



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGGTCCACATGGGTAGCAACAAGAGCAAGCCCAAGGATGCCAGCCA
1▶ M G S N K S K P K D A S Q

ApaI (631) **SfiI (697)**
601 GCGGCGCCGAGCCTGGAGCCCGCCGAGAACGTGCACGGCGTGGCGGGGGCGCTTTCCCGCCTCGCAGACCCCAAGCCAGCCTCGGCCGACGGC
13▶ R R R S L E P A E N V H G A G G G A F P A S Q T P S K P A S A D G

SacII (702) **NotI (730)** **Tth111I (772)** **Bsp120I**
701 CACCGCGGCCAGCGCGGCTTCGCCCCCGCGCCGAGCCCAAGCTGTTGCGAGGCTTCAACTCCTCGGACACCGTCCACCTCCCGCAGAGGGCGG
47▶ H R G P S A A F A P A A A E P K L F G G F N S S D T V T S P Q R A
801 GCCGCTGCGCGTGGAGTGACCACCTTTGTGGCCCTATGACTATGAGTCTAGGACGGAGACAGACCTGTCCTTCAAGAAAGGCGAGCGGCTCCAGAT
80▶ G P L A G G V T T F V A L Y D Y E S R T E T D L S F K K G E R L Q I
901 TGTCACAACACAGAGGGAGACTGGTGGCTGGCCACTCGCTCAGCACAGGACAGGCTACATCCCAAGCAACTACGTGGCGCCCTCCGACTCCATC
113▶ V N N T E G D W W L A H S L S T G Q T G Y I P S N Y V A P S D S I

PshAI (1034)
1001 CAGGCTGAGGAGTGGTATTTTGGCAAGATCACCAGACGGGAGTCAAGCGGTTACTGCTCAATGCAGAGAACCAGAGGGGACCTTCTCGTGCAGAGAAA
147▶ Q A E E W Y F G K I T R R E S E R L L L N A E N P R G T F L V R E
1101 GTGAGACCACGAAAAGGTGCTACTGCTCTCAGTGTCTGACTTCGACAAAGGCGCTCAACGTGAAGCACTACAAGATCCGCAAGCTGGACAGCGG
180▶ S E T T K G A Y C L S V S D F D N A K G L N V K H Y K I R K L D S G

DraIII (1296)
1201 CGGCTTCTACATCACCTCCCGCACCCAGTTCAACAGCCTGCAGCAGCTGGTGGCCTACTACTCCAACACGCCGATGGCCTGTGCCACCCGCTCACC
213▶ G F Y I T S R T Q F N S L Q Q L V A Y Y S K H A D G L C H R L T T
1301 GTGTGCCCCACGTCCAAGCCGACACTCAGGGCCTGGCCAAAGGATGCCTGGGAGATCCCTCGGGAGTCTGCGGCTGGAGGTCAAGCTGGGCCAGGGCT
247▶ V C P T S K P Q T Q G L A K D A W E I P R E S L R L E V K L G Q G

Asp718I (1432)
Acc65I (1432)
1401 GCTTTGGCGAGGTGTGGATGGGGACCTGGAACGGTACCACAGGTGGCCATCAAACCTGAAGCCTGGCACGATGTCTCCAGAGGCCCTTCTCGAGGA
280▶ C F G E V W M G T W N G T T R V A I K T L K P G T M S P E A F L Q E

BspHI (1508)
1501 GGCCAGGTGATGAAGAAGCTGAGGCATGAGAAGCTGGTGCAGTTGTATGCTGTGGTTTCAGAGGAGCCATTTACATCGTACCGGAGTACATGAGCAAG
313▶ A Q V M K K L R H E K L V Q L Y A V V S E E P I Y I V T E Y M S K

BsiWI (1694)
1601 GGGAGTTTGTGGACTTTCTCAAGGGGAGACAGGCAAGTACCTCGGGCTGCCTCAGCTGGTGGACATGGCTGCTCAGATCGCCTCAGGCATGGCGTACG
347▶ G S L L D F L K G E T G K Y L R L P Q L V D M A A Q I A S G M A Y
1701 TGGAGCGGATGAAGTACGTCACCGGGACCTTCGTGCAGCCAACATCCTGGTGGGAGAGAACCTGGTGTGCAAGTGGCCGACTTTGGGCTGGCTCGGCT
380▶ V E R M N Y V H R D L R A A N I L V G E N L V C K V A D F G L A R L

BbsI (1804)
1801 CATTGAAGACAATGAGTACACGGCGCGCAAGGTGCCAAATCCCATCAAGTGGACGGCTCCAGAAGCTGCCCTCTATGGCCGTTCCACATCAAGTCG
413▶ I E D N E Y T A R Q G A K F P I K W T A P E A A L Y G R F T I K S

BamHI (1916)
1901 GACGTGTGGTCTTCGGGATCCTGCTGACTGAGCTCACCAAAAGGACGGGTGCCCTACCCTGGGATGGTGAACCGGAGGTGCTGGACCAGGTGGAGC
447▶ D V W S F G I L L T E L T T K G R V P Y P G M V N R E V L D Q V E
2001 GGGGCTACCGGATGCCCTGCCCGCGGAGTGTCCCGAGTCCCTGCACGACCTCATGTGCCAGTGTGGCGGAAGGAGCCTGAGGAGCGGCCACCTTCGA
480▶ R G Y R M P C P P E C P E S L H D L M C Q C W R K E P E E R P T F E

XmaI (2155) **NheI (2182)**
2101 GTACCTGCAGGCTTCTGGAGGACTTACAGTCCACCGAGCCCGAGTACCAGCCGGGAGAACCTTAGGCACAGGCGGGCTAGCTGGCCAGACATG
513▶ Y L Q A F L E D Y F T S T E P Q Y Q P G E N L •

HpaI (2320) **MfeI (2331)**
2301 TTATAAGTGAATAAACAAAGTTAAACAACAATTGCATTATTTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCT

EcoRI (2416)
2401 CTACAAATGGTATGGAATCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCAT

2501 AGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACG

2601 TCTTCATTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAAT
2701 GTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGG
2801 ACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAG
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
2901 CACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGC
116 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 H
3001 CTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCT
82 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 E
3101 CAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGC
49 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 A
BspHI (3244)
BbsI (3240)
XmnI (3236)
3201 GACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCTATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGA
16 V E V L E L D Q Q S I N F T K M
AseI (3302)
3301 TGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACC
SpeI (3457)
3400 GCCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAG
SnaBI (3585)
3499 ACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAC
NdeI (3690)
3599 TGCCAAGTAGGAAAGTCCATAAGTTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGCCATATGAT
3699 ACACCTTGATGTACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCA
PacI (3876) BspLU11I (3886)
3799 TATTGACGTCAATGGGCGGGGTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGC
3897 AAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCA
3997 AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCG
4097 GATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCCAAGCTGGG
ApaLI (4200)
4197 CTGTGTGCACGAACCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAACCGGTAAGACACGACTTATGCCACTGGCA
4297 GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT
4397 TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACCGCTGGTAGCGGTGTTTTTTTGT
4497 TTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAA
PacI (4616) SwaI (4625) NotI (4635)
4597 GGGATTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGTTTTTGTGTGAATC
4697 GTAACATAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAGGTGCCAGAACATTTCTCTAT
4797 CGAA