



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

101 GAGAAAGTGGCGGGGTAACCTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

**NgoMIV (441)**

501 TCTGTTTGTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTGCCGAGCCATCTCTTAGGCGCTTGTGCTGCT MfeI (82)  
1 M C R A I S L R R L L L L

601 GCTGCTGCAGCTGCACAACCTAGTGTCACTCAAGGGAAGACGCTGGTGTGGGGAAGGAAAGGAAATCAGCAGAAGTCCCTGCGAGAGTCCAG AgeI (552)  
13 L L Q L S Q L L A V T Q G K T L V L G K E G E S A E L P C E S S Q

701 AAGAAGATCACAGTCTTACCTGGAAGTCTCTGACCAGAGGAAGATTCTGGGCGAGCATGGCAAAGGTGATTAATTAGAGGAGGTTGCGCTTCGAGT AseI (771)  
47 K K I T V F T W K F S D Q R K I L G Q H G K G V L I R G G S P S Q

801 TTGATCGTTTTGATCCAAAAAGGGGCATGGGAGAAAGGATCGTTTCTCTCATCATCAATAAACTTAAAGTGAAGACTCTCAGACTTATATCTGTGA  
80 F D R F D S K K G A W E K G S F P L I I N K L K M E D S Q T Y I C E

901 GCTGGAGAACAGGAAAGAGGAGGTGGAGTTGTGGGTGTTCAAAGTACCTCAGTCCGGGTACCAGCCTGTTGCAAGGGCAGAGCCTGACCCTGACCTTG Acc65I (958)  
113 L E N R K E E V E L W V F K V T F S P G T S L L Q G Q S L T L T L

1001 GATAGCAACTCTAAGTCTTAACCCCTTGACAGAGTGCAAACAAAAAGGTAAGTGTGCTAGTGGTTCAAAGTCTCTCCATGTCCAACCTAAGGG Bsu36I (1092)  
147 D S N S K V S N P L T E C K H K K G K V V S G S K V L S M S N L R

**XmnI (1149)**  
1101 TTCAGGACAGCGACTTCTGGAAGTGCACCGTGACCCTGGACCAGAAAAAGAACTGGTTTCGGCATGACACTCTCAGTGTGGGTTTTAGAGCAGACGCTAT  
180 V Q D S D F W N C T V T L D Q K K N W F G M T L S V L G F Q S T A I  
1201 CACGGCTATAAGAGTGGGAGAGTCAAGGAGTCTCTCCACTCAACTTTCAGAGGAAAGGGTGGGAGAGCTGATGTGGAAGGCAGAGAA G  
213 T A Y K S E G E S A E F S F P L N F A E E N G W G E L M W K A E K  
1301 GATTCTTTCTCCAGCCCTGGATCTCCTTCTCCATAAAGAACAAGAGGTGTCCGTACAAAAGTCCACCAAAGACCTCAAGCTCAGCTGAAGGAAACGC  
247 D S F F Q P W I S F S I K N K E V S V Q K S T K D L K L Q L K E T  
1401 TCCCACTACCCTCAAGATACCCAGGTCGCTTCAAGTGTGGTCTGGCAACCTGACTCTGACTCTGGCAAAGGGACACTGCATCAAGAAGTGAA  
280 L P L T L K I P Q V S L Q F A G S G N L T L T L D K G T L H Q E V N  
1501 CCTGGTGGTATGAAAGTGGCTCAGCTCAACAATACTTTGACCTGTGAGGTGATGGGACCTACCTCTCCCAAGATGAGACTGACCCTGAAGCAGGAGA  
313 L V V M K V A Q L N N T L T C E V M G P T S P K M R L T L K Q E N  
1601 CAGGAGGCCAGGCTCTGAGGAGCAGAAAGTAGTTCAAGTGGTGGCCCTGAGACAGGGCTGTGGCAGTGTCTACTGAGTGAAGGTGATAAGTCAAGA  
347 Q E A R V S E E Q K V V Q V V A P E T G L W Q C L L S E G D K V K

**BamHI (1709)**  
1701 TGGACTCCAGGATCCAGGTTTTATCCAGAGGGGTGAACAGACAGTGTCTGCTGGCTTGCCTGCTGGTGGCTCCTTCGGCTTTCTGGGTTTCTGGGCT  
380 M D S R I Q V L S R G V N Q T V F L A C V L G G S F G F L G F L G L

**BstAPI (1802)** **NgoMIV (1823)**  
1801 CTGCATCTCTGTGTGTCAGGTGCCGGCACCAACAGCGCCAGGCAGCAGCAATGTCTCAGATCAAGAGGCTCCTCAGTGAAGAAGACCTGCCAGTGC  
413 C I L C C V R C R H Q Q R Q A A R M S Q I K R L L S E K K T C Q C

**AvrII (1938)** **NheI (1966)**  
1901 CCCACCGGATGCAGAAGAGCCATAATCTCATCTGAGGCCACCTGACGCCACCCACCTGCTAGCTGGCCAGACATGATAAGATACATTGATG SapI (1914) StuI (1935) XcmI (1960) MscI (1972)  
447 P H R M Q K S H N L I •

2001 AGTTTGGACAACCACTAGAAATGCAAGTGAAGGCTTTATTTGTAAGTGTGATGCTATTGCTTTATTTGTAACCATTAAGCTGCAATAA

**HpaI (2104)** **MfeI (2115)**  
2101 ACAAGTTAAACAACAATTGCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATG

**EcoRI (2200)**  
2201 GAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGT

2301 TGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGGTTTGAAGTCTTCTTCTTTATG SapI (2382)

2401 TTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAAATATTGAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAG SspI (2439) Swal (2453)

2501 AATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAG

2601 CTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGA  
1+1 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  
SacI (2714) **BstXI (2743)**

2701 GCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGG  
110 A 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 (2878)

2801 TGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGA  
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

2901 GATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGTCTCATAGACATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCC  
44 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

XmnI (3020) AseI (3086)

3001 AGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAA  
10 L D Q Q S I N F T K M

SacI (3143)

3101 CAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCCATTTGCGTCAATG

SpeI (3241)

3201 GGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGA

SnaBI (3369)

3301 GTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCC

NdeI (3474)

3401 CATAAGGTCATGTACTGGGCATAATGCCAGGGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCA  
3501 AGTGGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCG

PacI (3660) SdaI (3652) BspLU11I (3670)

3601 GGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA  
3701 GGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCC  
3801 GACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTTCTC

ApaLI (3984)

3901 CCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCG  
4001 TTCAGCCCACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGAT  
4101 TAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTG  
4201 AAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGC  
4301 GCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAG

EagI (4420) NotI (4419)

PacI (4400) SwaI (4409)

4401 TTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCC  
4501 ATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCCAGGTGCCAGAACATTTCTCTATCGAA