



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **PshAI (575)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTAGGAGGGCCACCATGGCGACCACCGTCAGCACTCAGCGCGGG
1▶ M A T T V S T Q R G

BsrGI (604)
601 CCGGTGTACATCGGTGAGCTCCCGCAGGACTTCTCCGCATCACGCCACACAGCAGCAGCGGCAGGTCACGCTGGACGCCAGGCGGCCAGCAGCTGC
11▶ P V Y I G E L P Q D F L R I T P T Q Q Q R Q V Q L D A Q A A Q Q L

MscI (760)
701 AGTACGGAGGCGCAGTGGGCACCGTGGGCCGACTGAACATCACGGTGGTACAGGCAAAGTTGGCCAAGAATTACGGCATGACCCGCATGGACCCCTACTG
44▶ Q Y G G A V G T V G R L N I T V V Q A K L A K N Y G M T R M D P Y C
801 CCGACTGCGCCTGGGCTACGCGGTGTACGAGACGCCACCGGCACACAATGGCGCCAAGAATCCCCGCTGGAATAAGGTCATCCACTGCACGGTGCCCCA
77▶ R L R L G Y A V Y E T P T A H N G A K N P R W N K V I H C T V P P

BglIII (922)
XhoI (918) **Bsu36I (992)**
901 GCGGTGGACTCTTTCTATCTCGAGATCTTCGATGAGAGAGCCTTCTCCATGGACGACCGCATTGCCTGGACCCACATCACCATCCCCGAGTCCCTGAGGC
111▶ G V D S F Y L E I F D E R A F S M D D R I A W T H I T I P E S L R

BsrBI (1031)
1001 AGGGCAAGGTGGAGGACAAGTGGTACAGCCTGAGCGGGAGGCAGGGGACGACAAGGAGGGCATGATCAACCTCGTCATGTCTACGCGCTGCTTCCAGC
144▶ Q G K V E D K W Y S L S G R Q G D D K E G M I N L V M S Y A L L P A

XcmI (1148)
1101 TGCCATGGTATGCCACCCAGCCCGTGGTCTGATGCAACAGTGTACCAGCAGGGCGTTGGCTATGTGCCATCACAGGGATGCCCGCTGTCTGTAGC
177▶ A M V M P P Q P V V L M P T V Y Q Q G V G Y V P I T G M P A V C S

EagI (1228) **EcoO109I (1264)** **BspLU11I (1285)**
1201 CCCGGCATGGTGGCCGTGGCCCTGCCCGCCGCGTGAACGCCAGCCCGCTGTAGCGAGGAGGACCTGAAAGCCATCCAGGACATGTTCCCCAACAA
211▶ P G M V P V A L P P A A V N A Q P R C S E E D L K A I Q D M F P N

BsrBI (1316)
1301 TGGACCAGGAGGTGATCCGCTCCGTGCTGGAAGCCAGCGAGGGAACAAGGATGCCGCCATCAACTCCCTGCTGCAGATGGGGGAGGACCATAGAGCCT
244▶ M D Q E V I R S V L E A Q R G N K D A A I N S L L Q M G E E P •

MscI (1425)
NheI (1419)
1401 CTGCCTCGATGCCTTTTGCCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAACCTAGAATGCAGTGAAAAAATGCTTTTATT

HpaI (1557) **MfeI (1568)**
1501 TGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTTGCATTCATTTATGTTTCAGGTTCCAGG

EcoRI (1653)
1601 GGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGGTATGGAAATTTCTAATAACAGCATAGCAAACTTTAACCTCCAAATCAAGCC
1701 TCTACTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGT

SapI (1835) **SspI (1892)**
1801 TTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAAATATTCA

SwaI (1906) **EcoO109I (1967)**
1901 GAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTT

2001 GGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGGGGATGAGTTCTCAA
141▶ • N R T Y K L P I L E E I

BstXI (2196)
2101 TGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCAC
128▶ T 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
2201 CCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATG
95▶ R 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

StuI (2331)
2301 GCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCT
61▶ 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 R I A A G V H H K

BbsI (2477)
XmnI (2473)

2401 TGGTGCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATA
 28 N 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

AseI (2539)

2501 GTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGC

SpeI (2694)

2601 TCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGT

2701 CAAAAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCA

SnaBI (2822)

2801 TCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCACTGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTC

NdeI (2927)

2901 ATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCTCAAGTGGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAA

3001 GTCCTTATTGGCGTTACTATGGGAACATACGTCAATATTGACGTCAATGGGGCGGGTCTGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATG

PacI (3113)

SdaI (3105) BspLU11I (3123)

3101 TAACCGCTGCAGGTTAAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGC

3201 CCCCCTGACGAGCATCACA AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCG

3301 TCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCT

ApaLI (3437)

3401 CAGTTCGGTGTAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC

3501 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGT

3601 GGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA

3701 ACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG

EagI (3873)

PacI (3853) SmaI (3862) NotI (3872)

3801 TCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAGCGGCCGAATAAAATATCTTTATTTTC

3901 ATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCC

4001 AGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA