



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

101 GAGAAAGTGGCGGGGTAACGGAAAGTGTGTCGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGTCAAGTGCAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

**BspHI (560)**  
**AgeI (552)**  
501 TCTGTTTGTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTATCATGAACCGAAGCATTCCCGTGGAGTTGATGAATCAGA

601 ACCATTCCCGAGTCAATTGCTGAAACCGATCCCAGAATACTCTCCAGAAGAGGAATTGGAACCACTGCCCAATACAAGAACATGGCACCCAGCAGC

13> P F P S Q L L K P I P E Y S P E E E L E P P A P N T R N M A P S S

**BstEII (759)**  
701 TTGTCTGTCTCCAGTGCCTCCCTGAAACTGGCAAACCACAGCCTGTGTCAACAACAGGTACCTGCGAGCTAAAGTCTGGAGGAAGTGAAG

47> L S V L Q C P P L K L A N H Q P V S Q Q V T C L R A K V L E E G E

801 CCAGTTTCTTTAGAAGGCACCTGAACTTGCCAAAGATATTTCTCATGTTCTCTGGAGCCAGCGAGCTGAGTCTGAGCTCGGAGCCCTCCCTCCAGA

80> A S F F R R H P E L G K D I S S C S S G A S E P E S E L G A L P P E

901 GCATCGGTTACACTTACGAAAAACGAATAGATGGCTGGGATCTCAGCTTTGACGAGTCTCTGACTGGCCATGAATCAGACAAATCAGACCCA

113> H R F T L T E K R N R W L G S Q L S A A S P D T G H E S D K S D P

**Bsp120I (1072)**  
1001 AGTTTACCTAATGCTTTGGCAGACTCCTCAGTGGTGGCAAGAGATGATGCCCGGGCCCGGCCCGCTGGGCCACAGGCACAGGGCAGCCCCAG

147> S L P N A L A D S F S G G Q E M M P R P R P R P G P H R H R A A P

**SdaI (1197)**  
1101 ATGTGCCACGATAGACACTGGCTATGATTTCCAGCCCCAAGATGTCTGGGCATCAGGCAGTTGGAGAGGCCATTGCCCTCACCTCCTCGTGTACCT

180> D V P T I D T G Y D S Q P Q D V L G I R Q L E R P L P L T S S C Y L

1201 GCAGGACCTCCCTGGGCCTGAGGTCCAGGAATTGCCACCTCAGTTTGAAGTGGAGGATCCAATGAACGCCAGCTGCTGCCGCCCATCCTTCC

213> Q D L P G P L R S R E L P P Q F E L E R Y P M N A Q L L P P H P S

**Scal (1322)** **Bsp120I (1339)** **DraIII (1351)**  
1301 CCACAGGCCCCATGGAAGTGTGACTACTGCCCCGAGGGCCCTACCACCACAGGTGCCACAGGCCATGGCTACCTCCAGCAGCAGCCTACCAGC

247> P Q A P W N C Q Y Y C P G G P Y H H Q V P H G H G Y P P A A A Y Q

**Scal (1401)**  
1401 AAGTACTCCAGCCTGCTCTGCTGGCAGTCTCTCTGGGGCAAGGGCAAGAGGCCACGCCCTGTGAGAAGTGCATCCTGAATGACTCCAGCCCCA

280> Q V L Q P A L P G Q V L P G A R A R G P R P V Q K V I L N D S S P Q

**Bsu36I (1594)**  
1501 AGACCAAGAAGAGAGACCTGCACAGAGAGACTTCTTTCCCGAGGCTCCCGAGGGACCAGCTTACCGCCACCATCTAATGGAGTGGAAAGCCCTGAG

