



PvuI (7)
SgfI (6)

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCCGAGGTTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

XcmI (560)
NcoI (560)
BstEII (555)
AgeI (552) **BstXI (560)** **SmaI (598)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGGTACCATGGTGGTGGTGGCAGCCGCGCCGAACCCGGCCGACGG

1 M V V V A A A P N P A D G

NgoMIV (655)
SfiI (654)

601 GACCCCTAAAGTTCTGCTTGTGCGGGCAGCCGCTCCGCCGCGGAGCCCGGCCGAGCCCGGCCGAGCCCTGCCGCTCATGGTGCAGCCAGAGAGGGGCC

13 T P K V L L L S G Q P A S A A G A P A G Q A L P L M V P A Q R G A

BssHII (733)

701 AGCCCGGAGGCAGCGAGCGGGGGCTGCCCCAGGCGCAAGCGACAGCGCCTCACGCACCTGAGCCCGAGGAGAAGGCGCTGAGGAGGAACTGAAAA

47 S P E A A S G G L P Q A R K R Q R L T H L S P E E K A L R R K L K

801 ACAGAGTAGCAGCTCAGACTGCCAGAGATCGAAAGAAGGCTCGAATGAGTGAAGCAGCAAGTGGTAGATTTAGAAGAAGAGAACCAAAAACCTTTT

80 N R V A A Q T A R D R K K A R M S E L E Q Q V V D L E E E N Q K L L

Eco47III (965)

901 GCTAGAAAATCAGCTTTTACGAGAGAAAACATGGCCTTGTAGTTGAGAACCAGGAGTTAAGACAGCGCTTGGGGATGGATGCCCTGTTGTGAAGAG

113 L E N Q L L R E K T H G L V V E N Q E L R Q R L G M D A L V A E E

BstAPI (1054) **NcoI (1097)**

1001 GAGCGGAAGCCAAGGGGAATGAAGTGAGGCCAGTGGCCGGTCTGCTGAGTCCGAGCAGGTGCAGGCCAGTTGTACCCCTCCAGAACATCTCCCA

147 E A E A K G N E V R P V A G S A E S A A G A G A G P V V T P P E H L P

EcoRV (1138) **Tth11II (1168)**

1101 TGGATTCTGGCGTATTGACTCTTCAGATTGAGTCTGATATCCTGTTGGGCATTCTGGACAACCTGGACCCAGTCATGTTCTTCAAATGCCCTTCCCC

180 M D S G G I D S S D S E S D I L L G I L D N L D P V M F F K C P S P

1201 AGAGCCTGCCAGCTGGAGGAGCTCCAGAGGTCTACCAGAAAGACCCAGTTCTTACCAGCTCCCTTTCTGTGAGTGGGGACGTCATCAGCCAAG

213 E P A S L E E L P E V Y P E G P S S L P A S L S L S V G T S S A K

AseI (1309)

1301 CTGGAAGCCATTAATGAACATAATCGTTTTGACCACATATATACCAAGCCCTAGTCTTAGAGATACCTCTGAGACAGAGCCAAGCTAATGTGGTAG

247 L E A I N E L I R F D H I Y T K P L V L E I P S E T E S Q A N V V

EcoRI (1447) **BspEI (1494)**

1401 TGA AAAATCGAGGAAGCACCTCTCAGCCCTCAGAGAATGATCACCCCTGAATTCATTGTCTCAGTGAAGGAAGAACCTGTAGAAGATGACCTCGTTCGGGA

280 V K I E E A P L S P S E N D H P E F I V S V K E E P V E D D L V P E

1501 GCTGGGTATCTCAAATCTGCTTTCATCCAGCCACTGCCAAAGCCATCTTCTGCCTACTGGATGCTTACAGTACTGTTGATACGGGGGTTCCCTTTCC

313 L G I S N L L S S S H C P K P S S C L L D A Y S D C G Y G G S L S

BspLU11I (1610) **PvuII (1675)**

1601 CCATTCAGTGACATGTCTCTGCTTGGTGTAAACCATTCTGGGAGGACACTTTTGCCAATGAACTCTTCCCGAGCTGATTAGTGTCTAAGGAATGA

347 P F S D M S S L L G V N H S W E D T F A N E L F P Q L I S V •

MscI (1732)
NheI (1726)

1701 TCCAATACTGTTGCCCTTTCTTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGA AAAAAATG

HpaI (1864) **MfeI (1875)**

1801 CTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTATGTTTCAG

EcoRI (1960)

1901 GTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAA

2001 TCAAGCCTCTACTGAACTCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACCTTCTTTC

SapI (2142) **SspI (2199)**

2101 ATGGAGTTAAGATATAGTGTATTTTCCAAGTTTTGAACTAGCTCTTCATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAA

Swal (2213)
2201 ATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTT

2301 AGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGT
141 • N R T Y K L P I L

2401 TCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGC
130 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 G C P S

BstXI (2503)
2501 TGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAAT
97 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 S G I

StuI (2638)
2601 GGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACA
64 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 A G V

BbsI (2784)
2701 TGGTGCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCC
30 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 M

AseI (2846)
2801 TCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACTA
2901 AACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATT

SpeI (3001)
3001 TACTAGICAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAAC

SnaBI (3129)
3101 CGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGGGGCCATT

NdeI (3234)
3201 TACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCA
3301 ATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGGTCGTTGGGCGGTACGCCAGGGGGCCATTTACCGTA

PacI (3420)
PstI (3413)
SdaI (3412)
BspLU11I (3430)
3401 AGTTATGTAACGCCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAG
3501 GCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGC
3601 TCCCTCGTGGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTA

ApaLI (3744)
3701 GGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCT
3801 TGAGTCCAACCCGGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG
3901 AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGAT
4001 CCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC

PacI (4160) Swal (4169) NotI (4179)
4101 TACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTT
4201 TATTTTCATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGC
4301 TGTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA