



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

101 GAGAAGGTGGCGCGGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTTT

**BstEII (555)** **AgeI (552)** **NcoI (560)** **BglIII (584)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATGGGAGCTCCGGCGCTGCCCGAGATCTGGCAGCTGTA

13> M G A P A L P Q I W Q L Y

**FspI (658)**  
601 CCTCAAGAACTACCGCATCGCCACCTTCAAGAACTGGCCCTTCTGGAGGACTGCGCTGCGCACCAGAGCGAATGGCGGAGGCTGGCTTCATCCACTGC

13> L K N Y R I A T F K N W P F L E D C A C A P E R M A E A G F I H C

701 CCTACCGAGAACGAGCCTGATTTGGCCAGTGTTCCTGCTTAAAGGAATTGGAAGGCTGGGAACCGATGACAACCCGATAGAGGAGCATAGAAAAGC

47> P T E N E P D L A Q C F F C F K E L E G W E P D D N P I E E H R K

**EcoRI (859)**  
801 ACTCCCCTGGCTGCGCCTTCTCACTGTCAAGAAGCAGATGGAAGAACTAACCGTCAGTGAATTCTTGAAACTGGACAGACAGAGAGCAAGAACAAAAT

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

901 TGCAAAGGAGACCAACAAGCAAAAAGAGTTTGAAGAGACTGCAAAGACTACCCGTCAGTCAATTGAGCAGCTGGCTGCCTAATGCTGAGCCTTTGCT

113> A K E T N N K Q K E F E E T A K T T R Q S I E Q L A A •

**MscI (1039)** **NheI (1033)**  
1001 GAGATAACTTGGACCTGAGTGACATGCCACATCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAA

**HpaI (1171)**  
1101 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACATTGCATTCATTTTAT

**EcoRI (1267)**  
1201 GTTTCAGGTTTCCGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATAACAGCATAGCAAACTTTAAC

1301 CTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACC

**SapI (1449)**  
1401 TTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTT

**SspI (1506)** **SwaI (1520)** **EcoO109I (1581)**  
1501 TAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCC

1601 CCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGG

141> • N R T Y K L P

1701 GATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCA

133> 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 M G

**BstXI (1810)**  
1801 CAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAG

99> 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 A S

**StuI (1945)**  
1901 ACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGC

66> 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 A A

**BbsI (2091)** **XmnI (2087)**  
2001 CCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCATG

33> 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 K M

**AseI (2153)**  
2101 GTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGG

2201 TTCACTAAACGAGCTCTGCTTATATAGACTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCC

**SpeI (2308)**  
2301 GTTGATTTACTAGTCAAAAACAACTCCCAATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCAATTGATGACTG

**SnaBI (2436)**

2401 CAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCATGTACTGGCATAATGCCAGGCG

**NdeI (2541)**

2501 GGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATT

2601 GACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTGGGGCGGTGAGCCAGGCGGGCCATT

**PacI (2727)**

**PstI (2720)**

**SdaI (2719)**

**BspLU11I (2737)**

2701 TACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTT

2801 TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTCCCCC

2901 TGGAAAGCTCCCTCGTGCCTCTCCTGTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCA

**ApaLI (3051)**

3001 CGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCAGCCGCTGCGCTTATCCGGTAACT

3101 ATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGA

3201 GTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC

3301 TCTTGATCCGGCAAACAACCCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGGCAGAAAAAAGGATCTCAAGAAGATCCTTTGA

**EagI (3487)**

**PacI (3467) SmaI (3476) NotI (3486)**

3401 TCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAA

3501 ATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAA

3601 AATAGGCTGTCCCAGTCAAGTGCAGGTGCCAGAATTTCTCTATCGAA