



PvuI (7)
SgfI (6)
MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTATGTCGTGTACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGGC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTCCGTCGCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMI (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCCACGCTTTCCTGACCTGCTTGTCAACTCTACGCTTTTGTTTCGTTT

BspHI (560)
AgeI (552)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGTTCATGACATTTGCTGAGGACAAGACCTATAAGTATATCCG
601 AGACAACACAGCAAGTTTTGCTGTGTGACGTTCTGGAGATCGCTTACCTGTCTCCCTCACAGCTAGTGACCCAGGATCGACTGCGGGCTTCTCTAC
13▶ D N H S K F C C V D V L E I L P Y L S C L T A S D Q D R L R A S Y

NgoMI (752)
NaeI (752)
BglIII (791)
701 AGGCAGATCGGGAACCGGACACACTCTGGGACTCTTCAATAATCTCCAGCGCCGCTGGCTGGTGGGAGGTTCTCATCCGGCACTGACATCTGTG
47▶ R Q I G N R D T L W G L F N N L Q R R P G W V E V F I R A L Q I C

BsrBI (867)
801 AGTCGCTGGGCTGGCTGATCAAGTACTGAGTTTATCAGAGCTACCTGCTCCCGGACCTCACTCCGCTCCCTAGAGCCACTGCAGTTACCAGACTT
80▶ E L P G L A D Q V T R V Y Q S Y L P P G T S L R S L E P L Q L P D F

NcoI (954)
901 TCCTGCTGCGGTTTCTGGACCCTCTGCATTTGCGCCAGGTCAACAATCCCTGACCATGGCTTACGAGAGACCAAGTTGCCCAAGCCTGTCCAGGAC
113▶ P A A V S G P S A F A P G H N I P D H G L R E T P S C P K P V Q D

EcoRI (1026)
NruI (1064)
1001 ACCCAGCCACCAGAGTCCCGACTAGAGAATTGAGCAACTCCTCCAGACCACTCCGGGGCCGTCGCGAGGATGTCTGGTGGCTTTTGATACCCCTTC
147▶ T Q P P E S P V E N S E Q L L Q T N S G A V A R M S G G S L I P S
1101 CTAACAGCAGGCTCTCAGCCCTCAGCCCTCCAGAGAGCATCAAGAGCAAGAACCAGAACTGGGTGGCGCCACCGAGCAAAATGTTGCTCTGTTCCCAT
180▶ P N Q Q A L S P Q P S R E H Q E Q E P E L G G A H A A N V A S V P I

PshAI (1211)
Bsu36I (1257)
1201 AGCAACCTATGGACTGTGTCTCAACCGTTTCTTCCAGCCCTTCCAGTACTGCCCTGAGGACAAACCTTGTCTGGGGTACAGTATCAGCCCTA
213▶ A T Y G P V S P T V S F Q P L P R T A L R T N L L S G V T V S A L

BstEII (1357)
ScaI (1387)
1301 TCTGTGATACCTCTTTGTCCTCTGCTCACTGGATCAGCTTTTGAAGGGAGCTGGTGACCAGGCCAAAGCTGCCACCTGTTTCACTACTACACTCA
247▶ S A D T S L S S S S T G S A F A K G A G D Q A K A A T C F S T T L
1401 CCAATCTGTGACTACCAGCTCAGTGCCTTCTCCAGATTGGTCCAGTAAAACCATGTCTTCCAAGTGGCCCTCAGTCAAAGTCCACTGCTGCGGAT
280▶ T N S V T T S S V P S P R L V P V K T M S S K L P L S S K S T A A M

MscI (1592)
1501 GAGCTCTACTGTGCTCACCAATACAGCGCCATCAAAATTACCAGCAACTCAGTGTATGCGGGCACAGTGCCATCCAGAGTGCCTGCTAGTGTGGCCAAA
313▶ T S T V L T N T A P S K L P S N S V Y A G T V P S R V P A S V A K
1601 GCACCTGCCAACACAATACCACCTGAGAGGAAACAGCAAGCAAGCAAGGAGACCCCGGAGGTCAGCAACCAAGTCACTGAGGCAACAGACTG
347▶ A P A N T I P P E R N S K Q A K E T P E G P A T K V T T G G N Q T
1701 GACCAATAGCAGTATCAGGAGCTTGCCTGACCAGAGATGAGCAAGCCAGGTGTCTGGTATCCAGTGGACGAGCCATTCTCAGCCTGCTCTGT
380▶ G P N S S I R S L H S G P E M S G V L V S Q L D E P F S A C S V

NcoI (1845)
1801 GGACCTTGCATTAGCCCTAGCAGCTCCTTGGTCTCAGAACCAACCATGGTCCAGAGGAGAATGAGTATTCGCTCTTTAGAATCCAGGTAGACGAAAGC
413▶ D L A I S P S S S L V S E P N H G P E E N E Y S S F R I Q V D E S
1901 CCCAGTGTGATCTATTAGGAAGCCCTGAGCCACTAGCCACCCAGCAGCCCAAGAGAGAAACATTGTCCAGTTCAATGCCCTGGGCTAAGTGGC
447▶ P S A D L L G S P E P L A T Q Q P Q E E E E H C A S S M P W A K W

ApaLI (2012)
BamHI (2071)
2001 TTGGGGCCACCAGTGCCTCTTGGCTGATTCTGGCAGTGTGTACCGTAGTAGGCGCCTGGCCAGGGATCTATCCCTATGATGTGCCAGACTA
480▶ L G A T S A L L A V F L A V M L Y R S R R L A Q G S Y P Y D V P D Y

MscI (2174)
NdeI (2111)
NheI (2168)
2101 TGCTGGTATCCATATGATGTTCTCTGATTATGCTGGATACCCTTATGATGTGCCAGACTATGCTAAAGCTAGCTGGCCAGACATGATAAGATACATTGA
513▶ A G Y P Y D V P D Y A G Y P Y D V P D Y A •
2201 TGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCAATTATAAGCTGCAAT

HpaI (2306)
MfeI (2317)
2301 AAACAAGTTAAACAACAACATTCATTTTATGTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTA

EcoRI (2402)
2401 TGGAAATCTAAAATACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCT
2501 GTTGCCAATGTGATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTCTTCATTTCTTTA

SspI (2641)
SwaI (2655)
2601 TGTTTTAAATGACTGACCTCCACATTCCTTTTTAGTAAATATTAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGC

EcoO109I (2716)
2701 AGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTGGACTTAGGGAACAAGGAACCTTTAATAGAAATGGACAGCAAGAAAGGC

2801 AGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAG
 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 F C D P
 SacI (2916)
 Ecl136II (2916) BstXI (2945)

2901 GAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAAT
 111 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 V A V I
 StuI (3080)

3001 GGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGAGGCTCAATGTGGACAGCA
 78 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 H V A

3101 GAGATGATCTCCCACTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCT
 44 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 E V L E
 BspHI (3230)

3201 CCAGATCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA
 11 L D Q Q S I N F T K M
 SacI (3345)
 Ecl136II (3345)

3301 AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTCGCTCAA
 SpeI (3443)

3401 TGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTGATTACTAGTCAAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCCGT
 SnaBI (3571)

3501 GAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGT
 NdeI (3676)

3601 CCCATAAGGTGATGACTGGGCATAATGCCAGGCGGGCATTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGC
 CAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGG

3801 CGGGGGTCTTGGGCGGTGAGCCAGGCGGGCCATTACCGTAAAGTTATGTAACGCCTGCAGGTTAATTAAAGAACATGTGAGCAAAGGCCAGAAAAGGC
 SdaI (3854) PciI (3872)
 SbfI (3854) BspLU11I (3872)

3901 CAGGAACCGTAAAAAGCCGCGTGTGCGGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAC
 CCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTGTCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTTC

4101 TCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGTGGGCTGTGTGCACGAACCCCG
 ApaLI (4186)

4201 CGTTCAGCCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGG
 ATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGC

4401 TGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCCCGTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTAC
 GCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCT

4601 AGTTAATTAACATTTAAATCAGCGGCCCAATAAAAAATCTTTATTTTTCATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACATAACATACGCTCT
 EagI (4622)
 PacI (4602) SmaI (4611) NotI (4621)

4701 CCATCAAAAACAAAACGAAAACAAAACAACTAGCAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA