



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

Psp1406I (203) HindIII (245)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

SphI (560)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTGAGATGCCACCTCCTCGCTCCTCTTCTCCTCCTCTTCTCT
1 M P P P R L L F F L L F L

NcoI (605) PstI (667)
601 CACCCCATGGAAGTCAGGCCCGAGGAACCTCTAGTGGTGAAGGTGGAAGAGGGAGATAACGCTGTGCTGCAAGGGGACCTCAGATGGCCCC
13 T P M E V R P E E P L V V K V E E G D N A V L Q C L K G T S D G P

Th111I (711)
701 ACTCAGCAGCTGACCTGGTCTCGGGAGTCCCGCTTAAACCTTCTTAAACTCAGCCTGGGGCTGCCAGGCCTGGGAATCCACATGAGGCCCTGGCCA
47 T Q Q L T W S R E S P L K P F L K L S L G L P G L G I H M R P L A
801 TCTGGCTTTTTCATCTTCAACGTCTCTCAACAGATGGGGGGCTTCTACCTGTGCCAGCCGGGGCCCCCTCTGAGAAGGCTGGCAGCCTGGCTGGACAGT
80 I W L F I F N V S Q Q M G G F Y L C Q P G P P S E K A W Q P G W T V

AvrII (945)
901 CAATGTGGAGGGCAGCGGGAGCTGTTCCGGTGAATGTTTCCGACCTAGGTGGCTGGGCTGTGGCCTGAAGAACAGGTCTCAGAGGGCCCCAGCTCC
113 N V E G S G E L F R W N V S D L G G L G C G L K N R S S E G P S S

BspHI (1013) BglII (1055)
1001 CCTTCCGGGAAGCTCATGAGCCCCAAGCTGTATGTGTGGGCCAAAGACCGCCCTGAGATCTGGGAGGGAGAGCCTCCGTGTGTCACCAGGGGACAGCC
147 P S G K L M S P K L Y V W A K D R P E I W E G E P P C V P P R D S

NcoI (1127) Acc65I (1164)
1101 TGAACCAGAGCCTCAGCCAGGACCTCACCATGGCCCCTGGCTCCACACTCTGGCTGTCTGTGGGGTACCCCTGACTCTGTGTCCAGGGGCCCTCTC
180 L N Q S L S Q D L T M A P G S T L W L S C G V P P D S V S R G P L S

ApaLI (1210) PvuI (1257)
1201 CTGGACCCATGTGACCCCAAGGGCCTAAGTCATTGCTGAGCCTAGAGCTGAAGGACGATCGCCCGCCAGAGATATGTGGTAATGGAGACGGGTCTG
213 W T H V H P K G P K S L L S L E L K D D R P A R D M W V M E T G L

XmaI (1307) Th111I (1359) ScaI (1395)
1301 TTGTGGCCCGGGCCAGCTCAAGACGCTGGAAGTATTATTGTCACCGTGGCAACCTGACCATGTCACTTCCACCTGGAGATCACTGCTCGGCCAGTAC
247 L L P R A T A Q D A G K Y Y C H R G N L T M S F H L E I T A R P V

BstAPI (1404)
1401 TATGGCACTGGCTGCTGAGGACTGGTGGCTGGAAGTCTCAGCTGTGACTTTGGCTTATCTGATCTTCTGCTGTGTTCCCTTGTGGCATTCTTCTATCT
280 L W H W L L R T G G W K V S A V T L A Y L I F C L C S L V G I L H L
1501 TCAAAGAGCCCTGGTCTGAGGAGGAAAAGAAAGCAATGACTGACCCACCAGGAGATTCTTCAAAGTACGCTCCCCAGGAAGCGGGCCCGAGAAC
313 Q R A L V L R R K R K R M T D P T R R F F K V T P P P G S G P Q N
1601 CAGTACGGGAACGTGCTGTCTCTCCACACCCACCTCAGGCCTCGGACGCGCCAGCGTTGGCCGAGGCCTGGGGGGCACTGCCCGCTTATGGAA
347 Q Y G N V L S L P T P T S G L G R A Q R W A A G L G G T A P S Y G
1701 ACCPGAGCAGCTGCCAGCGGATGGAGCCTTGGGGTCCCGGAGCCCGGGAGTGGGCCAGGAAGAAGGGGAGGGCTATGAGGAACCTGA
380 N P S S D V Q A D G A L G S R S P P G V G P E E E G E G Y E E P D
1801 CAGTGAGGAGGACTCCGAGTTCTATGAGAACGACTCCAACCTTGGGCAGGACCAGCTCTCCAGGATGGCAGCGGCTACGAGAACCCTGAGGATGAGCCC
413 S E E D S E F Y E N D S N L G Q D Q L S Q D G S G Y E N P E D E P

BbsI (1915) SapI (1957)
1901 CTGGTCTGAGGATGAAGACTCCTTCCAACGCTGAGTCTTATGAGAACGAGGATGAAGAGCTGACCCAGCCGGTCCGAGGACAATGGACTTCTGA
447 L G P E D E D S F S N A E S Y E N E D E E L T Q P V A R T M D F L
2001 GCCCTCATGGGTGACCTGGGACCCAGCCGGGAAGCAACCTCCTGGGTCCAGTCTATGAGGATATGAGAGGAATCCTGTATGCAGCCCCCAGCT
480 S P H G S A W D P S R E A T S L G S Q S Y E D M R G I L Y A A P Q L

BsrBI (2100) BspHI (2130) XcmI (2179)
2101 CCGCTCCATTCGGGGCCAGCCTGGACCAATCATGAGGAAGATGCAGACTCTTATGAGAACATGGATAATCCCGATGGGCCAGCCAGCCTGGGGAGGA
513 R S I R G Q P G P N H E E D A D S Y E N M D N P D G P D P A W G G

DraIII (2223) NheI (2279)
2201 GGGGGCCGATGGGCACCTGGAGCACCAGGTGATCCTCAGTGGCCAGCCTGGATCTCCTCAAGTCCCAAGATTACAGCTAGCTGGCCAGACATGATA
547 G G R M G T W S T R •

2301 AGATAATTGATGAGTTTGGACAAACCACAAGTGAAGTGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACATTA

HpaI (2417) MfeI (2428)
2401 TAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTA

EcoRI (2513)
2501 CAAATGTGGTATGGAATCTAAATAACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGG

SapI (2695)
2601 CATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCT

2701 **SspI (2752)** **SwaI (2766)**
 TCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTT
 2801 TTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACA
 2901 **GCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCGGTGACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCAATGAGCAC**
 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 V
 3001 **AAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTG**
 115 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 R
 3101 **ACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAA**
 81 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 I
 3201 **TGTGGACAGCAGAGATGATCTCCCAGTCTTGGCTGATGGCCGCCGACATGGTGCTTGTGTCCATAGAGCATGGTGATCTTCTCAGTGGCGAC**
 48 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 V
 3301 **CTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGA**
 15 E V L E L D Q S I N F T K M
BbsI (3337) **XmnI (3333)** **AseI (3399)**
 3401 **TTAATTGTCAAACACGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCC**
SacI (3456)
 3501 **ATTTGCGTCAATGGGGCGGAGTTGTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTG**
SpeI (3554)
 3601 **GAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCA**
SnaBI (3682)
 3701 **AGTAGGAAAGTCCATAAGTGCATGTACTGGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACT**
NdeI (3787)
 3801 **TGATGTACTGCCAAGTGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTG**
PaeI (3973)
 3901 **ACGTCAATGGGCGGGGCTGTTGGGCGTCAAGCAGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGTTAA**
PstI (3966) **SdaI (3965)** **BspLU11I (3983)**
 4001 **CAGCAAAAGGCCAGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGA**
 4101 **GGTGGCAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCGACCCTGCCGTTACCGGATACCT**
ApaLI (4297)
 4201 **GTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTG**
 4301 **CACGAACCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCA**
 4401 **CTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT**
 4501 **CTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAG**
 4601 **CAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATT**
EagI (4733)
 4701 **TGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTAATCGTAACTA**
PaeI (4713) **SwaI (4722)** **NotI (4732)**
 4801 **ACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA**