaLI (3049)**

3001 CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTAT  
3101 CGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGT  
3201 TCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTC  
3301 TTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATC

**EagI (3485)**

**PacI (3465)**

**SwaI (3474)**

**NotI (3484)**

3401 TTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAAT  
3501 ATCTTTATTTTCATTACATCTGTGTGTTGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAA  
3601 TAGGCTGTCCCAGTGCAAGTGCCAGGTGCCAGAACATTTCTCTATCGAA