



100

PvuI (7) SgfI (6) MfeI (82) EcoNI (96)  
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) Bsu36I (291)  
201 Psp1406I (203) PvuII (239) EcoNI (287)  
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGACAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCGGTTGAGTGCCTGTCGCCCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) AgeI (552) BspHI (568) BbsI (581)  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTAGGAGGGCCATCATGACTCCTGGAAAGACCTCATTGGTGTCA  
601 CTGCTACTGCTGCTGAGCCTGGAGGCCATAGTGAAGGCAGGAATCACAATCCACGAAATCCAGGATGCCAAATCTGAGGACAAGAATTCCCGCGGA  
11▶ L L L L L S L E A I V K A G I T I P R N P G C P N S E D K N F P R  
701 CTGTGATGGTCAACCTGAACATCCATAACCGGAATACCAATCCAAAAGGCTCCTCAGATTACTACAACCGATCCACCTCACCTTGAATCTCCA  
44▶ T V M V N L N I H N R N T N T N P K R S S D Y Y N R S T S P W N L H

EcoRV (820)  
801 CCGCAATGAGGACCTGAGAGATATCCCTCTGTGATCTGGGAGGCAAAGTGGCCCACTTGGGCTGCATCAACGCTGATGGGAACGTGGACTACCACATG  
77▶ R N E D P E R Y P S V I W E A K C R H L G C I N A D G N V D Y H M

FspI (934)  
901 AACTCTGTCCCATCCAGCAAGAGATCTGGTCTGCGCAGGAGCCTCCACACTGCCCAACTCCTTCCGGCTGGAGAAGATACTGGTGTCCGTGGGCT  
111▶ N S V P I Q Q E I L V L R R E P P H C P N S F R L E K I L V S V G

DraIII (1023) MscI (1097) NheI (1091)  
1001 GCACCTGTGTACCCCGATTGTCCACCATGTGGCCTAAGAGCTCTGGGAGGCCACACTCCCAAAGCAGTTAGACTA GGAGAGCCGACCCGCTAGCTGG  
144▶ C T C V T P I V H H V A •  
1101 CCAGACATGATAAGATACATTGATGAGTTGGACAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTAT

HpaI (1229) MfeI (1240)  
1201 TTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTCATTTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAA

EcoRI (1325)  
1301 GTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACCTTAACTCCTCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGA  
1401 ATAAGGCATAGGCATCAGGGGCTGTGCAATGTGATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTAAGATATAGTATTTTCCCAAGGTT

SspI (1564) SwaI (1578)  
1501 TGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATG  
1601 AAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTGTGGACTTAGGGAACAAAGAACCTTTAAT  
1701 AGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCAT  
141▶ N R T Y K L P I L E E I T T K V L K G N M

BstXI (1868)  
1801 CTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAG  
119▶ E I 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  
1901 TAGGGGTGCTGACAGCCACAATGGTGTCAAAGCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACGACAGACAGTGACCCTGCCAA  
85▶ Y P 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

StuI (2003)  
2001 TGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGCTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGCTCATAGAGCATGGTGTCTT  
52▶ Y A 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

BbsI (2149) XmnI (2145)  
2101 CTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATA  
19▶ E T A V E V L E L D Q Q S I N F T K M

AseI (2211)  
2201 CTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACAGCTCTGCTTATATAGACCTCCACCGTACA

SpeI (2366)  
2301 CGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGG

SnaBI (2494)  
2401 GGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTA

NdeI (2599)  
2501 GATGTAAGTCCCAAGTAGGAAAGTCCCATAAAGTTCATGTACTGGGCATAATGCCAGCGGGCCATTTACCGTCTGACGTCAATAGGGGGCGTACTTGGC  
2601 ATATGATACTTGTGATGACTGCCAAGTGGGAGTTTACCCTAAATCTCCACCCATTGACGTCAATGGAAGTCCCTATTGGCGTTACTATGGGAACAT

PacI (2785)  
**PstI (2778)**  
**SdaI (2777)** **BspLU11I (2795)**

2701 ACGTCATTATTGACGTCAATGGCGGGGGTCGTTGGCGGTCAGCCAGGCGGCCATTTACC GTAAGTTATGTAACGCTGCAGGTTAA**TTAAGAACATG**  
 2801 TGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGAC  
 2901 GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCT  
 3001 TACCGGATACCTGTCCGCCTTTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGGTAGGTCGTTCCGCTCCAAG

**ApaLI (3109)**

3101 CTGGGCTGTGTGCACGAACCCCGTTCCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC  
 3201 TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC  
 3301 AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT  
 3401 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCAC

**EagI (3545)**

PacI (3525) SwaI (3534) **NotI (3544)**

3501 **GTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGTTTTTGTGT**  
 3601 GAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCC  
 3701 TCTATCGAA