



PvuI (7)
SgfI (6) **EcoNI (96)**
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
PvuII (239) **EcoNI (287)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

BspHI (560) **BspHI (587)**
AgeI (552)
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGGCGGCTACCTGAGATCACCGGTCATCATGAGGATATTTGCTGTCTTTATATTCATGACCTACTG
1▶ M R I F A V F I F M T Y W
601 GCATTTGCTGAACGCATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAGAGTATGGTAGCAATATGACAATTGAATGCAAATCCAGTAGAAAAA
13▶ H L L N A F T V T V P K D L Y V V E Y G S N M T I E C K F P V E K

BbsI (775)
701 CAATTAGACCTGGCTGCACTAATTGTCTATTGGAAATGGAGGATAAGAACATTATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTTTCAGCATAGTA
47▶ Q L D L A A L I V Y W E M E D K N I I Q F V H G E E D L K V Q H S

Bsp120I (812)
801 GCTACAGACAGAGGGCCCGCTTTGAAGGACCAGCTCTCCCTGGAAATGCTGCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGACCG
80▶ S Y R Q R A R L L K D Q L S L G N A A L Q I T D V K L Q D A G V Y R

BamHI (993)
901 CTGCATGATCAGCTATGGTGGTGGCCGACTACAAGCGAATTACTGTGAAAGTCAATGCCCATACAACAAAATCAACAAAAGAAATTTGGTTGTGGATCCA
113▶ C M I S Y G G A D Y K R I T V K V N A P Y N K I N Q R I L V V D P

BspLU11I (1021)
1001 GTCACCTCTGAACATGAACATGACATGTCAGGCTGAGGGCTACCCCAAGGCCGAAGTCATCTGGACAAGCAGTGACCATCAAGTCTGAGTGGTAAAGCCA
147▶ V T S E H E L T C Q A E G Y P K A E V I W T S S D H Q V L S G K T

HindIII (1126) **XmnI (1125)**
1101 CCACCACCAATTCGAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCACACTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCACCTTTTAGGAG
180▶ T T T N S K R E E K L F N V T S T L R I N T T T N E I F Y C T F R R

Bsu36I (1207) **PvuII (1223)**
1201 ATTAGATCCTGAGGAAAACCATACAGCTGAATTTGGTCCAGAACTACCTCTGGCACATCCTCAAATGAAAGGACTCACTTGGTAATTTCTGGGAGCC
213▶ L D P E E N H T A E L V I P E L P L A H P P N E R T H L V I L G A
1301 ATCTTATTATGCCTTGGTGTAGCACTGACATTCATCTCCGTTAAGAAAAGGAGAATGATGGATGTGAAAAATGTGGCATCAAGATACAACTCAA
247▶ I L L C L G V A L T F I F R L R K G R M M D V K K C G I Q D T N S

MscI (1442) **NheI (1436)**
1401 AGAAGCAAAGTGATACACATTTGGAGGAGACGTAATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAACCTAGAATGCAGT
280▶ K K Q S D T H L E E T •

HpaI (1574)
1501 GAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATT

EcoRI (1670)
1601 TATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTT
1701 AACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTC

SapI (1852)
1801 ACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGGTTTGAAGTACTCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTC

SspI (1909) **SwaI (1923)**
1901 TTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATAT
2001 CCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAG
1+1▶ • N R T Y K L

SacI (2184)
2101 GGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATG
134▶ P I L E E I T T K V L K G N M E I L V F C D P A Y D S I L E R C M

BstXI (2213)
2201 CCACAGGGGCTGACCACTGATGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAG
100▶ G C P S V V R I S R D V E D S Y P H R V A V I T D F D K Q G N S V A

StuI (2348)
2301 CAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGC
67▶ S G I A I A E A C V T V R G I Y A E I H V A S I I E G T K T R I A

BbsI (2494) **XmnI (2490)**
2401 CGCCCCGACATGGTGTCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTC
34▶ A G V H H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K

2501 ATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGA
0 M ← SacI (2556)

2601 CGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGT
SacI (2613)

2701 CCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCAGCCCATTGATGTA
SpeI (2711)

2801 CTGCCAAAACCGCATCATCATGGTAATAGCGGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTGATGACTGGGCATAATGCCAG
SnaBI (2839)

2901 GCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCC
NdeI (2944)

3001 ATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACGCCAGCGGGCC

3101 ATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT
PacI (3130)
PstI (3123)
SdaI (3122)
BspLU111 (3140)

3201 TTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCC

3301 CCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGC

3401 TCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTA
ApaLI (3454)

3501 ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTAC

3601 AGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGT

3701 AGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTT

3801 TGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAAT
EagI (3890)
PacI (3870) SwaI (3879) NotI (3889)

3901 AAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAG

4001 CAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA