



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGGAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACTGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGGC

PvuII (239) 301 GCCATCCACGCCGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

Bsu36I (291)
401 GGGCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

NgoMIV (441)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCATCATGCTTCAACATCCAGGCCAGGTCCTGCTCCGGA

AgeI (552) BspHI (560)
1▶ M M L Q H P G Q V S A S E

SapI (688)
601 AGTGAGTCTTCTGCCATCGTCCCTGCCTGTCCCTCCTGGTCACTGGTGTGTTGAGATTTTGTAACTGACGCCCTTTGTCAAGGAAGAGCTGAGG

13▶ V S A S A I V P C L S P P G S L V F E D F A N L T P F V K E E L R
701 TTTGCCATCCAGAACAAGCACCTCTGCCACCGGATGTCCTCTGCGCTGGAATCAGTCACTGTGAGCAGACAGACCCCTCGGGGTGTCCATCACAAAAGCCG

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

PvuII (857) 801 AGGTAGCCCTGAAGAAGATGAAAGGAAAAAGAGGCGACGAGAAAGAAATAAGATTGCAGCTCAAAGTGCCGAAACAAGAAGAAGGAGACGGAGTG

80▶ E V A P E E D E R K K R R R E R N K I A A A K C R N K K K E K T E C
PstI (901) 901 CCTGCAGAAAGAGTCGGAGAAGCTGAAAGTGTGAATGCTGAACTGAAGGCTCAGATTGAGGAGCTCAAGAACGAGAAGCAGCATTGATATACATGCTC

113▶ L Q K E S E K L E S V N A E L K A Q I E E L K N E K Q H L I Y M L

BbrPI (1014)
1001 AACCTTATCGGCCACGTGTATTGTCGGGCTCAGAATGGGAGGACTCCAGAAGATGAGAGAAACCTCTTTATCCAACAGATAAAAGAAGGAACATTGC

147▶ N L H R P T C I V R A Q N G R T P E D E R N L F I Q Q I K E G T L

MscI (1131)
NheI (1125) 1101 AGAGCTAAGCAGTCGTGGTATGGGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGC

180▶ Q S •

HpaI (1263) MfeI (1274)
1201 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAAACAACAATTGCATTCAATTTATGTTTCAGG

EcoRI (1359)
1301 TTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAT

1401 CAAGCCTCTACTTGAATCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTCA

SapI (1541) 1501 TGGAGTTAAGATATAGTGATTTTTCCCAAGGTTGAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAA

SspI (1598)
1601 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA

1701 GTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTT

141▶ • N R T Y K L P I L E
1801 CCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCT

130▶ 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 (1902) 1901 GACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATG

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 (2037) 2001 GCAATGGCTTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCATATGGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACAT

63▶ 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 H
BbsI (2183) 2101 GGTGCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCT

30▶ 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
XmnI (2179)
AseI (2245) 2201 CCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAA

2301 ACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTT

2401 **SpeI (2400)**
ACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACC

2501 **SnaBI (2528)**
GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTT

2601 **NdeI (2633)**
ACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGTACTGCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAA

2701 TGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAA

2801 **PstI (2812)** **SdaI (2811)** **PacI (2819)** **BspLU11I (2829)**
GTTATGTAACGCCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGG

2901 CTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCT

3001 CCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG

3101 **ApaI (3143)**
GTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT

3201 GAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGA

3301 AGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATC

3401 CGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

3501 **EagI (3579)** **PacI (3559)** **SwaI (3568)** **NotI (3578)**
ACGGGGTCTGACGCTCAGTGGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTT

3601 ATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCT

3701 GTCGCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA