



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

SgrAI (551) **NcoI (570)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGCGAAGGAGGGCCACCATGGCTTCGGGCAAGGCCAGGTCCTC
601 CCAGCAGGAGTGCAGAGCCTGCCCTGCCCTCTGCTTCTGAGGAGCAGGTAGCCCAGGACACAGAGGAGGTTTTCCGAGCTACGTTTTTACCGCCA
10▶ P R Q E C G E P A L P S A S E E Q V A Q D T E E V F R S Y V F Y R H
1▶ M A S G Q G P G P

BstEII (751) **XcmI (780)** **NcoI (780)**
701 TCAGCAGGAACAGGAGGCTGAAGGGGTGGCTGCCCTGCCGACCCAGAGATGGTCACCTTACCTCTGCAACCTAGCAGCACCATGGGGCAGTGGGACGG
43▶ Q Q E Q E A E G V A A P A D P E M V T L P L Q P S S T M G Q V G R

BstAPI (862) **PstI (869)** **BstAPI (881)** **ScaI (897)**
801 CAGCTCGCCATCATCGGGGACGACATCAACCGACGCTATGACTCAGAGTTCAGACCATGTTGCAGCACCCTGCAGCCCACGGCAGAGAATGCCTATGAGT
77▶ Q L A I I G D D I N R R Y D S E F Q T M L Q H L Q P T A E N A Y E

SapI (959)
901 ACTTCACCAAGATTGCCACCAGCCTGTTTGAGAGTGGCATCAATTGGGGCCGTGTGGTGGCTCTTCTGGGCTTCGGCTACCGTCTGGCCCTACAGTCTA
110▶ Y F T K I A T S L F E S G I N W G R V V A L L G F G Y R L A L H V Y

BstEII (1030) **AvrII (1021)** **SalI (1046)**
1001 CCAGCATGGCCTGACTGGCTTCTAGGCCAGGTGACCCGCTTCGTGGTGCATCTGCTGCATCACTGCATTGCCCGTGGATTGCACAGAGGGGTGGC
143▶ Q H G L T G F L G Q V T R F V V D F M L H H C I A R W I A Q R G G
1101 TGGGTGGCAGCCCTGAACCTGGGCAATGGTCCCATCCTGAACGTGCTGGTGGTCTGGGTGTGGTCTGTTGGCCAGTTTGGTACGAAGATTCTTCA
177▶ W V A A L N L G N G P I L N V L V V L G V V L L G Q F V V R R F F

BspHI (1202) **SmaI (1226)** **MscI (1278)** **NheI (1272)**
1201 AATCATGACTCCCAAGGGTGCCCTTTGGGTCCCGGTTCCAGACCCTGCCTGGACTTAAGCGAAGTCTTTGCCGCTAGCTGGCCAGACATGATAAGATACA
210▶ K S •
1301 TTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTG

HpaI (1410)
1401 CAATAAACAGTTAAACAACAACAAATTCATTCTATTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGT

EcoRI (1506)
1501 GGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGG

SapI (1688)
1601 GGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTT

SspI (1745) **SwaI (1759)**
1701 TTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATATTTAAATACATCATTGCAATGAAAATAATGTTTTTTATT
1801 AGGCAGAATCCAGATGCTCAAGGCCCTTCAATAATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAA
1901 AGCGAGCTTCTAGCTTTAGTTCTGTTGTAAGTGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAG
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

SacI (2020) **BstXI (2049)**
2001 TCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCA
112▶ 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 Y P H R V A V

StuI (2184)
2101 CAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGAC
79▶ 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 Y A E I H V
2201 AGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCCCGACATGGTCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACC
46▶ 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 E T A V E V

BspHI (2334) **BbsI (2330)** **XmnI (2326)** **AseI (2392)**
2301 AGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCTATTATACTATGCGGATATACTATGCCGATGATTAATTG
12▶ L E L D Q Q S I N F T K M

SacI (2449)
2401 TCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGGC

2500 GTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTTGACGTCAATGGGGTGGAGACTTGAAAT
SpeI (2547)
←

2599 CCCC GTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAG
SnaBI (2675)

2699 GAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGCCATATGATACACTTGATG
NdeI (2780)

2799 TACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTC

2899 AATGGGCGGGGTCGTTGGGCGGTACGCCAGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAG
PstI (2959) SdaI (2958) PacI (2966) BspLU11I (2976)
←

2997 CAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGT

3097 GCGGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTC

3197 CGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCAC
ApaLI (3290)

3297 GAACCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG

3397 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG

3497 CGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTTGTGTTGCAAGCAG

3597 CAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGG

3697 TCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACA
PacI (3706) SwaI (3715) EagI (3726) NotI (3725)

3797 TACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA