



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

**BstEII (555)** **AgeI (552)** **SfiI (576)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATTGGGCGTCCCACGGCCCTGGAGGCCGGCAGCTGGCG

1 M G V P T A L E A G S W R

**SapI (612)** **BamHI (604)** **AvrII (639)**  
601 CTGGGATCCCTGCTCTTCTGCTCTTCTGGTGGTCCCTAGTCCGGTGGCAGCCTTCAAGGTCGCCACGCCGATTCCCTGTATGTCTGTCCCAG

13 W G S L L F A L F L A A S L G P V A A F K V A T P Y S L Y V C P E

701 GGCAGAACGTCACCCTACCTGCAGGCTCTTGGCCCTGTGGACAAAGGGCAGCATGTGACCTTCTACAAGACGTGGTACCAGCTCGAGGGCGAGG

47 G Q N V T L T C R L L G P V D K G H D V T F Y K T W Y R S S R G E

801 TGCAGACCTGCTCAGAGCGCCGCCATCCGCAACCTCACGTTCCAGGACCTCACCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCAGCACCT

80 V Q T C S E R R P I R N L T F Q D L H L H H G G H Q A A N T S H D L

**FspI (959)**  
901 GGCTCAGCGCCACGGGCTGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTGGATAGCGGCCCTCTACTGCTGC

113 A Q R H G L E S A S D H H G N F S I T M R N L T L L D S G L Y C C

1001 CTGGTGGTGGAGATCAGGCACCACTCGGAGCACAGGTTCCATGGTGCATGGAGTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGG

147 L V V E I R H H H S E H R V H G A M E L Q V Q T G K D A P S N C V

1101 TGTACCCATCCTCCTCCAGGAGAGTAAAACATCACGGTGCAGCCCTGGTACGGGTGCATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCT

180 V Y P S S S Q E S E N I T A A A L A T G A C I V G I L C L P L I L L

1201 CCTGGTCTACAAGCAAAGGCAGGCAGCCTCAACCGCCGTGCCAGGAGCTGGTGCAGGATGGACAGCAACATTCAAGGGATTGAAAACCCCGCTTTGAA

213 L V Y K Q R Q A A S N R R A Q E L V R M D S N I Q G I E N P G F E

1301 GCCTACCACCTGCCAGGGGATACCGAGGCCAAAGTCAGGCACCCCTGTCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGCGGCATCTGCTTT

247 A S P P A Q G I P E A K V R H P L S Y V A Q R Q P S E S G R H L L

**BbsI (1441)** **Tth111I (1459)**  
1401 CGGAGCCACGACCCCTGTCTCCTCCAGGCCCGGAGAGCTTCTTCCATCCCTGGACCCTGCTCCTGACTCTCAAACCTTTGAGGTACATAGCC

280 S E P S T P L S P P G P G D V F F P S L D P V P D S P N F E V I •

**MscI (1512)** **NheI (1506)**  
1501 CAGCTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTG

**HpaI (1644)** **MfeI (1655)**  
1601 ATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAACAAATGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGA

**EcoRI (1740)**  
1701 GGTTTTTTAAAGCAAGTAAAACCTTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACTCCAAATCAAGCCTCTACTGATCC

1801 TTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTAAGATATAGTG

**SapI (1922)** **SspI (1979)** **Swal (1993)**  
1901 TATTTTCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAA

2001 TACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAAC

2101 AAAGAACCTTTAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGAC

141 • N R T Y K L P I L E E I T T K V

**SacI (2254)**  
2201 CAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTG

124 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 P S V V R I S R

2301 TCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGA

90 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 G I A I A E A C V

**StuI (2418)**  
2401 CAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGCTCCTACA

57 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 V H H K N D E Y

BbsI (2564)  
**XmnI (2560)**

2501 GAGCATGGTGATCTTCTCAGTGGCGACCTCCACGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTA  
24 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 (2626) SacI (2683)

2601 TACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAG  
←

SpeI (2781)

2701 ACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTGATTTACTAGICAAAACAACTCC  
←

2801 CATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGC  
←

SnaBI (2909)

2901 GATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATA  
←

NdeI (3014)

3001 GGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCG  
←

SdaI (3192)

3101 TTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGG  
←

PacI (3200) BspLU11I (3210)

3201 TTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGC  
←

3301 ATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGT  
←

3401 TCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAG  
←

ApaLI (3524)

3501 GTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGAC  
←

3601 ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGG  
←

3701 CTACACTAGAAGAAGCAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTATCGGCAAAACAAACCCGCT  
←

3801 GGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGT  
←

EagI (3960)

PacI (3940) SmaI (3949) NotI (3959)

3901 GGAACGAAAACCTACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGT  
←

4001 GTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGAAGTGCAG  
4101 GTGCCAGAACATTTCTCTATCGAA