

PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCGATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) **Bsu36I (291)**
Psp1406I (203) **PvuII (239)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTCTCAACTCTACGCTTTGTTTCGTTT

BstEII (555)
AgeI (552) **NcoI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCTCCGGTTGGCCGCGGTCTCTGCCGAGATCCT
EagI (635) 1 ▶ M A P G W P R S L P Q I L

BssHII (627)
601 CGTGTGGGATTCGCGCTTGGTGTGATGCGCGCCGGCCGGGGAGCAAGCACCAGGCACCTCCCATGCTCTAGCGGACGCTCTGGAGCGCGGACCTC
13 ▶ V L G F G L V L M R A A A G E Q A P G T S P C S S G S S W S A D L
BstAPI (707) **BstAPI (769)**
701 GACAAGTGCATGGACTGCGCTTCTGTCCAGCGCACCACACAGCAGCTTCTGCTGGGATGCGCCGACGACCTCTGCCACTTCAGGCTACTGTGGC
47 ▶ D K C M D C A S C P A R P H S D F C L G C A A A P P A H F R L L W
801 CCATTCTGGGGGCGCTCTAGTCTGGTCTGGTTTTGGCGCTGGTTTCTAGTTTCTGGTCTGGAGAAGATGCCCGGAGAGAAAAGTTTACTACCCC
80 ▶ P I L G G A L S L V L V L A L V S S F L V W R R C R R R E K F T T P
MscI (968)
NheI (962)
901 CATAGAGGAGACTGGTGGAGAGGGCTGCCAGGTGGCACTGATCCAGTGAAGAGCACCCGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTT
113 ▶ I E E T G G E G C P G V A L I Q •
1001 TGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAA

HpaI (1100) **MfeI (1111)** **EcoRI (1196)**
1101 GTTAACAACAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAAT
1201 TCTAAATACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCC
SapI (1378)

SspI (1435) **SwaI (1449)**
1401 AAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATC

EcoO109I (1510)
1501 CAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTC
1601 TAGCTTTAGTTCTGCTGACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCAT
141 ▶ • N R T Y K L P I L E E I T T K V L K G N M E I L V F C D P A Y
SacI (1710) **BstXI (1739)**
1701 AGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCAAATGGTGTG
109 ▶ D S I L E R C M G C P S V V R I S R D V E D S Y P H R V A V I T D
StuI (1874)
1801 AAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCACAGACAGTGCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATG
76 ▶ 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 A G E I H V A S I
1901 ATCTCCCACTTGGTCTGATGGCCGCCGACATGGTGTGTTGCTCCTCATAGAGATGGTGTCTTCTCAGTGGCGACCTCCACAGCTCCAGAT
42 ▶ 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 T A V E V L E L D
BbsI (2020) **AseI (2082)**
XmnI (2016)
2001 CCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGC
9 ▶ Q Q S I N F T K M
SacI (2139)
2101 GTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTCGCTCAATGGGGC


SpeI (2237)
2201 GGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCA

2301 AACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATA
SnaBI (2365)

2401 AGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTG
NdeI (2470)

2501 GGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGG

2601 TCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAA
Pacl (2656)
PstI (2649)
SdaI (2648) **BspLU11I (2666)**

2701 CCGTAAAAAGGCCGCGTTTCTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACA


2801 GGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGTCTCTGTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTT

2901 CGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCA
ApaLI (2980)

3001 GCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC

3101 AGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGC

3201 CAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTTCGCAAGCAGCAGATTACGCGCAG

3301 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAA
Pacl (3396)

3401 TTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCA
EagI (3416)
SwaI (3405) **NotI (3415)**

3501 AAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA