



PvuI (7)
SgfI (6) MfeI (82)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) PvuII (239) Bsu36I (291)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTGTTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTACCATGGCGCACGCTGGGAGAAGTGGTTACGATAACCGGGA
601 GATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGCTACGAGTGGGATGCGGGAGATGTGGCGCCGCCCGGGGGCCCGCCCGCACCG
13▶ I V M K Y I H Y K L S Q R G Y E W D A G D V G A A P P G A A P A P

SrfI (717) SandI (749)
701 GGCTTCTTCTCCTCCAGCCCGGCACACGCCCATCCAGCCGCATCCCGGACCCGGTCCGACGACCTCGCCACTACAGACCCCGGCTGCCCCGGCG
47▶ G F F S S Q P G H T P H P A A S R D P V A R T S P L Q T P A A P G

SacII (803) NgoMIV (859)
801 CCGCCGCGGGGCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGACCCTCCGCCAGGCGCGGACGACTTCTCCCGCCGCTACCGCCGCGACTTCGC
80▶ A A A G P A L S P V P P V V H L T L R Q A G D D F S R R Y R R D F A

PvuII (913) BstXI (953) SapI (969)
901 CGAGATGTCCAGCCAGCTGCACCTGACGCCCTTACCAGCGGGGATGCTTTGCCACGGTGGTGGAGGAGCTTTCAGGGACGGGGTGAAGTGGGGGAGG
113▶ E M S S Q L H L T P F T A R G C F A T V V E E L F R D G V N W G R
1001 ATTGTGGCCTTCTTTGAGTTCGGTGGGGTTCATGTGTGGAGAGCGTCAACCGGGAGATGTGCGCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGT
147▶ I V A F F E F G G V M C V E S V N R E M S P L V D N I A L W M T E

BamHI (1124) SphI (1175)
1101 ACCTGAACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCTTTGTGGAAGTGTACGGCCCCAGCATGCGGCCCTCTGTTTGATTTCTC
180▶ Y L N R H L H T W I Q D N G G W D A F V E L Y G P S M R P L F D F S

BbsI (1212)
1201 CTGGCTGTCTGAAGACTGCTCAGTTTGGCCCTGGTGGGAGCTTGCATCACCTGGTGCCTATCTGGGCCACAAGTGAAGTCAACATGCCTGCCCC
213▶ W L S L K T L L S L A L V G A C I T L G A Y L G H K •

MseI (1316)
NheI (1310)
1301 AAACAAATATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATT

HpaI (1448) MfeI (1459)
1401 TGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAGTTAAACAACAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGT

EcoRI (1544)
1501 GGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGA
1601 ATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTATGAGTTTAAAGATAT

SapI (1726) SspI (1783) SmaI (1797)
1701 AGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAATATTCAGAAATAATT
1801 TAAATACATCATTGCAATGAAAAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGG
1901 GAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTT
141▶ N R T Y K L P I L E E I T T K

BstXI (2087)
2001 TGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGA
125▶ V L K G N M E I L V F C D P A Y D S I L E R C M G C P S V V R I S
2101 TCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCA
92▶ 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 S G I A I A E A

StuI (2222)
2201 CAGACAGTGACCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCCT
58▶ 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 A G V H H K N D E

BbsI (2368)
XmnI (2364)
2301 CATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCGT
25▶ Y L M T I K E T A V E V L E L D Q Q S I N F T K M

AseI (2430)
2401 ATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTAT

SpeI (2585)

2501 ATAGACCTCCCACGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCC GTT GATTACTAGTCAAAACAAA

2601 CTCCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAA

SnaBI (2713)

2701 TAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTC

NdeI (2818)

2801 AATAGGGGGCGTACTTGGCATATGATACACTTGTGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATT

PstI (2997)

SdaI (2996)

2901 GGC GTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGGGGGTCTTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAA GTTATGTAACGCTG

PacI (3004)

BspLU11I (3014)

3001 CAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGAC

3101 GAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTC

3201 CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGT

ApaLI (3328)

3301 GTAGGTCGTTGCTCCAAGCTGGGTGTGTGCACGAACCCCGTT CAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA

3401 AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACT

3501 ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCAC

3601 CGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT

EagI (3764)

PacI (3744) SwaI (3753)

NotI (3763)

3701 CAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCT

3801 GTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGT

3901 GCAGGTGCCAGAACATTTCTCTATCGAA