



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

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGGCC **Bsu36I (291)**

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

**NgoMIV (441)**

**NcoI (560)**  
**BstEII (555)**  
**KasI (535)** 501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCACCATGGCTTTAGAGATCCACATGTCAGACCCCATGTGCCT **AgeI (552)** **BspLU11I (578)**

601 CATCGAGAACTTTAATGAGCAGCTGAAGGTTAATCAGGAAGCTTTGGAGATCCTGTCTGCCATTACGCAACCTGTAGTTGTGGTAGCGATTGTGGCCTC **1 M A L E I H M S D P M C L**

13 I E N F N E Q L K V N Q E A L E I L S A I T Q P V V V A I V G L

701 TATCGCACTGGCAATCCTACCTGATGAACAAGCTGGCTGGGAAGAACAAGGGCTTCTCTGTTGCATCTACGGTGCAGTCTCACACCAAGGGAATTTGGA **47 Y R T G K S Y L M N K L A G K N K G F S V A S T V Q S H T K G I W**

801 TATGGTGTGTGCCTCATCCCACTGGCCAAATCACACATTAGTTCTGCTTGCACCCGAGGGCCTGGGAGATGTAGAGAAGGCTGACAACAAGAATGATAT **80 I W C V P H P N W P N H T L V L L D T E G L G D V E K A D N K N D I**

**BglII (902)** 901 CCAGATCTTTGCACTGGCACTCTTACTGAGCAGCACCTTTGTGTACAATACTGTGAACAAAATTGATCAGGGTGCATCGACCTACTGCACAATGTGACA **BsrGI (941)** **DraIII (988)**

113 Q I F A L A L L L S S T F V Y N T V N K I D Q G A I D L L H N V T

1001 GAACTGACAGATCTGCTCAAGGCAAGAACTCACCCGACCTTGACAGGGTTGAAGATCCTGCTGACTCTGCGAGCTTCTCCAGACTTAGTGTGGACTC **BglII (1008)** **XcmI (1081)**

147 E L T D L L K A R N S P D L D R V E D P A D S A S F F P D L V W T

1101 TGAGAGATTTCTGCTTAGGCCTGGAAATAGATGGCAACTTGTACACCAGATGAATACCTGGAGAATTCCTAAGGCCAAAGCAAGGTAGTGATCAAAG **StuI (1116)** **Bsu36I (1170)**

180 L R D F C L G L E I D G Q L V T P D E Y L E N S L R P K Q G S D Q R

**Bst1107I (1229)** 1201 AGTTCAAAATTTCAATTTGCCCGTCTGTGTATACAGAAGTTCTTTCAAAAAAGAAATGCTTTATCTTTGACTTACCTGCTCACAAAAAAGCTTGGC **213 V Q N F N L P R L C I Q K F F P K K K C F I F D L P A H Q K K L A**

1301 CAACTTGAACACTGCCTGATGATGAGCTAGAGCCTGAATTTGTCAACAAGTACAGAATTCCTGTTCTACATCTTTAGCCATTCTATGACCAAGACTC **247 Q L E T L P D D E L E P E F V Q Q V T E F C S Y I F S H S M T K T**

**PshAI (1449)** 1401 TTCCAGGTGGCATCATGGTCAATGGATCTCGTCTAAAGAACCTGGTGTGACCTATGTCAATGCCATCAGCAGTGGGGATCTGCCTTGATAGAGAATGC **280 L P G G I M V N G S R L K N L V L T Y V N A I S S G D L P C I E N A**

1501 AGTCTGGCCTTGCTCAGAGAGAGAACTCAGCTGCAGTGCAAAAGGCCATTGCCACTATGACCAGCAAATGGGCCAGAAAGTGCAGCTGCCATGGAA **NcoI (1592)**

313 V L A L A Q R E N S A A V Q K A I A H Y D Q Q M G Q K V Q L P M E

**BspHI (1658)** 1601 ACCCTCCAGGAGCTGCTGGACCTGCACAGGACCAGTGAGAGGGAGGCCATTGAAGTCTTCATGAAAACTCTTTCAAGGATGTAGACCAAAGTTTCCAGA **BbsI (1654)**

347 T L Q E L L D L H R T S E R E A I E V F M K N S F K D V D Q S F Q

1701 AAGAAATTGGAGACTCTACTAGATGCAAAACAGAATGACATTTGTAACAGGAACCTGGAAGCATCTCGGATTATTGCTCGGCTTTACTTAAGGATATTT **380 K E L E T L L D A K Q N D I C K R N L E A S S D Y C S A L L K D I F**

**XbaI (1806)** 1801 TGGTCTCTAGAAGAAGCAGTGAAGCAGGGAATTTATTCTAAGCCAGGAGGCCATAATCTCTTATTGAGAAAACAGAAAGTGAAGGCAAAAGTACTAT **ScaI (1892)**

413 G P L E E A V K Q G I Y S K P G G H N L F I Q K T E E L K A K Y Y

1901 CGGAGCCTCGAAAAGGAATACAGGCTGAAGAAGTTCTGCAGAAATTTAAAGTCCAAGGAGTCTGTGAGTCATGCAATATTACAGACTGACCAGGCTC **447 R E P R K G I Q A E E V L Q K Y L K S K E S V S H A I L Q T D Q A**

2001 TCACAGAGACGAAAAAAGAAGAAAGAGGCACAAAGTGAAGCAGAAAGCTGAAAAGGCTGAAGCGCAAAGGTTGGCGCGATTCAAAGGCAGAACGAGCA **BstAPI (2097)**

480 L T E T E K K K K E A Q V K A E A E K A E A Q R L A A I Q R Q N E Q

2101 AATGATGCAGGAGAGGGAGAGACTCCATCAGGAACAAGTGAGACAAATGGAGATAGCCAAACAAAATTGGCTGGCAGAGCAACAGAAAATGCAGGAACAA **513 M M Q E R E R L H Q E Q V R Q M E I A K Q N W L A E Q Q K M Q E Q**

2201 CAGATGCAGGAACAGGCTGCACAGCTCAGCACAACATCCAAGCTCAAAATAGAAGCCTTCTCAGTGCAGCTCCAGCACGCCAGAGACTGTTAAATACG **547 Q M Q E Q A A Q L S T T F Q A Q N R S L L S E L Q H A Q R T V N N**

**MscI (2356)** 2301 ATGATCCATGTGTTTACTCTAAAGTGCTAAATATGGAGTTTCTTTTTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCAC **NheI (2350)**

580 D D P C V L L •

2401 AACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAAC **HpaI (2488)** **MfeI (2499)**

2501 AATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGGTATGGAATTCTAAAAATACAG

2601 CATAGCAAACTTTAACCTCAAATCAAGCCTCTACTGAACTCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAG

2701 **SapI (2766)**  
 CTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGAC

2801 **Swal (2837)** **EcoO109I**  
 CCCCCACATTCCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAG

2901 **GCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTC**  
 141 • N

3001 **CTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGA**  
 138 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 C D P A Y D S I L

3101 **BstXI (3127)**  
 GCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTG  
 105 E R C M G C 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

3201 **StuI (3262)**  
 CCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTC  
 72 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 V A S I I E G T

3301 **TTGGTCTGATGGCCGCCGACATGGTGTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCTGTGAGAGA**  
 38 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 V L E L D Q Q S I

3401 **BbsI (3408)** **AseI (3470)**  
 TGTGAAGTCTTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTC  
 5 N F T K M

3501 **TCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACG**

3601 **SpeI (3625)**  
 ACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCA

3701 **SnaBI (3753)**  
 CGCCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATCGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGACT

3801 **NdeI (3858)**  
 GGCATAATGCCAGGCGGGCATTACCCTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCG

3901 **TAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTTGGCGGT**

4001 **SdaI (4036)** **PacI (4044)** **BspLU11I (4054)**  
 CAGCCAGGCGGGCATTACCCTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGC

4101 **CGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGA**

4201 **TACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGG**

4301 **ApaLI (4368)**  
 CGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTG

4401 **CGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT**

4501 **GTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG**

4601 **GAAAAAGAGTTGGTAGCTTGTATCCGGCAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATC**

4701 **PacI (4784)** **Swal (4793)**  
 TCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTTCATGGCTAGTTAATTAACATTTAAA

4801 **EagI (4804)**  
**NotI (4803)**  
 TCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAA

4901 **ACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA**