



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

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGGTTCGCGCCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

**BstEII (555)**  
**AgeI (552)** **NcoI (560)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCGTCGTTACGGTGAAGGCCTATCTTCTGGGCAA

1 M A S F T V K A Y L L G K

**EagI (674)**  
**SacII (671)** **XmaI (681)**  
601 GGAGGAGCGACCCGCGAGATCCGCCGTTTCTGCTTACAGCCGGAGCGGAGCGGAAGCCCAAGCCGCGCCGGCCGGGGCCCTGCGAGAGG

13 E E A T R E I R R F S F C F S P E P E A E A Q A A A G P G P C E R

701 CTGCTGAGCCGAGTGGCTGTGCTGTTCCCCACGCTGAGGCCTGGCGGCTTCCAGGCGCACTACCGCGATGAGGATGGGACTTGGTTGCCTTTTCCAGTG

47 L L S R V A V L F P T L R P G G F Q A H Y R D E D G D L V A F S S

**DraIII (893)**  
801 ATGAGGAGCTGACAATGGCTATGTCCTATGTGAAAGATGACATCTTCCGCATCTACATTAAGAGAAGAAGGAGTGGCGGCGGAACATCGCCACCATG

80 D E E L T M A M S Y V K D D I F R I Y I K E K K E C R R E H R P P C

**ApaI (925)**  
901 TGCTCAGGAGGCACCCCGAAACATGGTGACCCCAATGTGATCTGTGATGGTTGCAACGGGCCTGTGGTGGGAACTGCTATAAGTGCAGTGTGTGCCCA

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

**MscI (1077)**  
1001 GACTACGACCTGTGACGCGTGTGCGAGGGGAAGGGCCTGCACAGGGAACAGCAAGCTCATCTTTCCCAACCCCTTTGGCCACTCTCTGATAGCTTCT

147 D Y D L C S V C E G K G L H R E H S K L I F P N P F G H L S D S F

**XcmI (1165)**  
1101 CTCATAGCCGCTGGCTTCGGAAGCTGAAACATGGACACTTTGGCTGGCTGGCTGGGAGATGGGCCACCGGGAACTGGAGCCACGTCCTCCTCGTGC

180 S H S R W L R K L K H G H F G W P G W E M G P P G N W S P R P P R A

1201 AGGGGATGGCCGCTTCCCTACAGCTGAGTCAGTCTGCCACCAGAAGATCCCAATGTCAATTTCTGAAGAATGTGGGGGAGAGTGTGGCAGCT

213 G D G R P C P T A E S A S A P P E D P N V N F L K N V G E S V A A

1301 GCCCTCAGCCCTTAGGCATTGAGGTTGACATTGATGTGAAACATGGAGGGAAGAGAAGCCGCTGACACCCACTACCCAGAAAGTTCCAGCACAGGCA

247 A L S P L G I E V D I D V E H G G K R S R L T P T T P E S S S T G

**SapI (1433)**  
1401 CAGAAGACAAGAGTAACACTCAGCCAAGCAGCTGCTTTCGGAAGTCAGCAAACCTGACGGGGCTGGGAGGGCCCTGCTCAGTCTCTGACAGAGCAAT

280 T E D K S N T Q P S S C S S E V S K P D G A G E G P A Q S L T E Q M

1501 GAAAAAGATAGCCTTGGAGTCGGTGGGACAGCCAGAGGAACAGATGGAGTCGGGAACTGCTCAGGAGGAGACGATGACTGGACACATTTGTCTTCAAAA

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

**XbaI (1665)**  
1601 GAAGTGGACCCATCTACAGTGAAGTCCAGTCTCTACAGATGCCAGAATCGGAAGGGCAAGCTCTAGACCCCTCACAGGAAGGACCCACAGGGCTGA

347 E V D P S T G E L Q S L Q M P E S E G P S S L D P S Q E G P T G L

**NcoI (1775)**  
1701 AGGAAGCTGCCCTATACCCACATCTCCACCAGAGGCTGATCCCCGGCTGATTGAGTCCCTCTCCAGATGCTGTCCATGGGTTTCTCGGATGAAGGCGG

380 K E A A L Y P H L P P E A D P R L I E S L S Q M L S M G F S D E G

**BstBI (1866)** **NheI (1895)**  
1801 CTGGCTCACCAGGCTCTACAGACCAAGAATTACGACATCGGGGCTGCTGGACACGATCCAGTATTGAAAGCACCTCCACCATTGTGATAGTGTAG

413 W L T R L L Q T K N Y D I G A A L D T I Q Y S K H P P P L •

**MscI (1901)**  
1901 CTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCT

**HpaI (2033)** **MfeI (2044)**  
2001 TTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAACAATTGCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTTAAA

**EcoRI (2129)**  
2101 GCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGG

2201 ATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTGACGCTCACCTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAA

**SapI (2311)** **SspI (2368)** **SwaI (2382)**  
2301 GGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAATAATTTAAATACATCATTGC

2401 AATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTT

2501 TAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGC TTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCAT  
 141 • N R T Y K L P I L E E I T T K V L K G N  
 SacI (2643) BstXI (2672)  
 2601 TCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATC  
 120 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 D  
 2701 AGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCCTG  
 87 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  
 2801 CCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGA  
 53 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 I  
 XmnI (2949)  
 2901 TCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGA  
 20 K E T A V E V L E L D Q Q S I N F T K M  
 AseI (3015) SacI (3072)  
 3001 TATACTATGCCGATGATTAATTGTCAA AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCG  
 SpeI (3170)  
 3101 TACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCA  
 SnaBI (3298)  
 3201 ATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATA  
 3301 CGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACT  
 NdeI (3403)  
 3401 TGGCATATGATACTTGTACTGCTCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGA  
 PacI (3589)  
 3501 ACATACGTCAATTATTGACGTCAATGGGCGGGGTCTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACCGCTGCAGGTTAATTAAGAA  
 PstI (3582) SdaI (3581) BspLUIII (3599)  
 3601 CATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAAT  
 3701 CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCGTGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGC  
 3801 CGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTC  
 ApaLI (3913)  
 3901 CAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCG  
 4001 CCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAA  
 4101 GAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAACAACACCGCTGGTAGCGGTGG  
 4201 TTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGAAAA  
 EagI (4349)  
 4301 TCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGTTTTT  
 PacI (4329) SmaI (4338) NotI (4348)  
 4401 GTGTGAATCGTAACTAACATACGCTCTCCATCAAACAACGAAACAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACA  
 4501 TTTCTCTATCGAA