313> D Q E E R P A Q R D F S F P R L P R D Q L Y R P P S N G V E A P E

1601 GAGTCCTTGGACCTTCTGCAGAGCTGAGACCACATGGTCCCAAGGCTCCATCCCTAGCTGCCGTGCTAGACCCCTAGCAACCCCTTAGCCCGAGGAA

347> E S L D L P A E L R P H G P Q A P S L A A V P R P P S N P L A R G

**BstXI (1766)**  
1701 CTCTAAGAACCAGCAATTTGCCAGAAGAATTACGAAAGTCTTTATCACTTATTCTATGGACACAGCCATGGAGGTGGTGAATTTGTGAACCTTTCTGTT

380> T L R T S N L P E E L R K V F I T Y S M D T A M E V V K F V N F L L

**XmnI (1803)** **EcoRV (1855)** **Eco47III (1874)** **BsaBI**  
1801 GGTGAACGGCTTCCAAACTGCGATTGACATATTTGAGGATAGAATCCGGGGTATTGATATCATAAATGGATGGAGCGCTATCTTCGAGATAAGACAGTG

413> V N G F Q T A I D I F E D R I R G I D I I K W M E R Y L R D K T V

1901 ATGATAATCGTAGCAATCAGCCCCAAATACAAACAGGATGTGGAAGGCCTGAGTGCAGCTGGACGAGGACGAGCATGGCTTACATACTAAGTACATTC

447> M I I V A I S P K Y K Q D V E G A E S Q L D E D E H G L H T K Y I

**SapI (2061)**  
2001 ATCGGATGATGCAGATTGAGTTCATAAGTCAAGGAGCATGAAGTTCAGATTCATCCCTGTGCTTTCCAAATGCCAAGAAGGAGCATGTGCCGACCTG

480> H R M M Q I E F I S Q G S M N F R F I P V L F P N A K K E H V P T W

2101 GCTTCAGAACACTCATGTTTACAGCTGGCCCAAGAATAAGAAAAACATCCTGTGCGGCTGCTCAGGGAGGAAGATGTGGCTCCTCCCGAGGCCCT

513> L Q N T H V Y S W P K N K N I L L R L L R E E E Y V A P P R G P

**Acc65I (2217)** **NheI (2242)**  
2201 CTGCCACCTTTCAGGTGGTACCCTTGTGACGATGGCCACTCGCTAGTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAA

547> L P T L Q V V P L •

**HpaI (2380)**  
2301 TGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGTGAATAAACAAGTTAAACAACAATTGCAT

**EcoRI (2476)**  
2401 TCATTTTATGTTTCAGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAAATACAGCATAGCAA

2501 AACTTAAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGC

**SapI (2658)**  
2601 AGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTCTTTCATTTCTTTATGTTTTAAATGACTGACCTCCACA

2701 **SspI (2715)** **SwaI (2729)**  
 TTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCA

2801 TAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTGA  
 141 • N R T Y

2901 CTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTG  
 136 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 E R

3001 **BstXI (3019)**  
 CACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGC  
 102 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 G N S

3101 **StuI (3154)**  
 TCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCT  
 69 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 K T R

3201 **XmnI (3296)**  
 GATGGCCGCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAG  
 36 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 N F

3301 **BbsI (3300)** **AseI (3362)**  
 GTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTT  
 2 T K M

3401 ATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTTG

3501 **SpeI (3517)**  
 GAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATT

3601 **SnaBI (3645)**  
 GATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGTGTACTGCCAAGTAGGAAAGTCCATAAGGTCACTGACTGGGCATAA

3701 **NdeI (3750)**  
 TGCCAGGCGGGCCATTTACCGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGAGTTTACCGTAAATACT

3801 CCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGGCGTACGCCAGG

3901 **SdaI (3928)** **PaeI (3936)** **BspLU11I (3946)**  
 CGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGC

4001 TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGC

4101 GTTTCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCT

4201 **ApaLI (4260)**  
 CATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTAT

4301 CCGGTAACATATCGTCTTGTAGTCCAAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGG

4401 TGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGA

4501 GTTGGTAGCTCTTGTATCCGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAG

4601 **EagI (4696)** **NotI (4695)**  
 ATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGG

4701 **PaeI (4676)** **SwaI (4685)**  
 CGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACA

4801 AACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA