



**PvuI (7)**  
**SgfI (6)** MfeI (82) EcoNI (96)  
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

**HindIII (245)** **Bsu36I (291)**  
**Psp1406I (203)** PvuII (239) EcoNI (287)  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

**SphI (560)** BbsI (574)  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCAGCATGCCGTTTGTGAAGACAAGACCTATAAGTATATCTG  
1 M P F A E D K T Y K Y I C  
601 CCGCAATTCAGCAATTTTTGCAATGTGGATGTTGTAGAGATTCTGCCTACCTGCCCTGCCTCACAGCAAGAGACCAGGATCGACTGCGGGCCACCTGC  
13 R N F S N F C N V D V V E I L P Y L P C L T A R D Q D R L R A T C  
701 AACTCTCAGGGAACCGGACACCTCTGGCATCTCTCAATACCTTCAGCGCGGCCCGGCTGGGTGGAGTACTTCATTGCGGCACTGAGGGGCTGTG  
47 T L S G N R D T L W H L F N T L Q R R P G W V E Y F I A A L R G C  
801 AGCTAGTTGATCTCGCGGACGAAGTGGCCTCTGTCTACGAGAGCTACCAGCCTCGACCTCGGACCTCCCGCCAGACCCACTGGAGCCACCGTCACTTCC  
80 E L V D L A D E V A S V Y E S Y Q P R T S D R P P D P L E P P S L P  
901 TGCTGAGAGGCCAGGGCCCGCCACACCTGCTGCGGCCACAGCATCCCTACAACAGCTGCAGAGAGAAGGAGCAAGTTACCCATGCCTGTCCAGGAG  
113 A E R P G P P T P A A A H S I P Y N S C R E K E P S Y P M P V Q E  
EcoRI (1026)  
1001 ACCAGGCGCCAGAGTCCCCAGGAGAGAATTGAGAGCAAGCCCTGCAGACGCTCAGCCCCAGAGCCATCCAAGGAATCCAGATGGTGGCCCCCTGGAGT  
147 T Q A P E S P G E N S E Q A L Q T L S P R A I P R N P D G G P L E  
1101 CCTCCTCTGACCTGGCAGCCCTCAGCCCTCTGACCTCCAGCGGGCATCAGGAGAAGGACAGAACTGGGAGTACCCACACAGCAGGTGCGACCTCCAG  
180 S S S D L A A L S P L T S S G H Q E K D T E L G S T H T A G A T S S  
1201 CCTCACACCATCCCGTGGCCTGTGCTCCATCTGTCTCCTTCCAGCCCTGGCCCGTTCACCCCCAGGGCAAGCCGCTTGCCTGGACCCACAGGGTCA  
213 L T P S R G P V S P S V S F Q P L A R S T P R A S R L P G P T G S  
1301 GTTGATCTACTGGCACCTCCTTCTCCTCCTATCCCCGCTGGCTTGGCCTTGCAGGGGTCAGAGGGTAAACAGGGTGCAGAGAGTACCAGGCCGAGC  
247 V V S T G T S F S S S S P G L A S A G A A E G K Q G A E S D Q A E  
1401 CTATCATCTGCTCAGTGGGGCAGAGGCACCTGCCAAGCTCTGCCCTCAAAGTGCCTACCACCTTGCCTGTAACACAGTGGCCCTGAAAGTGGC  
280 P I I C S S G A E A P A N S L P S K V P T T L M P V N T V A L K V P  
1501 TGCAACCCAGCATCTGTCAGCACAGTGCCTCCAAGTGGCAACTAGCTCAAAGCCCTGGTGCAGTGCCTTCAATGCGCTACCAATCCAGCACCA  
313 A N P A S V S T V P S K L P T S S K P P G A V P S N A L T N P A P  
1601 TCCAAATTGCCATCAACTCAACCCGTGCTGGCATGGTGCATCCAAGTGCCTACTAGCATGGTGTCTACCAAGGTGTCTGCCAGCACAGTCCCCACTG  
347 S K L P I N S T R A G M V P S K V P T S M V L T K V S A S T V P T  
NcoMIV (1744)  
1701 ACGGGAGCAGCAGAAATGAGGAGACCCAGCAGCTCCAACACCCGCGCGCCACTGGAGGCAGCTCAGCCTGGCTAGACAGCAGCTTTGAGAATAGGGG  
380 D G S S R N E E T P A A P T P A G A T G G S S A W L D S S F E N R G  
XcmI (1889)  
1801 CCTGGGTGGAGCTGAGTAAGCCTGGCGTGTGGCATCCAGGTAGACAGCCGTTCTCGGGCTGCTTCGAGGATCTTGCCATCAGTGCAGCACCTCC  
413 L G S E L S K P G V L A S Q V D S P F S G C F E D L A I S A S T S  
NcoI (1917) BbrPI (1966)  
1901 TTGGGCATGGGGCCCTGCCATGGCCAGAGGAGAATGAGTATAAGTCCGAGGGCACCTTTGGGATCCACGTGGCTGAGAACCCAGCATCCAGCTCCTGG  
447 L G M G P C H G P E E N E Y K S E G T F G I H V A E N P S I Q L L  
2001 AGGGCAACCTGGCCACCTGCGGACCCGGATGGCGGCCAGGCCACAAGCCGACCGGAAGTTCAGGAGAGGGAGGTGCCATGCCACAGGCCCTCACC  
480 E G N P G P P A D P D G G P R P Q A D R K F Q E R E V P C H R P S P  
MscI (2191)  
2101 TGGGGCTCTGTGGCTCCAGGTGGCTGTGACAGGGGTGCTGGTAGTCACACTCCTGGTGGTGTACCGGCGCGTCTGCACTAGGCTAGCTGGCCAGAC  
513 G A L W L Q V A V T G V L V V T L L V V L Y R R R L H •  
2201 ATGATAAGATACATTGATGAGTTTGACAAACCACTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAA

**HpaI (2323)** MfeI (2334)  
2301 CCATTATAAGCTGCAATAAACAAGTTAAACAACAATTCATTTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAA

EcoRI (2419)  
2401 CCTCTACAAATGTGGTATGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGG  
2501 CATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCAAGGTTTGAAGT

**SapI (2601)** **SspI (2658)** SwaI (2672)  
2601 AGCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAATAATTTAAATACATCATTGCAATGAAAAA

2701 AATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAT  
2801 TGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCTCAAT  
141 • N R T Y K L P I L E E I T T K V L K G N M E I  
SacI (2933) BstXI (2962)  
2901 GAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGG  
117 L 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  
StuI (3097)  
3001 TGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGG  
83 H 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  
3101 CCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCCTCATAGAGCATGGTATCTTCTCAGT  
50 E 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  
BbsI (3243)  
3201 GGGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGC  
17 A V E V L E L D Q Q S I N F T K M  
XmnI (3239)  
3301 CGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTA  
AseI (3305) SacI (3362)  
3401 CCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTTGACGTCAATGGGGTGA  
SpeI (3460)  
3501 GACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA  
SnaBI (3588)  
3601 CTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTACCCTCATTGACGTCAATAGGGGGCTACTTGGCATATGA  
NdeI (3693)  
3701 TACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCA  
PacI (3879)  
3801 TTATTGACGTCAATGGGGGGGGTCTGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAATAAGAACATGTGAGCA  
SdaI (3871) BspLU11I (3889)  
3901 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAA  
4001 GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGG  
4101 ATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTTCGCTCCAAGCTGGGC  
ApaLI (4203)  
4201 TGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAG  
4301 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATT  
4401 TGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTT  
4501 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTAAAG  
EagI (4639)  
4601 GGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCG  
PacI (4619) Swal (4628) NotI (4638)  
4701 TAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATC  
4801 GAA