



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGGTCTGCGCCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **SphI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAGCATGCAACCAATCCTGCTTCTGCTGGCCTTCCTCCTGCT

601 GCCAGGGCAGATGCAGGGGAGATCATCGGGGACATGAGGCCAAGCCCACTCCCGCCCTACATGGCTTATCTTATGATCTGGGATCAGAAGTCTCTG
13▶ P R A D A G E I I G G H E A K P H S R P Y M A Y L M I W D Q K S L

Bsp120I (785)
701 AAGAGGTGCGGTGGCTTCTGATACAGACGACTTCGTGCTGACAGCTGCTACTGTTGGGAAGCTCCATAATGTCACCTTGGGGGCCACAATATCA
47▶ K R C G G F L I Q D D F V L T A A H C W G S S I N V T L G A H N I

PstI (895)
801 AAGAACAGGAGCCGACCCAGCAGTTTATCCCTGTGAAAAGACCCATCCCCATCCAGCCTATAATCCTAAGAATTCTCCAACGACATCATGCTACTGCA
80▶ K E Q E P T Q Q F I P V K R P I P H P A Y N P K N F S N D I M L L Q

Bsu36I (939) **NgoMIV (994)**
901 GCTGGAGAGAAAGCCAAAGCGGACCAGAGCTGTGCAGCCCTCAGGCTACCTAGCAACAAGGCCAGGTGAAGCCAGGGCAGACATGCAGTGTGGCCGGC
113▶ L E R K A K R T R A V Q P L R L P S N K A Q V K P G Q T C S V A G

1001 TGGGGCAGACGGCCCCCTGGGAAACACTCACACACTACAAGAGGTGAAGATGACAGTGCAGGAAGATCGAAAGTGCGAATCTGACTTACGCCATT
147▶ W G Q T A P L G K H S H T L Q E V K M T V Q E D R K C E S D L R H

SmaI (1130)
1101 ATTACGACAGTACCATTGAGTTGTGCGTGGGGACCCAGAGATAAAAAGACTTCCTTTAAGGGGACTCTGGAGGCCTCTTGTGTGAACAAGGTGGC
180▶ Y Y D S T I E L C V G D P E I K K T S F K G D S G G P L V C N K V A

BsrGI (1269)
1201 CCAGGGCATTGTCTCCTATGGACGAAACAATGGCATGCCTCCACGAGCCTGCACCAAAGTCTCAAGCTTTGTACTGGATAAAGAAAACCATGAAACGC
213▶ Q G I V S Y G R N N G M P P R A C T K V S S F V H W I K K T M K R

MscI (1321)
1301 TACTAACTACAGGAAGCTAGTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTG
247▶ Y •

HpaI (1453) **MfeI (1464)**
1401 AAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTATTTATGTTTCAGGTTACAGGGGA

EcoRI (1549)
1501 GGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTA
1601 CTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTTCATGGAGTTAA

SapI (1731) **SspI (1788)**
1701 GATATAGTGTATTTTCCAAAGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAA

SwaI (1802)
1801 TAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGAC

1901 TTAGGGAACAAAGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGT
141▶ • N R T Y K L P I L E E I T

SacI (2063) **BstXI (2092)**
2001 GGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTG
127▶ T K V 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

2101 ATGGATCTGTCCACTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTT
93▶ I S R D 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

StuI (2227)
2201 CAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGT
60▶ A C V 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

BbsI (2373)
XmnI (2369)
2301 GTCCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGA
27▶ D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M

2401 **AseI (2435)** **SacI (2492)**
GTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAAACGAGCTCTG

2501 **SpeI (2590)**
CTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTACTAGTCAAA

2601
ACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCAT

2701 **SnaBI (2718)**
GGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTG

2801 **NdeI (2823)**
ACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCC

2901
CTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAAC

3001 **PacI (3009)** **PstI (3002)** **SdaI (3001)** **BspLU11I (3019)**
GCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCC

3101
CTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCG

3201
CTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGT

3301 **ApaLI (3333)**
TCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACC

3401
CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCC

3501
TAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAA

3601
ACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTG

3701 **EagI (3769)** **PacI (3749)** **Swal (3758)** **NotI (3768)**
ACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTA

3801
CATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTG

3901
CAAGTGCAGGTGCCAGAACATTTCTCTATCGAA