



**PvuI (7)**  
**SgfI (6)** MfeI (82) EcoNI (96)  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
Psp1406I (203) PvuII (239) EcoNI (287)  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
**NaeI (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)** **Bsp120I (588)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATTGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGAT  
1▶ M A A A A A A G A G P E M  
**SacII (603)** **KasI (661)**  
601 GGTCCGGCGGCAGGTGTTTCGACGTGGGGCCGCGCTACACCAACCTCTCGTACATCGGGGAGGGCGCCTACGGCATGGTGTGCTGCTTATGATAATGTC  
13▶ V R G Q V F D V G P R Y T N L S Y I G E G A Y G M V C S A Y D N V  
701 AACAAAGTTTCGAGTAGCTATCAAGAAAATCAGCCCTTTGAGCACCAGACCTACTGCCAGAGAACCCCTGAGGGAGATAAAAATCTTACTGCGCTTCAGAC  
47▶ N K V R V A I K K I S P F E H Q T Y C Q R T L R E I K I L L R F R

**EcoO109I (875)**  
801 ATGAGAACATCATTGGAATCAATGACATTATTCGAGCACAACCATCGAGCAAATGAAAGATGTATATATAGTACAGGACCTCATGGAACAGATCTTTA  
80▶ H E N I I G I N D I I R A P T I E Q M K D V Y I V Q D L M E T D L Y

**Psp1406I (991)**  
901 CAAGCTCTTGAAGACACAACACCTCAGCAATGACCATATCTGCTATTTTCTCTACCAGATCCTCAGAGGGTAAATATATCCATTGAGTAAACGTTCTG  
113▶ K L L K T Q H L S N D H I C Y F L Y Q I L R G L K Y I H S A N V L  
1001 CACCGTGACCTCAAGCCTTCCAACCTGTGCTCAACACCACCTGTGATCTCAAGATCTGTGACTTTGGCTGGCCCGTGTGAGATCCAGACCATGATC  
147▶ H R D L K P S N L L N T T C D L K I C D F G L A R V A D P D H D

**MscI (1124)** **EcoRI (1161)**  
1101 ACACAGGGTTCCTGACAGAATATGTGGCCACACGTTGGTACAGGGCTCCAGAATTATGTTGAATTCAGGGCTACACCAAGTCCATTGATATTTGGTC  
180▶ H T G F L T E Y V A T R W Y R A P E I M L N S K G Y T K S I D I W S

**PvuII (1267)** **BamHI (1294)**  
1201 TGTAGGCTGCATTCTGGCAGAAATGCTTTCTAACAGGCCATCTTTCCAGGGAAGCATTATCTTGACCAGCTGAACACATTTTGGGATTCTTGGATCC  
213▶ V G C I L A E M L S N R P I F P G K H Y L D Q L N H I L G I L G S

**NcoI (1381)**  
1301 CCATCACAAGAAGACCTGAATTGTATAATAAAATTTAAAGCTAGGAACCTATTTGCTTTCTCTTCCACACAAAAATAAGGTGCCATGGAACAGGCTGTTCC  
247▶ P S Q E D L N C I I N L K A R N Y L L S L P H K N K V P W N R L F

**BstXI (1412)**  
1401 CAAATGCTGACTCCTAAAGCTCTGGACTTATTGGACAAAATGTTGACATTAACCCACACAAGAGGATTGAAGTAGAACAGGCTCTGGCCACCCATATCT  
280▶ P N A D S K A L D L L D K M L T F N P H K R I E V E Q A L A H P Y L  
1501 GGAGCAGTATTACGACCCGAGTGACGAGCCATCGCCGAAGCACCATTCAAGTTGACATGGAATGGATGACTTGCCTAAGGAAAAGCTCAAAGAATA  
313▶ E Q Y Y D P S D E P I A E A P F K F D M E L D D L P K E K L K E L

**MscI (1683)**  
**NheI (1677)**  
1601 ATTTTGAAGAGACTGCTAGATTCCAGCCAGGATACAGATCTTAAATTTGTCAGGACAAGGGCTCAGAGGACTGGACGCTAGCTGGCCAGACATGATAAG  
347▶ I F E E T A R F Q P G Y R S •  
1701 ATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATA

**HpaI (1815)** MfeI (1826)  
1801 AGCTGCAATAAACAGTTAAACAACAATTGCATTCAATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACA

**EcoRI (1911)**  
1901 AATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCA  
2001 TCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTAGCTCTTC

**SspI (2150)** **SwaI (2164)**  
2101 ATTTCTTTATGTTTTAAATGCAGTACCTCCACATTCCCTTTTATGATAAATATTGAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTT

**EcoO109I (2225)**  
2201 TTATTAGGAGAATCCAGATGCTCAAGGCCCTTCAATAATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGC

**SacI (2425)** **BstXI (2454)**  
2301 AAGAAAGCGAGCTTCTAGCTTTAGTTCCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAA  
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  
2401 AGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGAC  
114▶ 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

2501 AGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATG **StuI (2589)**  
81 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 Y A E I  
2601 TGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGTGGTCCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCT  
47 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 E T A V E  
**BspHI (2739)**

2701 CCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATT **AseI (2797)**  
14 V L E L D Q Q S I N F T K M  
**XmnI (2731)**

2801 AATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCCAT **SacI (2854)**

2901 TTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGTGGAGACTTGG **SpeI (2952)**

3000 AAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAA **SnaBI (3080)**

3100 GTAGGAAAGTCCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTT **NdeI (3185)**  
3200 GATGTACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGAAACATACGTCATTATTGA

3300 CGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCGAGGTTAA TTAAGAACATGTGAGCAAAGG **PstI (3364)** **SdaI (3363)** **PacI (3371)** **BspLU11I (3381)**  
3398 CCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAG  
3498 AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACC

3598 TGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGT **ApaLI (3695)**  
3698 GCACGAACCCCCGTTTCCGCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC  
3798 ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTA  
3898 TCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAA  
3998 GCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATT

4098 TTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACT **EagI (4131)** **PacI (4111)** **Swal (4120)** **NotI (4130)**  
4198 AACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA