



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555) **BamHI (581)**
KasI (535) **AgeI (552)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCACCATGGGAACCCAAAGCCACGGATCCTGCCCTGGCTGGT
1▶ M G T P K P R I L P W L V

PvuII (604)
601 GTCGCAGCTGGACCTGGGCAACTGGAGGGCGTGGCTGGGTGAACAAGGCCGACGCGCTTCCGCATCCCTTGAAGCACGGCCTACGGCAGGATGCA
13▶ S Q L D L G Q L E G V A W V N K S R T R F R I P W K H G L R Q D A
701 CAGCAGGAGGATTTCCGAATCTCCAGGCTGGGCGGAGGCCACTGGTGCATATGTTCCCGGAGGGATAAGCCAGACCTGCCAACCTGGAAGAGGAATT
47▶ Q Q E D F G I F Q A W A E A T G A Y V P G R D K P D L P T W K R N
NdeI (749) **XmaI (757)**
801 TCCGCTCTGCCCTCAACCGCAAAGAGGTTGCGTTTAGCAGAGGACCGGAGCAAGGACCCCTACGACCCACATAAAATCTACGATTTTGAAGTCAAGG
80▶ F R S A L N R K E G L R L A E D R S K D P H D P H K I Y E F V N S G
BsrBI (801) **BspEI (930)** **ScaI (952)** **XmnI (970)**
901 AGTTGGGGACTTTTCCAGCCAGACACCTCTCCGGACACCAATGGTGGAGGCAGTACTTCTGATACCCAGGAAGACATTCTGGATGAGTTACTGGTAAC
113▶ V G D F S Q P D T S P D T N G G G S T S D T Q E D I L D E L L G N
SauI (1026)
1001 ATGGTGTGGCCCACTCCAGATCCGGGACCCCAAGCCTGGCTGTAGCCCCTGAGCCCTGCCCTCAGCCCCTGCGGAGCCCAGCTTGGACAATCCCA
147▶ M V L A P L P D P G P P S L A V A P E P C P Q P L R S P S L D N P
1101 CTCCTTCCCAAACCTGGGGCCCTCTGAGAACCCTGAAGCGGCTGTTGGTCCCGGGGAAGAGTGGGAGTTCGAGGTGACAGCCTTCTACCGGGGCCG
180▶ T P F P N L G P S E N P L K R L L V P G E E W E F E V T A F Y R G R
MscI (1282)
1201 CCAAGTCTCCAGCAGACCATCTCTGCCGGAGGCGCTGCGGCTGGTGGGGTCCGAAGTGGGAGACAGGACGCTGCCTGGATGGCCAGTCCACATGCCA
213▶ Q V F Q Q T I S C P E G L R L V G S E V G D R T L P G W P V T L P
1301 GACCCTGGCATGTCCCTGACAGACAGGGGAGTGTGAGCTACGTGAGGCATGTGCTGAGCTGCCTGGTGGGGGACTGGCTCTCTGGCGGGCCGGCAGT
247▶ D P G M S L T D R G V M S Y V R H V L S C L G G G L A L W R A G Q
1401 GGCTCTGGGCCACGCGGCTGGGGCACTGCCACACATACTGGGCAGTGAAGGAGGCTGCTCCCAACAGCGGCATGGGCTGATGGCGAGTCCCAA
280▶ W L W A Q R L G H C H T Y W A V S E E L L P N S G H G P D G E V P K
BglII (1542)
1501 GGACAAGGAAGGAGCGTGTGTTGACCTGGGGCCCTTATTGTAGATCTGATTACCTTACGGAAGGAAGCGGACGCTCACCACGCTATGCCCTCTGGTTC
313▶ D K E G G V F D L G P F I V D L I T F T E G S G R S P R Y A L W F
Bsu36I (1674) **BbrPI (1668)** **XmaI (1697)**
1601 TGTGTGGGGAGTCATGGCCCCAGGACCCGCTGGACCAAGAGGCTCGTGATGGTCAAGGTTGTGCCACGTGCCTCAGGGCCTTGGTAGAAATGGCCC
347▶ C V G E S W P Q D Q P W T K R L V M V K V V P T C L R A L V E M A
PstI (1795) **SdaI (1794)**
1701 GGGTAGGGGTGCTCCTCCTGGAGAATACTGTGGACCTGCACATTGACAACAGCCACCCTCTCCCTCACCTCCGACCAGTACAAGGCTACCTGCA
380▶ R V G G A S S L E N T V D L H I D N S H P L S L T S D Q Y K A Y L Q
BstXI (1824)
1801 GGACTTGGTGGAGGCATGGATTTCCAGGGCCCTGGGAGACCTGAGCCCTCGTCTCATGGTGTGCCTCAACCCCTGTTCCCCACCACCTCAACC
413▶ D L V E G M D F Q G P G E T •
MscI (1911) **NheI (1905)**
1901 AATAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGA

HpaI (2043) **MfeI (2054)**
2001 TGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGAG

EcoRI (2139)
2101 GTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCT
2201 TTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGT

SapI (2321) **SspI (2378)** **SwaI (2392)**
2301 ATTTTCCCAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAAT
2401 ACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACA

2501 AAGGAACCTTTAATAGAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACC
 141 • N R T Y K L P I L E E I T T K V
 SacI (2653) BstXI (2682)

2601 AGCTTGCCATTTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGT
 123 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 V V R I S R D

2701 CCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGAC
 90 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 A I A E A C V

2801 AGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATAG
 57 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 H K N D E Y
 XmnI (2959)

2901 AGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTAT
 23 L M T I K E T A V E V L E L D Q Q S I N F T K M
 AseI (3025) SacI (3082)

3001 ACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGA
 SpeI (3180)

3101 CCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCC
 SnaBI (3308)

3201 ATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCG
 NdeI (3413)

3301 ATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAG
 NdeI (3413)

3401 GGGCGTACTTGGCATATGATACTTGTACTGCTGCAAGTGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGT
 PstI (3592) SdaI (3591) PacI (3599)

3501 TACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCAGGT
 BspLU11I (3609)

3601 TAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCA
 TCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTT
 CCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTTCGGTGTAGG
 ApaLI (3923)

3901 TCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACA
 CGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGC
 TACTACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTG
 GTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTG
 EagI (4359) PacI (4339) SmaI (4348) NotI (4358)

4301 GAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTTCATTACATCTGTGTG
 TGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAGG
 TGCCAGAACATTTCTCTATCGAA