



**PvuI (7)**  
**SgfI (6)** **MfeI (82)** **EcoNI (96)**  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
**PvuII (239)** **EcoNI (287)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTGCCTGCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
**NaeI (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
**KasI (535)** **AgeI (552)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCCACCATGGAAGATCCACACAAGAGTAACACGACAGAGACTGC  
601 ATCTCAGCCTGGTTCAACCGTTGCGGGGCTCACGTTTCTCAGATAGTACATCAGGTGTCTGTTATCAGAAAGTGAGGAGTCTCAGGACTCATCTGAC  
13▶ S Q P G S T V A G P H V S Q I V H Q V S S L S E S E E S Q D S S D

**BamHI (728)** **KasI (740)**  
701 AGCATAGGCTCCTCACAGAAAGCTCACGGGATCTGGCCGGCGCCCTACAGGAAAATTTGAAAGACCTCTCTTCTGAAGATACACGGGGCAGAA  
47▶ S I G S S Q K A H G I L A R R P S Y R K I L K D L S S E D T R G R  
801 AAGGGAAAGGAGAAAATCCAGCATTTCTGCCATCAGCTATGTCTGTTCCAGCCCCATCTATCAGACGAGCAGCGGACAGTACATTGCCATTGCCCC  
80▶ K G E G E N P S I S A I T S M S V P A P I Y Q T S S G Q Y I A I A P

**MscI (917)** **PstI (949)** **ScaI (979)**  
901 AAACGGAGCCTTACATTTGGCCAGTCCAAGCACGGATGGAGTGCAGGCATTAACCATGACAAAATCAAGCAGTACTCAGCAGGGGACGATC  
113▶ N G A L H L A S P S T D G V Q A L Q T L T M T N S S S T Q Q G T I

**BsrGI (1059)**  
1001 CTCCAGTATGCACAGACCTCTGACGGACAGCAGATACTCGTCCCGAGCAACCAGGTGGTTGTACAGACTGCATCAGGAGATATGCAGACCTACCAGATCC  
147▶ L Q Y A Q T S D G Q I L V P S N Q V V V Q T A S G D M Q T Y Q I  
1101 GTACCACGCCATCTGCCAGTCTCTCCACAGACCGTGGTGTAGACTTCTCCTGTGACTTTACATCTCAGACAACAAAGACAGATGACCCCTCAACTAAG  
180▶ R T T P S A T S L P Q T V V M T S P V T L T S Q T T K T D D P Q L R  
1201 AAGAGAAATACGACTGATGAAAAACAGAGAAGCTGCCGAGAGTCCCGCGGAAGAAGAGTACGTGAAGTGCCTGGAGAACCCTGTTGCTGTTCTG  
213▶ R E I R L M K N R E A A R E C R R K K K E Y V K C L E N R V A V L

**MscI (1387)**  
**NheI (1381)**  
1301 GAAAATCAAATAAACTCTAATAGAGGAGCTAAAGACTTTGAAAGACCTTTATTCTCATAAAAGTGTGGTTGATCTTTAAAGCTAGCTGGCCAGACATGA  
247▶ E N Q N K T L I E E L K T L K D L Y S H K S V •  
1401 TAAGATACATTGATGAGTTTGGACAAACCAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCAT

**HpaI (1519)** **MfeI (1530)**  
1501 TATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCATTTATGTTTCAGGTTACAGGGGAGGTGGGGAGGTTTTTAAAGCAAGTAAACCTC

**EcoRI (1615)**  
1601 TACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTGAATCCTTTTCTGAGGGATGAATAAGGCATA  
1701 GGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTAGCT

**SspI (1854)** **SwaI (1868)**  
1801 CTTCAATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATG  
1901 TTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGA  
2001 CAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGC  
114▶ N R T Y K L P I L E E I T T K V L K G N M E I L

**SacI (2129)** **BstXI (2158)**  
2101 ACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCC  
115▶ 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 P H R

**StuI (2293)**  
2201 TGACAGCCACAATGGTGTCAAAGCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTC  
82▶ 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 Y A E  
2301 AATGTGGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGCTCCTATAGAGCATGGTATCTTCTCAGTGGCG  
49▶ 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 E T A

**BspHI (2443)**  
**BbsI (2439)**  
**XmnI (2435)**  
2401 ACCTCCACGAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCCTATAGTGTGATGCTATTATACTATGCCGATATACTATGCCGAT  
15▶ V E V L E L D Q Q S I N F T K M

**AseI (2501)** **SacI (2558)**  
2501 GATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGC

2601 CCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGAC  
SpeI (2656)  
←

2700 TTGGAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTG  
SnaBI (2784)

2800 CCAAGTAGAAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATAC  
NdeI (2889)

2900 ACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTA

3000 TTGACGTCAATGGGGGGGGTCTGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAA  
PstI (3068)  
SdaI (3067)  
PacI (3075)  
BspLU11I (3085)  
←

3098 AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG

3198 TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAAGTCCCTCGTGCCTCTCCTGTCCGACCCTGCCGTTACCGGA

3298 TACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCT

3398 GTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGC  
ApaLI (3399)

3498 AGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTT

3598 GGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTGTTT

3698 GCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGG

3798 GATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGGTTTTTTGTGTAATCGT  
PacI (3815)  
SwaI (3824)  
EagI (3835)  
NotI (3834)

3898 AACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGACAGGTGCCAGAACATTTCTCTATCG

3998 AA