



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

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTATGCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTCGCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

**AgeI (552)** **BspHI (568)** **BssHII (589)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTAGGAGGGCCATCATGAACAAGTTGCTGTGCTGCGCGCTCGT  
1 M N K L L C C A L V

**Psp1406I (635)** **XmnI (633)**  
601 TTTCTGGACATCTCCATTAAGTGGACCACCCAGGAAACGTTTCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAAT  
11 F L D I S I K W T T Q E T F P P K Y L H Y D E E T S H Q L L C D K

**Acc65I (708)** **BsrGI (729)**  
701 GTCCTCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGAAGACCGTGTGCGCCCTTGCCTGACCACTACTACACAGACAGCTGGCACACCAG  
44 C P P G T Y L K Q H C T A K W K T V C A P C P D H Y Y T D S W H T S  
801 TGACGAGTGTCTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGGAGTGAATCGCACCCACAACCCGCTGTGCGAATGCAAGGAAGGG  
77 D E C L Y C S P V C K E L Q Y V K Q E C N R T H N R V C E K E G  
901 CGTACCTTGAGATAGAGTTCTGCTTGAACATAGGAGCTGCCCTCCTGGATTGGAGTGGTCAAGCTGGAACCCAGAGCGAAATACAGTTTGCAAAA  
111 R Y L E I E F C L K H R S C P P G F G V V Q A G T P E R N T V C K  
1001 GATGTCCAGATGGGTTCTTCTCAAATGAGACGTCTAAAGCACCTGTAGAAAACACACAAATTGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGG  
144 R C P D G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G

**BspEI (1125)**  
1101 AAATGCAACACACGACAACATATGTTCCGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGTGAGGAGGCATTCTCAGGTTTGTCT  
177 N A T H D N I C S G N S E S T Q K C G I D V T L C E E A F F R F A  
1201 GTTCTACAAAATTCAGCCTAACTGGCTTAGTGTCTTGGTAGACAATTTGCCTGGCACAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAAC  
211 V P T K F T P N W L S V L V D N L P G T K V N A E S V E R I K R Q  
1301 ACAGCTCACAAAGAACAGACTTTCCAGCTGCTGAAGTTATGAAACATCAAAAACAAAGACCAAGATATAGTCAAGAAGATCATCAAGATATTGACCTCTG  
244 H S S Q E Q T F Q L L K L W K H Q N K D Q D I V K K I I Q D I D L C

**HindIII (1469)**  
1401 TGA AACACAGCGTGACGCGCACATTGGACATGCTAACCTCACCTTCGAGCAGCTTCGTAGCTTATGGAAGCTTACCGGAAAGTGGAGCAGAA  
277 E N S V Q R H I G H A N L T F E Q L R S L M E S L P G K K V G A E

**SphI (1521)** **EcoO109I (1597)**  
1501 GACATTGAAAAACAATAAAGGCATGCAAAACCCAGTGACCAGATCCTGAAGCTGCTCAGTTTGTGGCAATAAAAAATGGCGACCAAGACACCTTGAAGG  
311 D I E K T I K A C K P S D Q I L K L L S L W R I K N G D Q D T L K

**BsrGI (1699)**  
1601 GCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACCTTCCAAAACGTCACTCAGAGTCTAAAGAAGACCATCAGGTTCCCTTACAGCTTCACAAT  
344 G L M H A L K H S K T Y H F P K T V T Q S L K K T I R F L H S F T M

**BstEII (1737)** **MscI (1783)**  
1701 GTACAAAATGTATCAGAAGTTATTTTAGAAAATGATAGTAAACAGGTCAAATCAGTAAAAATAAGCTGTTATAACTGGAAATGGCCATTGAGCTGTTT  
377 Y K L Y Q K L F L E M I G N Q V Q S V K I S C L •

**MscI (1845)**  
1801 CCTACAATTGGCGAGATCCCATGGATGAGTAACTGTTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGC

**HpaI (1977)**  
1901 AGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCA

**EcoRI (2073)**  
2001 TTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAAC  
2101 TTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGC

**SapI (2255)**  
2201 CTCACCTTCTTTCATGGAGTTTAAAGATAGTGTATTTTCCAAAGTTTGAAGTACTCTTCTTTATGTTTTAAATGCACTGACCTCCACATTC

**SspI (2312)** **SwaI (2326)** **EcoO109I (2387)**  
2301 CCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAA  
2401 TATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTT  
141 • N R T Y K

**SacI (2587)**  
2501 GAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCGCAC  
135 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 E R C

2601 **BstXI (2616)**  
101 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 G N S V

2701 **StuI (2751)**  
68 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 K T R I

2801 **XmnI (2893)**  
35 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 N F T

2901 **AseI (2959)**  
1 K M

3001 **SacI (3016)**  
TGACGGTTACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTGGAA

3101 **SpeI (3114)**  
AGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGAT

3201 **SnaBI (3242)**  
GTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAAGGTCATGTA CTGGGCATAATGC

3301 **NdeI (3347)**  
CAGGCGGGCATTACCCTGTCATTGACGTCAATAGGGGGCTACTTGCCATATGATACACTTGATGTA CTGCCAAGTGGGCAGTTTACCCTAAATACTCCA

3401 **PacI (3533)**  
3501 **SdaI (3525)** **BspLU11I (3543)**  
GCCATTTACCCTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGCTGG  
3601 CGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGCTT  
3701 TCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGCGCTTTCTCAT

3801 **ApaLI (3857)**  
AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCCTTATCCG

3901 GTA ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCACTGGCAGCAGCCACTGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGC

4001 TACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTT

4101 GGTAGCTCTTGATCCGGCAAACAAACCCGCTGGTAGCGGTGGTTTTTTTGGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATC

4201 **EagI (4293)**  
CTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGC  
**PacI (4273)** **SwaI (4282)** **NotI (4292)**

4301 AATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAAAC  
4401 TAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA