



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA **EcoNI (96)**

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **HindIII (245)** **Bsu36I (291)**  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC **EcoNI (287)**

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

**KasI (535)** **AgeI (552)** **BspHI (560)**  
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCATCATGAAATCACTCTCATATAGAGAATCTGGATGAAGA **XcmI (676)**  
13 M K Y H S H I E N L D E D

601 TGGATATACTCAATTAGACTTCAGCACTCAAGACATCCATAAAAGGCCAGGGGATCAGAGAAAGGAAGCCGGCTCCATCTTCACCTTGAGAGCCATT  
13 G Y T Q L D F S T Q D I H K R P R G S E K G S R A P S S P W R P I

**PstI (743)**  
701 GCAGTGGGTTTAGGAATCCTGTGCTTTGTGGTAGTAGTGGTTCGTCAGTGTAGGTGCCCTAGCATTGGAACACAAATTCAGGGAGAAATCCAGAA G  
47 A V G L G I L C F V V V V A A V L G A L A F W R H N S G R N P E  
801 AGAAAGACAATTCATCAAGAAATAAGAGACACCAAGCCACAGAATCATCTTTAGATGAGAAGGTGGCTCCCAAGGCATCCCAAACTACAGG  
80 E K D N F P S R N K E N H K P T E S S L D E K V A P S K A S Q T T G

**Ppu10I (934)** **NsiI (934)**  
901 AGGTTTTTCTCAGCCTTGCCTTCCAAATTGGACCATGCATGGGAAGAGCTGTACCTATTTAGCTTCTCAGGAAATTCCTGGTATGGAAGTAAGAGACAC  
113 G F S Q P C L P N W T M H G K S C Y L F S F S G N S W Y G S K R H  
1001 TGCTCCAGCTAGGTGCTCATCTACTGAAGATAGACAACCTCAAAGAATTTGAGTTCATTGAAAGCCAAACATCATCTCACCATATTACTGCATTTTGG A  
147 C S Q L G A H L L K I D N S K E F E F I E S Q T S S H H I T A F W

**StuI (1101)** **NcoI (1129)**  
1101 TAGGCCTTTCCCGCAATCAGAGTGAAGGGCCATGGTTCGGGAGGATGGATCAGCATTCTTCCCAACTCGTTTCAAGTCAGAAATACAGCTCCCCAGGA  
180 I G L S R N Q S E G P W F W E D G S A F F P N S F Q V R N T A P Q E

**HindIII (1200)** **NheI (1297)**  
1201 AAGCTTACTGCACAATTGTGATGGATTGATGATCAGAGGTCTACAACCAATCTGCAATACTTCTTCATACAGTATCTGTGAGAAGGAACTGTAAGCT  
213 S L L H N C V W I H G S E V Y N Q I C N T S S Y S I C E K E L •

**MscI (1303)**  
1301 AGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTG

**HpaI (1435)**  
1401 CTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAAACAACAATTGCATTATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTTA

**EcoRI (1531)**  
1501 AAGCAAGTAAACCTCTACAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAG  
1601 GGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTATTTC

**SspI (1770)** **SwaI (1784)**  
1701 AAGGTTTGAAGTACTGCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATT

**EcoO109I (1845)**  
1801 GCAATGAAAATAAATGTTTTTATTAGCGAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACC  
1901 TTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCC  
1414 • N R T Y K L P I L E E I T T K V L K G

**SacI (2045)**  
2001 ATTCATCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCA  
121 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 D V E  
2101 TCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCAGCAGACCCAATGGCAATGGCTTCAGCAGACAGCAGTGCACC  
87 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 T V R

**StuI (2209)**  
2201 TGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGTCTCATAGAGCATGGT  
54 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 L M T

**BbsI (2355)** **XmnI (2351)**  
2301 GATCTTCTCAGTGGGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCC  
21 I K E T A V E V L E L D Q Q S I N F T K M

**AseI (2417)** **SacI (2474)**  
2401 GATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCAC

2501 CGTACACGCCTACGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAAAACAAACTCCCATTGACGT  
2601 CAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAA  
**SnaBI (2700)**  
2701 TACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCACTGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTA  
**NdeI (2805)**  
2801 CTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGG  
**PacI (2991)**  
**PstI (2984)**  
**SdaI (2983)**  
2901 GAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAG  
**BspLU11I (3001)**  
3001 AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAA  
3101 ATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCT  
3201 GCGGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCG  
**ApaLI (3315)**  
3301 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTAT  
3401 CGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG  
3501 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGT  
3601 GGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAA  
**EagI (3751)**  
**PacI (3731)** **SwaI (3740)** **NotI (3750)**  
3701 ACTCACGTTAAGGGATTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTT  
3801 TTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAA  
3901 CATTCTCTATCGAA