



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTGTTTCGTTT

AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTCAACATGTCTGGTTGTCTGGCCACCAGCCCGCGCGGCC
601 TTTTCCGTTAGCGTTGCTGCTTTTGTCTGCTCGGCCAGATTGGTCTTCCATCTCCTTCCATCTGCCATTAECTCTCGAAGTGCCTCCGTGAG
13▶ F P L A L L L L F L L G P R L V L A I S F H L P I N S R K C L R E

BglIII (737) **BsiWI (731)** **FspI (770)**
701 GAGATTCACAAGGACCTGCTAGTGACTGGCGGTACGAGATCTCCGACCAGTCTGGGGCGCTGGCGGCTGCGCAGCCACCTCAAGATCACAGATTCTG
47▶ E I H K D L L V T G A Y E I S D Q S G G A G G L R S H L K I T D S
801 CTGGCCATATTCTACTCCAAGAGGATGCAACCAAGGGAAATTTGCCTTACCCTGAAGATTATGACATGTTTGAAGTGTGTTTGGAGCAAGGG
80▶ A G H I L Y S K E D A T K G K F A F T T E D Y D M F E V C F E S K G
901 AACAGGGCGGATACCTGACCAACTCGTATCTAGACATGAAGCATGGAGTGGAGGCGAAAAATTACGAAGAGATTGCAAAAGTTGAGAAGCTCAAACCA
113▶ T G R I P D Q L V I L D M K H G V E A K N Y E E I A K V E K L K P
1001 TTAGAGGTAGACTGCGACGCTAGAAGACCTTTCAGAATCTATTGTAATGATTTTGCCTACATGAAGAAGAGAGAAGGAGATGCGTGATACCAACG
147▶ L E V E L R R L E D L S E S I V N D F A Y M K K R E E E M R D T N
1101 AGTCAACAAACTCGGGTCTATACTCAGCATCTTTCAATGTTCTGTCTCATTGGACTAGCTACCTGGCAGGCTTCTACTGCGACGCTTCTTCAA
180▶ E S T N T R V L Y F S I F S M F C L I G L A T W Q V F Y L R R F F K

NheI (1246) **BstXI (1243)** **MscI (1252)**
1201 GGCCAAGAAATTGATTGAGTAATGAATGAGGCATATTCTCTCCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC
213▶ A K K L I E •

HpaI (1384) **MfeI (1395)**
1301 AGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAATT

EcoRI (1480)
1401 GCATTCATTTTATGTTTCAGGTTGAGGGGAGGTGTTGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATA
1501 GCAAAACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGT

SapI (1662)
1601 TTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCAAGTGGTGAAGTACTAGCTCTTCATTTCTTTATGTTTAAATGCACTGACCTCC

SspI (1719) **Swal (1733)**
1701 CACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCC
1801 TTCATAATATCCCCAGTTTAGTGTGGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGG
141▶ • N R T
SacI (1994)

1901 TGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTC
137▶ 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 D S I L E
BstXI (2023)
2001 TCTGCACATGCCACAGGGGTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGG
104▶ 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 F D K Q G
StuI (2158)
2101 TTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGG
70▶ 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 I I E G T K T
2201 TCCTGATGGCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTT
37▶ 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 Q Q S I N
XmnI (2300) **AseI (2366)**
2301 GAAGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCA
4▶ F T K M

2401 **SacI (2423)**
GCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACAT

2501 **SpeI (2521)**
TTTGAAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCCACGCC

2601 **SnaBI (2649)**
CATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGC

2701 **NdeI (2754)**
ATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAA

2801 TACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGCGGTCAGC

2901 **PacI (2940)**
PstI (2933)
SdaI (2932)
CAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCG

3001 TTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACC

3101 AGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCT

3201 **ApaLI (3264)**
TTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCCACCGCTGCCCC

3301 TTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG

3401 GCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAA

3501 AAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAA

3601 **PacI (3680) SwaI (3689) NotI (3699)**
GAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAG

3701 **EagI (3700)**
CGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAA

3801 AACAACTAGCAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA