



PvuI (7)
SgfI (6)
MfeI (82)

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552)
NcoI (560)
EcoRV (570)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCCATGGCTCCGATATCTGTGCTGGTGTCCGCTTGGC

DraIII (640)
BbrPI (663)

601 CACCTTCTGCCATCTGACTGTCCTGCTGGTGGACAGCACCACGGTGTGACGAAATGCAACATCACGTGCAGCAAGATGACATCAAAGATACCTGTAGCT

13▶ T F C H L T V L L A G Q H H G V T K C N I T C S K M T S K I P V A

701 TTGCTCATCCHACTCAACAGAACAGGCATCATGCGGCAACCGCAATCATCTTGGAGACGAGACAGCACAGGCTGTTCTGTGCCGACCCGAAGGAGC

47▶ L L I H Y Q Q N Q A S C G K R A I I L E T R Q H R L F C A D P K E

801 AATGGGTCAAGGACGCGATGACGATCTGGACCGCAGGCTGCTGCCCTAACTCGAAATGGCGGCACCTTCGAGAAGCAGATCGGCGAGGTGAAGCCAG

80▶ Q W V K D A M Q H L D R Q A A A L T R N G G T F E K Q I G E V K P R

901 GACCACCCTGCCGCGGGGAATGGACGAGTCTGTGGTCTGGAGCCGAAGCCACAGGCGAAAGCAGTAGCTGGAGCCGACTCCTTCTCCAGGAA

113▶ T T P A A G G M D E S V V L E P E A T G E S S S L E P T P S S Q E

1001 GCACAGAGGGCCTGGGACCTCCCGAGAGCTGCCGACGGCGTACTGGTTCCTCAGGGACAGGCTCCCCCGACGCCAAAGGCTCAGGATGGAGGGC

147▶ A Q R A L G T S P E L P T G V T G S S G T R L P P T P K A Q D G G

BstXI (1167)

1101 CTGTGGGCACGGAGCTTTTCCGAGTGCCTCCGCTCCTCACTGCCGCCACGTGGCAGAGTTCTGCTCCCCACCACTGGGCCAGCCTCTGGGCTGAGGC

180▶ P V G T E L F R V P P V S T A A T W Q S S A P H Q P G P S L W A E A

StuI (1241)

1201 AAAGACCTCTGAGGCCCGTCCACCCAGGACCCCTCCACCCAGGCCTCCTACTGCTCCTCCAGCCAGAGGAGAATGCTCCGTCTGAAGGCCAGCGT

213▶ K T S E A P S T Q D P S T Q A S T A S S P A P E E N A P S E G Q R

BsrBI (1342)

1301 GTGTGGGGTCAGGGACAGAGCCCGAGGCAAGAACTCTGTGAGCGGAGGAGATGGGTCCCGTCCAGCGCACACGGATGCCTTCCAGGACTGGGGGC

247▶ V W G Q G Q S P R P E N S L E R E E M G P V P A H T D A F Q D W G

PvuII (1476)

1401 CTGGCAGCATGGCCACGTCTGTGGTCCCTGTCTCCTCAGAAGGGACCCCGAGCAGGGAGCCAGTGGCTTTCAGGCAGCTGGACCCCTAAGGCTGAGGA

280▶ P G S M A H V S V V P V S S E G T P S R E P V A S G S W T P K A E E

NcoI (1514)

1501 ACCATCCATGCCACCATGGACCCCGAGGCTGGCGTCTTATCACTCCTGTCCCTGACGCCAGGCTGCCACCCGGAGGCAGGCGGTGGGGCTGCTG

313▶ P I H A T M D P Q R L G V L I T P V P D A Q A A T R R Q A V G L L

1601 GCCTTCTTGGCTCCTCTTCTGCTGGGGTGGCCATGTTACCTACCAGAGCCTCAGGGCTGCCCTCGAAAGATGGCAGGAGAGATGGCGGAGGGCC

347▶ A F L G L L F C L G V A M F T Y Q S L Q G C P R K M A G E M A E G

NdeI (1733)
NheI (1788)

1701 TTCGCTACATCCCCGGAGCTGTGGTAGTAATTCATATGTCCTGGTGGCCGTGAACTCCTCTGGCCTGTGTCTAGTTGTTTATTGCTAGCTGGCCA

380▶ L R Y I P R S C G S N S Y V L V P V •

1801 GACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTG

HpaI (1926)
MfeI (1937)

1901 TAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTA

EcoRI (2022)

2001 AAACCTCTACAAATGTGGTATGGAAATTTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATA

2101 AGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGA

SapI (2204)
SspI (2261)
SwaI (2275)

2201 ACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAA

2301 ATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGA

2401 AATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTATCTC

141 ◀ • N R T Y K L P I L E E I T T K V L K G N M E

2501 AATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAG
 118 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 R D V E D S Y
 2601 GGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGT
 84 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 C V T V R G I Y
 StuI (2700)
 2701 AGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTGCTCATAGAGCATGGTGTCTTCTC
 51 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 Y L M T I K E
 BbsI (2846)
 XmnI (2842)
 2801 AGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTA
 18 T A V E V L E L D Q Q S I N F T K M
 AseI (2908) SacI (2965)
 2901 TGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCTACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGC
 SpeI (3063)
 3001 CTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAACTCCCATTGACGTCAATGGGGT
 SnaBI (3191)
 3101 GGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGAT
 NdeI (3296)
 3201 GTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATA
 3301 TGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACG
 PacI (3482)
 PstI (3475)
 SdaI (3474) BspLU11I (3492)
 3401 TCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAITTAAGAACATGTGA
 3501 GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCGCGTGTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCT
 3601 CAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGGCTCTCCTGTTCGACCTGCCGCTTAC
 3701 CGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCCAAGCTG
 ApaLI (3806)
 3801 GGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGG
 3901 CAGCAGCCACTGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGT
 4001 ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTT
 4101 GTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTT
 EagI (4242)
 PacI (4222) SmaI (4231) NotI (4241)
 4201 AAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAA
 4301 TCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCT
 4401 ATCGAA