



125

PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGGCC
PvuII (239)
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
Bsu36I (291)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCATCATGAAGATGAGACGCTACAAGCTTTTCTCATGTTCTG
1▶ M K M R R Y K L F L M F C
601 TATGGCCGGCCTGTGCCTCATCTCCTTCTGCACCTTCTCAAGACCCTGTCTATGTACCTTCCCCGAGAAGTGGCCTCCCTCAGCCCTAACCTGGTG
13▶ M A G L C L I S F L H F F K T L S Y V T F P R E L A S L S P N L V
701 TCCAGCTTTTCTGGAACAATGCCCGGTACGCCCCAGGCCAGCCCCGAGCCAGGAGGCCCTGACCTGCTGCGTACCCCACTTACTCCCACTCGCCCC
47▶ S S F F W N N A P V T P Q A S P E P G G P D L L R T P L Y S H S P

DraIII (841)
801 TGCTGCAGCCGCTGCCGCCAGCAAGGCGGCGGAGGAGCTCCACCGGTTGGACTTGGTGTGCCCGAGGACACCACCGAGTATTTCTGCGCACCAAGGC
80▶ L L Q P L P P S K A A E E L H R V D L V L P E D T T E Y F V R T K A

BstXI (926) **Bsu36I (970)**
901 CGCGGGCTGTCTTCAAACCCGGCACCAAGATGCTGGAGAGGCCGCCCGGGACGGCCGGAGGAGAAGCCTGAGGGGGCCAACGGCTCCTCGGCCCGG
113▶ G G V C F K P G T K M L E R P P P G R P E E K P E G A N G S S A R

Asp718I (1010)
Acc65I (1010)
1001 CGGCCACCCCGGTACCTCCTGAGCGCCGGGAGCGCACGGGGGGCCGAGGCGCCCGCGCAAGTGGTGGAGTGCCTGTGCCTGCCCGGCTGGCACGGAC
147▶ R P P R Y L L S A R E R T G G R G A R R K W V E C V C L P G W H G

BsrBI (1150)
PvuII (1101) **Scal (1127)** **XcmI (1145)**
1101 CCAGCTGCGGCGTGGCCACTGTGGTGCAGTACTCCAACCTGCCACCAAGGAGCGGCTGGTGCCAGGGAGGTGCCGCGCCGCTCATCAACGCCATCAA
180▶ P S C G V P T V V Q Y S N L P T K E R L V P R E V P R R V I N A I N
1201 CGTCAACCACGAGTTCGACCTGTGACGTGCGCTTCCACGAGCTGGCGACGTGGTGGACGCTTTGTGGTGTGCGAGTCCAACCTCACGGCTTATGGG
213▶ V N H E F D L L D V R F H E L G D V V D A F V V C E S N F T A Y G

BsrBI (1309)
NotI (1305)
1301 GAGCCGCGCCGCTCAAGTTCGGGAGATGCTGACCAATGGCACCTTCGAGTACATCCGCCACAAGGTGCTCTATGTCTTCTGGACCACTTCCCGCCG
247▶ E P R P L K F R E M L T N G T F E Y I R H K V L Y V F L D H F P P
1401 GCGGCGCGGACGAGCGGCTGGATCGCCGACGACTACCTGCGCACCTTCTCACCAGGACGGGCTCGCGGCTGCGCAACCTGCGCCCGACGACGCTT
280▶ G G R Q D G W I A D Y L R T F L T Q D G V S R L R N L R P D D V F
1501 CATCATTGACGATGCGGACGAGATCCCGGCCGTGACGGCGTCTTTTCTCAAGCTCTACGATGGTGGACCGAGCCCTTCCGCTTCCACATGCGCAAG
313▶ I I D D A D E I P A R D G V L F L K L Y D G W T E P F A F H M R K
1601 TCGCTACGCGTCTTCTGGAAGCAGCCGGCACCTGGAGTGGTGTGACGGTGCACGGTGGACATGCTGCAGGCAGTGTATGGGCTGGACGGCATCC
347▶ S L Y G F F W K Q P G T L E V V S G C T V D M L Q A V Y G L D G I

Scal (1715)
1701 GCCTGCGCCCGCCAGTACTACCCATGCCAACTTCAGACAGTATGAGAACCAGCCGACATCCTGGTGCAGTGGTGGTGGGAGCCCTGCA
380▶ R L R R R Q Y Y T M P N F R Q Y E N R T G H I L V Q W S L G S P L H
1801 CTTGCGCGGCTGGCACTGCTCCTGGTGTTCACGCCGAGGGCATCTACTTCAAGCTCGTGTCCGCCAGAATGGCGACTTCCACGCTGGGGTACTAC
413▶ F A G W H C S W C F T P E G I Y F K L V S A Q N G D F P R W G D Y

SacII (1926)
1901 GAGGACAAGCGGACCTGAACTACATCCGCGGCTGATCCGCACCGGGGCTGGTTGACGGCACGACGAGGAGTACCCGCCTGAGACCCAGCGAGC
447▶ E D K R D L N Y I R G L I R T G G W F D G T Q Q E Y P P A D P S E

BspLU11I (2000) **AgeI (2036)**
2001 ACATGTATGCGCCCAAGTACCTGCTGAAGAAGTACGACCGGTTCCACTACCTGCTGGACAACCCCTACAGGAGCCAGGAGCACGGCGCGGGGGT
480▶ H M Y A P K Y L L K N Y D R F H Y L L D N P Y Q E P R S T A A G G W

SacII (2109) **XbaI (2159)** **NheI (2195)**
2101 GCGCCACAGGGGTCGAGGGAAGGCGCCCGCCGGGCAAACCTGGACGAGGCGGAAGTCTAGAGCTGCATGATCTGATAGGGTTTGTGACAGGGCTAG
513▶ R H R G P E G R P P A R G K L D E A E V •

MscI (2201)
2201 CTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCT

HpaI (2333) **MfeI (2344)**
2301 TTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA AATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGAGGTTTTTAA

EcoRI (2429)
2401 GCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGG
2501 ATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGAGTAAAGATATAGTGTATTTCCAA

2601 **SspI (2668)** SwaI (2682)
 GGTTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGC

2701 AATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTT

2801 TAATGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCAT
 141 • N R T Y K L P I L E E I T T K V L K G N
BstXI (2972)

2901 TCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATC
 120 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 D

3001 AGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACAGCACAGACAGTGACCCTG
 87 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 R

StuI (3107)
 3101 CCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCACAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTCTCATAGAGCATGGTGA
 53 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 I
BspHI (3257)

XmnI (3249)
 3201 TCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCTCTATAGTGAAGTCTATTATACTATGCCGA
 20 K E T A V E V L E L D Q Q S I N F T K M

AseI (3315)
 3301 TATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCG

SpeI (3470)
 3401 TACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTC

SnaBI
 3500 AATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGAATAGCGATGACTAAT

3600 ACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTAC

NdeI (3703)
 3700 TTGGCATATGATACACTTGATGTACTGCCAAGTGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGG

SdaI (3881)PacI (3889)
 3800 AACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCC T G C A G G T T A A T T A A

BspLU11I (3899)
 3898 GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAA

3998 AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCC

4098 TGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCG

ApaLI (4213)
 4198 CTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTA

4298 TCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTA

4398 GAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGG

4498 TGGTTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAA

PacI (4629) SwaI (4638) NotI (4648)
 4598 AACTCACGTTAAGGGATTTTGGTATGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGTTT

4698 TTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGA

4798 ACATTTCTCTATCGAA