



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

**AgeI (552)** **SphI (568)**  
501 TCTGTTTGTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGTAGGAGGGCCAGCATGCCAATCACTCGAATGCGGATGAGACCC 1 M P I T R M R M R P

**AseI (615)** **XcmI (633)** **BsaBI (641)** **NcoI (678)**  
601 TGGCTAGAGATGCAGATTAATCCAACCAAATCCAGGGCTGATCTGGATCAATAAAGAAGAGATGATCTCCAGATCCATGGAAAGCAGCTGCTAAGC 11 W L E M Q I N S N Q I P G L I W I N K E E M I F Q I P W K H A A K

**BspEI (733)**  
701 ACGGCTGGGACATCAACAAGGATGCCTGTCTGTTCGGAGCTGGGCCATTACACAGGCCGATACAAAGCAGGAGAAAAGAGCCAGATCCCAAGACATG 44 H G W D I N K D A C L F R S W A I H T G R Y K A G E K E P D P K T W

801 GAAGGCAAATCCGTTGTGCCATGAACCTCCGACAGCTCAGGAAAGTGAAGGATCAGAGTAGGAACAAGGGCAGCTCTGCTGTGCGGGTGTACCGG 77 K A N F R C A M N S L P D I E E V K D Q S R N K G S S A V R V Y R

901 ATGCTGCCACCCCTACCCAGGAACAGAGGAAAGAGAGAAAGTCCAAGTCCAGCCGAGACACTAAGAGCAAAACCAAGAGGAAGCTGTGTGGAGATGTTA 111 M L P P L T R N Q R K E R K S K S S R D T K S K T K R K L C G D V

1001 GCCCGGACACTTTCTGATGGACTCAGCAGCTACCCCTACCTGATGACCACAGCAGTTACACCACTCAGGGCTACCTGGGTGAGGACTTGGATATGGA 144 S P D T F S D G L S S S T L P D D H S S Y T T Q G Y L G Q D L D M E

**DraIII (1123)** **NdeI (1158)**  
1101 AAGGGACATAACTCCAGCACTGTCCCGTGTGTCGTCAGCAGCAGTCTCTGAGTGGCATATGCAGATGGACATTATACCAGATAGCACCCTGATCTG 177 R D I T P A L S P C V V S S S L S E W H M Q M D I I P D S T T D L

1201 TATAACCTACAGGTGTCACCCATGCCTTCCACCTCCGAAGCCGCAACAGACGAGGATGAGGAAGGGAAGATAGCCGAAGACCTTATGAAGCTCTTTGAAC 211 Y N L Q V S P M P S T S E A A T D E D E E G K I A E D L M K L F E

**ClaI (1323)** **SandI (1356)** **EcoO109I (1356)** **PvuII (1388)**  
1301 AGTCTGAGTGGCAGCCGACACATCGATGGCAAGGGATACTTGTCTAATGAGCCAGGACCCAGCTCTCTTGTCTATGGAGACTCAGCTGCAAAGA 244 Q S E W Q P T H I D G K G Y L L N E P G T Q L S S V Y G D F S C K E

**XhoI (1420)** **BspLU11I (1448)** **XcmI (1480)**  
1401 GGAACAGAGATTGACAGCCCTCGAGGGGACATTGGGATAGGCATACAACATGTCTTACGGAGATGAAGAATATGGACTCCATCATGTGGATGGACAGC 277 E P E I D S P R G D I G I G I Q H V F T E M K N M D S I M W M D S

**ApaLI (1549)** **NheI (1565)** **MscI (1571)**  
1501 CTGCTGGGCAACTCTGTGAGGCTGCCGCCCTTATTACAGGCCATTCTTGTGACCATAGTTTGGGCTAGCTGGCCAGACATGATAAGATACATTGATGA 311 L L G N S V R L P P S I Q A I P C A P •

1601 GTTTGGACAAACCACAAC TAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAA

**HpaI (1703)** **MfeI (1714)** **EcoRI**  
1701 CAAGTTAAACAACAACAATTGCATTCAATTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGG 1801 AATTCTAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTT

**SapI (1981)**  
1901 GCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGT

**SspI (2038)** **SwaI (2052)**  
2001 TTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAATATTGAGAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGA

**EcoO109I (2113)**  
2101 ATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGC

2201 TTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTCCATTCTCAATGAGCACAAAGCAGTCAGGAG 111 N R T Y 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

**SacI (2313)** **BstXI (2342)**  
2301 CATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGT 110 Y D S I L E R 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

**StuI (2477)**  
2401 GTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAG 77 D F D K Q G N S 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

2501 ATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACAGCTCCA 43 I I E G T K T R 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

**XmnI (2619)** **AseI (2685)**  
2601 GATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTGCAAAAC 10 D Q Q S I N F T K M

2701 AGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACGTACACGCCTACCGCCATTTCGCTCAATGG

SacI (2742)

---

2801 GGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAG

SpeI (2840)

---

2901 TCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCC

SnaBI (2968)

---

3001 ATAAGTCATGTACTGGGCATAATGCCAGGCGGGCCATTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAA

NdeI (3073)

---

3101 GTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGG

---

PacI (3259)

PstI (3252)

SdaI (3251)

BspLU11I (3269)

3201 GGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATAAGAACTGTGAGCAAAGGCCAGCAAAGGCCAG

---

3301 GAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG

---

3401 ACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCC

---

ApaLI (3583)

3501 CTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGCT

---

3601 TCAGCCCAGCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT

---

3701 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGA

---

3801 AGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCG

---

PacI (3999)

3901 CAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGT

---

EagI (4019)

Swal (4008)    NotI (4018)

4001 TAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCA

4101 TCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA