



**PvuI (7)**  
**SgfI (6)** **EcoNI (96)**  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**Psp1406I (203)** **PvuII (239)** **EcoNI (287)**  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

**NgoMIV (441)**  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

**AgeI (552)** **BspHI (568)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTAGGAGGGCCATCATGAAAGGGTGTCTCTTATCTAATGTAC  
1 M K G C S S Y L M Y

**PshAI (610)** **PstI (680)**  
601 TCCTTTGGGGGACTTTTGTCCCTATGGATTCTTCTGGTGTCTCCACAAACCAATGCACTGTGAGATACAACGTAGTGTACTGCAGCCATTTGAAGCTAA  
11 S F G G L L S L W I L L V S S T N Q C T V R Y N V A D C S H L K L  
701 CACACATACTGATGATCTTCCCTCTAACATAACAGTGTGAATCTTACTCACAACCAACTCAGAAGATTACCACCTACCAACTTTACAAGATACAGCCA  
44 T H I P D D L P S N I T V L N L T H N Q L R R L P P T N F T R Y S Q

**XcmI (829)**  
801 ACTTGCTATCTTGGATGCAAGATTTAACTCCATTTCAAAAAGTGGAGCCAGAAGTGTGCCAAAATACTCCCTTTGTTGAAAGTATTGAACCTGCAACATAAT  
77 L A I L D A G F N S I S K L E P E L C Q I L P L L K V L N L Q H N  
901 GAGCTCTCAGATTTCTGATCAAACTTTGTCTTCTGACGAACTGACAGAAGTCTGATCTAATGTCTAACTCAATACACAAAATTAAGCAACCCCTT  
111 E L S Q I S D Q T F V F C T N L T E L D L M S N S I H K I K S N P  
1001 TCAAAAACAGAAGAATCTAATCAAATAGATTTGTCTCATAATGTTTATCATCTACAAAAGTGGGAACGGGGTCCAAGTGGAGAAGCTCCAAGAAGT  
144 F K N Q K N L I K L D L S H N G L S S T K L G T G V Q L E N L Q E L  
1101 GCTCTTAGCAAAAATAAAATCCTTGCCTTGCAGAGTGAAGAAGTGTGAGTTTCTTGGCAATCTCTTCTTACGAAAAGTGGACTTGTATCAAATCCACTT  
177 L L A K N K I L A L R S E E L E F L G N S S L R K L D L S S N P L

**XmaI (1211)** **BstXI (1223)**  
1201 AAAGAGTTCTCCCGGGGTGTTTCCAGACAATTGGCAAGTTATTCGCCCTCCTCTTGAACAACGCCCAACTGAACCCCACTCACAGAGAAGCTTTGCT  
211 K E F S P G C F Q T I G K L F A L L L N N A Q L N P H L T E K L C

**PvuII (1347)**  
1301 GGGAACTTCAAACACAAGCATCCAGAATCTCTCTGCTAACAACAGCTGCTGGCCACCAGCGAGAGCACTTTCTCTGGGCTGAAGTGGACAAATCT  
244 W E L S N T S I Q N L S L A N N Q L L A T S E S T F S G L K W T N L  
1401 CACCAGCTCGATCTTCTTACAACAACCTCCATGATGTCGGCAACGGTTCCTTCTCCTATCTCCAAGCCTGAGGTATCTGTCTCTGGAGTACAACAAT  
277 T Q L D L S Y N N L H D V G N G S F S Y L P S L R Y L S L E Y N N

**Acc65I (1546)**  
1501 ATACAGCGTCTGTCCCTCGCTCTTTTTATGGACTCTCCAACCTGAGGTTGAAGCGAGCATTACTAAGCAAAGTGTTCACCTGCTTCCAC  
311 I Q R L S P R S F Y G L S N L R Y L S L K R A F T K Q S V S L A S  
1601 ATCCCAACATTGACGATTTTCCCTTCAATGGTAAAAATTTGGAATATCTCAACATGGATGACAATAATATTTCAAGTACCAAAAGCAATACCTTCCAC  
344 H P N I D D F S F Q W L K Y L E Y L N M D D N N I P S T K S N T F T  
1701 GGGATTGGTGAGTCTGAAGTACCTAAGTCTTCCAAAAGTTCACAAGTTTGAACCTTAAACAAATGAAACATTTGTGTCACTTGTCTCATTCTCCCTTG  
377 G L V S L K Y L S L S K T T F S L Q T L T N E T F V S L A H S P L  
1801 CTCACTCTCAACTTAACGAAAAATCACATCTCAAAAATAGCAATGGTACTTTCTTGGTTAGGCCAACTCAGGATACTTGTCTCGGCCTTAATGAAA  
411 L T L N L T K N H I S K I A N G T F S W L G Q L R I L D L G L N E

**BglII (1951)**  
1901 TTGAACAAAAACTCAGCGCCAGGAATGGAGAGGTCTGAGAAATATTTGAGATCTACTATCTTATAACAAATACCTCCAAGTGTCTACCAGTTTCCTT  
444 I E Q K L S G Q E W R G L R N I F E I Y L S Y N K Y L Q L S T S S F

**EcoRV (2058)**  
2001 TGCATTGGTCCCAAGCCTTCAAAGACTGATGCTCAGGAGGGTGGCCCTTAAAAATGTGGATATCTCCCTTACCTTTCCGCCCTTTCGTAACCTTGACC  
477 A L V P S L Q R L M L R R V A L K N V D I S P S P F R P L R N L T

**XbaI (2165)**  
2101 ATTCTGGACTTAAGCAACAACAATAGCCAACATAAATGAGGACTTGTGGAGGGTCTTGAAGTCTAGAAATCCTGGATTTTCAGCACAATAAAGTAACTTAG  
511 I L D L S N N N I A N I N E D L L E G L E N L E I L D F Q H N N L  
2201 CCAGGCTCTGAAACGCGCAAAACCCGGTGGTCCCGTTAATTTCTGAAGGGGCTGTCTCACCTCCACATCTTGAATTTAGAGTCCAACGGCTTAGATGA  
544 A R L W K R A N P G G P V N F L K G L S H L H I L N L E S N G L D E

**BstBI (2328)**  
2301 AATCCAGTGGGGTTTTCAAGAACTTATTCGAACATAAGAGCATCAATCTAGGACTGAATAACTTAAACAAACTTGAACCAATCATTTTTTGATGACCAG  
577 I P V G V F K N L F E L K S I N L G L N N L N K L E P F I F D D Q  
2401 ACATCTAAGGTCACTGAACCTCAGAAGAAGCTCATAACATCTGTTGAGAAGGATGTTTTCGGGCCGCTTTTCAAAACCTGAACAGTTTAGATATGC  
611 T S L R S L N L Q K N L I T S V E K D V F G P P F Q N L N S L D M

**BbrPI (2519)** **HpaI (2544)**  
2501 GCTTCAATCCGTTTGCAGTGCACGTGTGAAAGTATTTCTGGTTTGTAACTGGATCAACCAGACCCACACTAATATCTCTGAGCTGTCCACTCACTACCT  
644 R F N P F D C T C E S I S W F V N W I N Q T H T N I S E L S T H Y L  
2601 CTGTAACACTCCACATCATTATTATGGCTTCCCGCTGAAGCTTTTCGATACATCATCTGTAAAGACAGCGCCCTTTGAACCTCTTTCATAATCAGC  
677 C N T P H H Y Y G F P L K L F D T S S C K D S A P F E L L F I I S

**XcmI (2701)**  
2701 ACCAGTATGCTCCTGTTTTTATACTTGTGGTACTGCTCATTACATCGAGGGCTGGAGGATCTTTTTACTGGAATGTTTCAAGTGCATCGGATTCTTG  
711 T S M L L V F I L V V L L I H I E G W R I S F Y W N V S V H R I L

**Tth11I (2874)**  
2801 GTTTCAGGAAATAGACACACAGGCTGAGCAGTTTGAATATACAGCCTACATAATTCATGCCATAAAGACAGAGACTGGGTCTGGGAACATTTCTCCCC  
744 G F K E I D T O A E O F E Y T A Y I I H A H K D R D W V W E H F S P

2901 AATGGAAGAACAAGACCAATCTCTCAAATTTTGCCTAGAAGAAAGGGACTTTGAAGCAGGCGTCTTGGACTTGAAGCAATTGTTAATAGCATCAAAA  
777▶ M E E Q D Q S L K F C L E E R D F E A G V L G L E A I V N S I K R  
3001 AGCCGAAAAATCATTTCGTTATCACACACCATTTATTAAGACCCTCTGTGCAAGATTCAAGGTACATCACGCAGTTGACGAAGCTATTGAGCAA  
811▶ S R K I I F V I T H H L L K D P L C R R F K V H A V Q Q A I E Q  
3101 ATCTGATTCAATTATACTGATTTTCTCCAGAATATTCCAGATTATAAACTAAACCATGCACCTGTGTTGCGAAGAGGAATGTTAAATCTCATTGCAT  
844▶ N L D S I I L I F L Q N I P D Y K L N H A L C L R R G M F K S H C I  
EcoRI (3272) BamHI (3285)  
3201 CTTGAAGTGGCCAGTTGAGAAAGACGGATAAATGCCTTTCATCATAAATGCAAGTAGCACTTGGATCTCGGAATTCAGCACATGGATCCTATCCCTAT  
877▶ L N W P V Q K E R I N A F H H K L Q V A L G S R N S A H G S Y P Y  
NdeI (3325) NheI (3382)  
3301 GATGTGCCAGACTATGCTGGCTATCCATATGATGTTCTGATTATGCTGGATACCCTTATGATGTGCCAGACTATGCCTAAAGCTAGTGGCCAGACATG  
911▶ D V P D Y A G Y P Y D V P D Y A G Y P Y D V P D Y A •  
3401 ATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCA  
HpaI (3520)  
3501 TTATAAGCTGCAATAAACCAAGTTAAACAACAACCAATTGCATTCAATTTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCT  
EcoRI (3616)  
3601 CTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCAT  
SapI (3798)  
3701 AGGCATCAGGGGCTGTTGCCAATGTCATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTCCCAAGTTTGAAGTAC  
SwaI (3869)  
3801 TCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTGAGAAATAATTTAAATACATCATTGCAATGAAAAATAAT  
EcoO109I (3930)  
3901 GTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGG  
4001 ACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAG  
141▶ • N R T Y K L P I L E E I T T K V L K G N M E I L  
BstXI (4159)  
4101 CACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGC  
116▶ 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 S Y P H  
StuI (4294)  
4201 CTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACGACAGACAGTGCCTGCCAATGTAGGCCT  
82▶ 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 G I Y A E  
4301 CAATGTGGACAGCAGAGATGATCTCCAGTCTTGGCTCTGATGGCCGCCGACATGGTGTGTTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGC  
49▶ 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 K E T A  
BspHI (4444)  
4401 GACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGA  
16▶ V E V L E L D Q Q S I N F T K M  
AseI (4502)  
4501 TGATTAATTTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCG  
SpeI (4657)  
4601 CCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCATGGGGTGGAGAC  
SnaBI (4785)  
4701 TTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTG  
NdeI (4890)  
4801 CCAAGTAGGAAAGTCCATAAGTTCATGTAAGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCAATGACGTCATAGGGGGCGTACTTGGCATATGATAC  
4901 ACTTGATGTAAGTCCAAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTA  
PacI (5076)  
PstI (5069)  
SdaI (5068) BspLU11I (5086)  
5001 TTGACGTCATAGGGCGGGGCTGTTGGCGGTGACCCAGGCGGGCCATTTACCGTAAATGTAACGCCTGCAGGTTAATTAAGAACATGTAGCAAAA  
5101 GGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAATAATCGACGCTCAAGTC  
5201 AGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTGTCGCTCTCTGTTCCGACCTGCCGTTACCGGATA  
5301 CCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGT  
ApaLI (5400)  
5401 GTGCACGAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACATCGTCTTGTAGTCCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCAG  
5501 CCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGG  
5601 TATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGTTC  
5701 AAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAACTCAGTTAAGGGA

**EagI (5836)**

Pacl (5816) SwaI (5825) **NotI (5835)**

5801 TTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTA

5900 ACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGA  
6000 A