



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
**MfeI (82)**  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGGCCCGCCGCCCTACCTGAGGCC  
**PvuII (239)**  
**Bsu36I (291)**  
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
**NaeI (441)** 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

**KasI (535)** 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCATCATGATGCCTAAGCATTGCCTTAGGTCTCCTCATCAT  
**AgeI (552)** 1▶ M M P K H C L L G L L I I  
**BspHI (560)**

601 ACTCTTGAGCAGTGAACAGAAATACAACCAGCTCGTGTATCTGACGCCCCAGAAGTCCGATTTTCAGTCCAGAAATTTCCACAATTTTGCAGTGG  
**SspI (685)**  
13▶ L L S S A T E I Q P A R V S L T P Q K V R F Q S R N F H N I L H W  
701 CAAGCAGGGAGCTCTCTCCAGCAACAACAGCATCTACTTTGTGAGTACAAGATGTATGGACAGAGCAATGGGAAGATAAAGTTGACTGTGGGGGA  
47▶ Q A G S S L P S N N S I Y F V Q Y K M Y G G Q S Q W E D K V D C W G  
801 CCACGGCCTCTGTGACCTGACCAATGAAACCTTAGACCCATACGAGCTGTATTACGGAGGGTGTGACGCCTGTGCTGGACCCACTCTGCCTG  
80▶ T T A L F C D L T N E T L D P Y E L Y Y G R V M T A C A G R H S A W

**NcoI (922)** 901 GACCAGGACACCCGCTTCACTCCATGGTGGGAAACAAAAGTATGATCCTCCGGTCTGACTATAACCCGAGTTAACGCATCTTTGCGGGTCTTCTCCGT  
**HpaI (970)**  
113▶ T R T P R F T P W W E T K L D P P V V T I T R V N A S L R V L L R

**NcoI (1043)**  
**Ppu10I (1037)**  
**NsiI (1037)** 1001 CCTCAGAGTTGCCAAATAGAAACCAAAGTGGAAAAATGCATCCATGGAAACTTACTACGGCTTAGTATACAGAGTTTCCACAATCAACAATCACTAG  
**Bst1107I (1066)**  
147▶ P P E L P N R N Q S G K N A S M E T Y Y G L V Y R V F T I N N S L  
1101 AGAAGGAGCAAAAAGCCTATGAAGGACTCAGAGAGCTGTTGAAATTGAAGGTCTGATACCTCATTCCAGCTACTGCGTAGTGGCTGAAATGTACCAGCC  
180▶ E K E Q K A Y E G T Q R A V E I E G L I P H S S Y C V V A E M Y Q P

**MscI (1282)**  
**NheI (1276)** 1201 CATGTTTGACAGAAGAAGCCCAAGAAGCAAGGAGAGATGTGTGCAGATTCCATGAACTGGTCTGAGGCGCTAAAACGCTAGCTGGCCAGACATGATAAGA  
213▶ M F D R R S P R S K E R C V Q I P •

1301 TACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAA

**HpaI (1414)** 1401 GCTGCAATAAACAAGTTAACAACAACAATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAA

**EcoRI (1510)**  
1501 ATGTGGTATGGAATTCTAAATAACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCAT  
1601 CAGGGCTGTTGCCAATGTGATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTAAGATATAGTATTTTCCAAGGTTTGAAGTCTCTTCA

**SspI (1749)** 1701 TTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTT  
**Swal (1763)**

**EcoO109I (1824)** 1801 TATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCA  
1901 AGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAA  
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

**BstXI (2053)** 2001 GCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACA  
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

**StuI (2188)** 2101 GCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGT  
80▶ 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 H  
2201 GGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCCGACATGGTGTCTTGTCTCTATAGAGCATGGTATCTTCTCAGTGGCGACCTC  
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

**BspHI (2338)**  
**BbsI (2334)** 2301 CACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCATGATGGCCCTCCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTA  
**XmnI (2330)** 14▶ V L E L D Q Q S I N F T K M  
2401 ATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATT

**AseI (2396)**

2501 TGCCTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGGA  
SpeI (2551) ←

2600 AATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAG  
SnaBI (2679)

2700 TAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCATTACCCTGATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTG  
NdeI (2784)

2800 ATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGAC

2900 GTCAATGGGGCGGGTCTGTTGGGCGGTGAGCCAGGCGGGCATTACCCTGTAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGC  
PstI (2963) SdaI (2962) PacI (2970) BspLU11I (2980) ←

2998 CAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGA

3098 GGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAAGTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCT

3198 GTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTG  
ApaLI (3294)

3298 CACGAACCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCA

3398 CTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT

3498 CTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCCGCTGGTAGCGGTGTTTTTTTGTGTTGCAAG

3598 CAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATT

3698 TGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTAATCGTAACTA  
PacI (3710) SmaI (3719) EagI (3730) NotI (3729)

3798 ACATACGCTCTCCATCAAAACAAAACGAAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGACGGTGCCAGAACATTTCTCTATCGAA