



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCGCTTGTCTCAACTCTACGTTCTTTGTTTCGTTT

NcoI (560)
KasI (535) **BstEII (555)** **AgeI (552)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGAATACGCCCTCTGACGCTTCACTGGACCCCGAAGC
1 M E Y A S D A S L D P E A
601 CCCGTGGCCTCCCGCGCCCCGCGCTCGCGCTGCGCGTACTGCTTTGGCCCTGGTCCGCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCGCC
13 P W P P A P R A R A C R V L P W A L V A G L L L L L L L A A A C A
701 GTCTTCTCGCCTGCCCTGGGCGTGTCCGGGCTCGCGCTCGCCCGGCTCCCGCGCCAGCCGAGACTCCCGGAGGGTCCCGAGCTTTGCCCCGACG
47 V F L A C P W A V S G A R A S P G S A A S P R L R E G P E L S P D
801 ATCCCGCCGGCCTTTGGACCTGCGGCAGGGCATGTTTGCAGCTGGTGGCCAAAATGTTCTGCTGATCGATGGGCCCTGAGCTGGTACAGTGACCC
80 D P A G L L D L R Q G M F A Q L V A Q N V L L I D G P L S W Y S D P
901 AGGCCTGGCAGGCGTGTCCCTGACGGGGGCTGAGCTACAAAGAGGACAGAAAGGAGCTGGTGGTGGCCAAGGCTGGAGTCTACTATGTCTTCTTCAA
113 G L A G V S L T G G L S Y K E D T K E L V V A K A G V Y Y V F F Q
BstAPI (1062) **MscI (965)**
1001 CTAGAGCTGCGGCGCGTGGTGGCCGGCAGGGCTCAGGCTCCGTTTCACTTGGCTGCACCTGCAGCCACTGCCTCTGCTGCTGGGGCCGCCCTGG
147 L E L R R V V A G E G S G S V S L A L H L Q P L R S A A G A A A L
1101 CTTTGACCGTGGACCTGCCACCCGCTCCTCCGAGGCTCGAACTCGGCCCTCGGTTTCCAGGGCCGCTTGTGACCTGAGTGCCGGCCAGCGCCTGGG
180 A L T V D L P P A S S E A R N S A F G F Q G R L L H L S A G Q R L G
BstAPI (1225) **KasI (1252)** **BstEII (1278)**
1201 CGTCCATCTTCACTGAGGCCAGGGCACGCCATGCTGCGCAGCTTACCAGGGCGCCACAGTCTTGGGACTCTTCCGGGTGACCCCGAAATCCAGCC
213 V H L H T E A R A R H A W Q L T Q G A T V L G L F R V T P E I P A
MscI (1373)
1301 GGAATCCCTTACCAGGCTCGGAATAACGCCAGCCTGGGTGCAGCCACCTGGACAGAGTCCGAATGCTAGCTGGCCAGACATGATAAGATACATTGAT
247 G L P S P R S E •
1401 GAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATA

HpaI (1505) **MfeI (1516)**
1501 AACAAAGTTAAACAACAACAAATGCATTCAATTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTAT

EcoRI (1601)
1601 GGAATCTAAAATACAGCATAGCAAACCTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTG

SapI (1783)
1701 TTGCCAATGTCATTAGCTGTTGACGCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGTTTGAACCTAGCTCTTCATTTCTTTAT

SspI (1840) **SwaI (1854)**
1801 GTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCA
1901 GAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGA
2001 GCTTCTAGCTTTAGTTCTGCTGACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGG
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
2101 AGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACTTGTGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATG
111 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 P H R V A V I
2201 GTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAG
77 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 A E I H V A S
2301 AGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGCATGGTCTGTTGCTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACAGCTC
44 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 T A V E V L E
2401 CAGATCCTGCTGAGAGATGTTGAAGGCTTCTATGGTGGCCCTCTATAGTGAGTCTGATTATACTATGCCGATATACTATGCCGATGATTAATTGCAAA
11 L D Q Q S I N F T K M

2501 ACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACGCCCATTTGCGTCAAT
SacI (2544)

2601 GGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTG
SpeI (2642)

2701 AGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTC
SnaBI (2770)

2801 CCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCC
NdeI (2875)

2901 AAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGC

3001 GGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGAAAAGGCC
PacI (3061)
PstI (3054)
SdaI (3053) BspLU11I (3071)

3101 AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC
3201 CGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCCTTCT

3301 CCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCCAAGCTGGGCTGTGTGCACGAACCCCC
ApaLI (3385)

3401 GTTCAGCCCAGCCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA

3501 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCT

3601 GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACG

3701 CGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTA

3801 GTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTC
EagI (3821)
PacI (3801) SmaI (3810) NotI (3820)

3901 CATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA