



PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245) **Bsu36I (291)**

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGGCCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

SphI (560) **NheI (585)**

501 TCTGTTTGTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAGCATGCCAGCCTCATCTCCTTTCTGTAGCCCCAAAGG
1▶ M P A S S P F L L A P K G

Bsp120I (618)
NcoI (695)

601 GCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGCCGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGACAGCTCTGGGGCCGTGGCTTGTGCCATG
 13▶ P P G N M G G P V R E P A L S V A L W L S W G A A L G A V A C A M

Bsu36I (732)

701 GCTCTGCTGACCCAAACAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCAGGGGACAGGAGGCCCTCCAGAATGGGGAAGGGTATCCCT
 47▶ A L L T Q Q T E L Q S L R R E V S R L Q G T G G P S Q N G E G Y P
 801 GGCAGAGTCTCCCGAGCAGAGTCCGATGCCCTGGAAGCCTGGGAGAGTGGGGAGAGATCCCGAAAAGGAGAGCAGTCTCACCCAAAACAGAAAGAA
 80▶ W Q S L P E Q S S D A L E A W E S G E R S R K R R A V L T Q K Q K K

StuI (999)

901 GCAGACTCTGTCTGCACCTGGTCCCATTAACGCCACCTCCAAGGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGCGGTGGGAGA
 113▶ Q H S V L H L V P I N A T S K D D S D V T E V M W Q P A L R R G R

XcmI (1091)

1001 GGCCTACAGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGCTCTGTTTCAAGACGTGACTTTACCATGGGTC
 147▶ G L Q A Q G Y G V R I Q D A G V Y L L Y S Q V L F Q D V T F T M G

XhoI (1109)
RsrII (1172) **PvuII (1188)**

1101 AGTGGTGTCTCGAGAAGGCAAGGAGCAGGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCGGACCGGGCTACAACAGCTGCTATAG
 180▶ Q V V S R E G Q G R Q E T L F R C I R S M P S H P D R A Y N S C Y S

BbsI (1207)
XmaI (1250)

1201 CGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTGATAATCCCGGGCAAGGGGAAACTTAACCTCTCTCCACATGGAACCTTCTGGGG
 213▶ A G V F H L H Q G D I L S V I I P R A R A K L N L S P H G T F L G

NheI (1345)

1301 TTTGTAAACTGTGATTGTGTTATAAAAAGTGGCTCCAGAAATTCGCTAGCTCGACATGATAAGATACATTGATGAGTTTGGACAAAACCAACTAGAAT
 247▶ F V K L •

1401 GCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCA

HpaI (1508)
MfeI (1519)

1501 AATAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGG

EcoRI (1604)

1601 TATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGG

SapI (1786)

1701 CTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTATTTTCCCAAGTTTGAAGTACTAGCTCTTCATTTCTT

SspI (1843)
SwaI (1857)

1801 TATGTTTTAAATGCAGTACCTCCACATTCCCTTTTATGAAAATATTCAGAAAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAG
 1901 GCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACAAAGGAACCTTAAATAGAATTGGACAGCAAGAAAG
 2001 CGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAGCAGTC
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

SacI (2118)

2101 AGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACA
 112▶ 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 V A V

StuI (2282)

2201 ATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAG
 78▶ 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 H V A
 2301 CAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAG
 45▶ 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

BbsI (2428)
XmnI (2424)
AseI (2490)

2401 CTCCAGATCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTC
 12▶ E L D Q Q S I N F T K M

2501 AAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTC
SacI (2547)

2601 AATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTTGACGTCAATGGGGTGGAGACTTGGAAATCCCC
SpeI (2645)

2701 GTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAA
SnaBI (2773)

2801 GTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACT
NdeI (2878)

2901 GCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATG

3001 GCGGGGGTCTGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCGTCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAG
PacI (3064) SdaI (3056) BspLU11I (3074)

3101 GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAA
BspLU11I (3074)

3201 ACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTT

3301 TCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACC
ApaLI (3388)

3401 CCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACA

3501 GGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCT

3601 GCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGCAAGCAGCAGATT

3701 ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGG

3801 CTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCT
PacI (3804) SnaI (3813) EagI (3824) NotI (3823)

3901 CTCCATCAAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA