



100

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

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGGC **HindIII (245)** **Bsu36I (291)**
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGTCAAGTGCAGACC

NgoMIV (441) 401 GGGCCTTTGTCCGGGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) 501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTTGAGTGCAGTGCAGGAGGCACAACATGTCGTCTTACACCTCTTCTA **AgeI (552)** **BspLU11I (575)**
601 CCTGGCGCTCTGCTTGTCTCACCTTACCAGCTCCACCACAGCTGGACCAGAGACCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGA **BspEI (788)**
8▶ L A L C L L T F T S S T T A G P E T L C G A E L V D A L Q F V C G
701 CCGAGGGGCTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTGCGAGGGCACCTCAGACAGGCAATTGGATGAGTGTGCTTCCGGAGCTGTG
42▶ P R G F Y F N K P T G Y G S S I R R A P Q T G I V D E C C F R S C

BsrBI (852) 801 ATCTGAGGAGACTGGAGATGTAAGTGTGCCCCACTGAAGCTACAAAAGCAGCCGCTCTATCCGTGCCAGGCCACACTGACATGCCAAGACTCAGAA **NheI (998)**
75▶ D L R R L E M Y C A P L K P T K A A R S I R A Q R H T D M P K T Q K
901 GGAAGTACATTTGAAGAACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGC
108▶ E V H L K N T S R G S A G N K T Y R M •

MscI (1004) 1001 TAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATT

HpaI (1136) 1101 GCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTAAACAACAACAAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTT **MfeI (1147)**

EcoRI (1232) 1201 AAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGA
1301 GGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCC

SspI (1471) 1401 CAAGGTTTGAAGTCTCTTCAATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAAATATTAAATACATCAT **SwaI (1485)**

EcoO109I (1546) 1501 TGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAAC
1601 CTTAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGTTGACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGC
141▶ • N R T Y K L P I L E E I T T K V L K G

SacI (1746) 1701 CATTCTCTCAATGAGCACAAGCAGTCCAGGAGCATAGTCCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTC
121▶ N M 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
1801 ATCAGAGTAGGGGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACC
88▶ D S 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

StuI (1910) 1901 CTGCCAATGATAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCCGACATGGTGTCTTGTCTCATAGAGCATGG
54▶ R G I 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

BspHI (2060) 2001 TGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCTGATGGCCCTCTATAGTGCATGATTATACTATGC
21▶ I K E T A V E V L E L D Q Q S I N F T K M **BbsI (2056)** **XmnI (2052)**

AseI (2118) 2101 CGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCA **SacI (2175)**

SpeI (2273) 2201 CCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACG
2301 TCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTA

SnaBI (2401) 2401 ATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTGGCATAATGCCAGGCGGGCATTACCGTCAATGACGTCAATAGGGGGCGT

NdeI (2506) 2501 ACTTGGCATATGATACACTTGTACTGCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATG

PacI (2692)
PstI (2685)
SdaI (2684)

2601 GGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAA

BspLU11I (2702)

2701 GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAA

2801 AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTCCGACCC

2901 TGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCG

ApaLI (3016)

3001 CTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTA

3101 TCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTA

3201 GAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCCTGGTAGCGG

3301 TGGTTTTTTTGGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAA

EagI (3452)

PacI (3432) SwaI (3441) NotI (3451)

3401 AACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTT

3501 TTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGA

3601 ACATTTCTCTATCGAA