



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAATGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) **NcoI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCCATGGCGAAGACCTACGATTACCTGTTCAAGCTGCTGCT

601 GATCGGGGACTCGGGGTAGGGAAGACCTGTGCTCCTGTTCCGCTTCTCCGAGGACGCCTTCAACTCCACATTCATCTCTACCATAGGAATTGACTTTAAA

130▶ I G D S G V G K T C V L F R F S E D A F N S T F I S T I G I D F K

NgoMIV (754) **BstBI (770)**

EagI (752) **BsrBI (763)**

701 ATTAGACCATAGAGCTCGATGGCAAGAGGATTAAGTGCAGATATGGGACCGCCGAGGAGCGGTTTTCGAACAATCACGACAGCCTACTACAGGG

47▶ I R T I E L D G K R I K L Q I W D T A G Q E R F R T I T T A Y Y R

SphI (885)

NcoI (803)
BspEI (857)
SapI (880)

801 GTGCCATGGGTATCATGCTGGTCTACGACATTACCAATGAGAAGTCTTTGACAACATCCGGAATTGGATTGCGAACATTGAAGAGCATGCCTCTGCAGA

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

901 CGTGGAGAAGATGATACTGGGAATAAGTGTGATGTGAATGACAAGAGACAGGTGTCCAAGGAACGGGGAGAAAAGCTGGCACTCGACTATGGGATCAAG

113▶ V E K M I L G N K C D V N D K R Q V S K E R G E K L A L D Y G I K

XcmI (1022) **NsiI (1040)** **EcoRV (1063)**

1001 TTCATGGAGACCAGTGC AAAAGGCCAACATCAATGTGGAGAATGCATTTTCACTCTTGCCAGGGATATCAAAGCAAAAATGGACAAAAAATTGGAAGGGA

147▶ F M E T S A K A N I N V E N A F F T L A R D I K A K M D K K L E G

NcoI (1119) **Tth111I (1187)** **NheI (1198)**

1101 ACAGCCCAGGGGAGCAGCCATGGAGTCAAGATCACAGTGGAGCAGCAGAAGAGGACCAGCTTCTTCCGGTGCAGTCTCCTGTGAGGACAAGGTCTCGC

180▶ N S P Q G S S H G V K I T V E Q Q K R T S F F R C S L L •

MscI (1204)

1201 TAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATT

HpaI (1336) **MfeI (1347)**

1301 GCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGAGGTTTTTT

EcoRI (1432)

1401 AAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGA

1501 GGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCC

SapI (1614)
SspI (1671)
SwaI (1685)

1601 CAAGTGGTGAAGTCTCTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCAT

EcoO109I (1746)

1701 TGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTATGAGTTGGACTTAGGGAACAAAGGAAC

1801 CTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGC

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

BstXI (1975)

1901 CATTCTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGTCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTC

121▶ 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 R D V E

2001 ATCAGAGTAGGGGTCCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCAGACAGTACC

88▶ 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 C V T V

StuI (2110)

2101 CTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGTCCTCATAGAGCATGG

54▶ 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 Y L M T

XmnI (2252)

2201 TGATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGC

21▶ I K E T A V E V L E L D Q Q S I N F T K M

2301 **AseI (2318)**
CGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCA
2401 **SpeI (2473)**
CCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACG
2501 TCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTA
SnaBI (2601)
2601 ATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGT
NdeI (2706)
2701 ACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTACTG
PacI (2892)
2801 GGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCAGGTTAAITAA
SdaI (2884)
BspLU11I (2902)
2901 GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAA
3001 AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGCCTCTCCTGTTCCGACCC
3101 TGCCGCTTACCGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCG
ApaLI (3216)
3201 CTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTA
3301 TCGCCACTGGCAGCAGCCACTGTTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTA
3401 GAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGTGGTAGCGG
3501 TGGTTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAA
EagI (3652)
3601 **PacI (3632) SmaI (3641) NotI (3651)**
AACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTT
3701 TTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGA
3801 ACATTTCTCTATCGAA