



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAACCTGGAAAGTGTGCTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) BspHI (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCCATGAAAGTCTCTGCCGCCCTTCTGTGCCTGCTGCTCAT
1▶ M K V S A A L L C L L L I

BstAPI (640)
601 AGCAGCCACCTTCATTCCCAAGGGCTCGCTCAGCCAGATGCAATCAATGCCCGAGTACCTGCTGCTATAACTTACCAATAGGAAGATCTCAGTGCAG
13▶ A A T F I P Q G L A Q P D A I N A P V T C C Y N F T N R K I S V Q

NruI (704)
701 AGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCAAAGAAGCTGTGATCTTCAAGACCATTGTGGCAAGGAGATCTGTGCTGACCCCAAGC
47▶ R L A S Y R R I T S S K C P K E A V I F K T I V A K E I C A D P K

XcmI (818) **NheI (891)**
NcoI (818) **BbsI (852)** **PstI (886)**
801 AGAAGTGGGTTACAGATTCCATGGACCACCTGGACAAGCAAACCCAACTCCGAAGACTTGAACACTCACTCCACAACCCAAGAATCTGCAGCTAGCTGG
80▶ Q K W V Q D S M D H L D K Q T Q T P K T •

901 CCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTAT

HpaI (1029) MfeI (1040)
1001 TTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAATTGCATTCATTTTATGTTTCAGGTTGAGGGGAGGTGTGGGAGGTTTTTAAAGCAA

EcoRI (1125)
1101 GTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGA
1201 ATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTCCAAGGTT

SapI (1307) **SspI (1364)** **SwaI (1378)**
1301 TGAAGTCTCTTCATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTATGAAAATATTCAGAAATAATTTAAATACATCATTGCAATG

EcoO109I (1439)
1401 AAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTATGAGTTGGACTTAGGGAACAAAGAACCTTTAAT
1501 AGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCATTTCAT
141◀ • N R T Y K L P I L E E I T T K V L K G N M

SacI (1639) **BstXI (1668)**
1601 CTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAG
119◀ 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 D S
1701 TAGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTTCAGCAGACAGTGCACCTGCCAA
85◀ 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 R G I

StuI (1803)
1801 TGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGATCTT
52◀ 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 I K

BbsI (1949)
XmnI (1945)
1901 CTCAAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATA
19◀ E T A V E V L E L D Q Q S I N F T K M

AseI (2011) **SacI (2068)**
2001 CTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACA

SpeI (2166)
2101 CGCCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTGATTACTAGTCAAACAAACTCCCATTGACGTCAATGG

SnaBI (2294)
2201 GGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTA

2301 GATG TACTGCCAAGTAGGAAAGTCCCAT AAGGTCATG TACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGC **NdeI (2399)**

2401 ATATGATACACTTGATG TACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACAT

PacI (2585)
PstI (2578)
SdaI (2577) **BspLU11I (2595)**

2501 ACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAATTAAGAACATG

2601 TGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGAC

2701 GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTCCGACCTGCCGCT

2801 TACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAG

ApaLI (2909)

2901 CTGGGCTGTGTGCACGAACCCCCGTT CAGCCCAGCCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC

3001 TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC

3101 AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTT

3201 TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCAC

EagI (3345)
PacI (3325) SwaI (3334) **NotI (3344)**

3301 GTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGT

3401 GAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTTC

3501 TCTATCGAA