



PvuI (7)
SgfI (6)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCTACCTGAGATCACCGGTAGGAGGGCCACCATGGCTGGTGATCTTTCAGCAGGTTTCTTC

ScaI (638) **AgeI (552)** **NcoI (568)**
601 ATGGAGGAACCTTAATACATACCGTCAGAAGCAGGGAGTAGTACTTAAATATCAAGAACTGCCTAATTCAGGACCTCCACATGATAGGAGGTTTACATTTCC

11▶ M E E L N T Y R Q K Q G V V L K Y Q E L P N S G P P H D R R F T F

BstAPI (756)
701 AAGTTATAATAGATGGAAGAGAAATTTCCAGAAGGTGAAGGTAGATCAAAGAAGGAAGCAAAAATGCCGACGCAAAATAGCTGTTGAGATACTTAATAA

44▶ Q V I I D G R E F P E G E G R S K K E A K N A A A K L A V E I L N K

NcoI (859) **StuI (875)**
801 GGAAAAGAAGGCAGTTAGTCCTTATTATTGACAACAACGAATTTCTCAGAAGGATTATCCATGGGAATTACATAGGCCCTTATCAATAGAATTGCCAG

77▶ E K K A V S P L L L T T T N S S E G L S M G N Y I G L I N R I A Q

901 AAGAAAAGACTAACTGTAATATTGAACAGTGTGCATCGGGGGTGCATGGGCCAGAAGGATTTTCATTATAAATGCAAAATGGACAGAAAAGATATAGTA

111▶ K K R L T V N Y E Q C A S G V H G P E G F H Y K C K M G Q K E Y S

1001 TTGGTACAGGTTCTACTAAACAGGAAGCAAAACAATTTGGCCGCTAAACTGCATATCTCAGATATTATCAGAAGAACTCAGTAAATCTGACTACCT

144▶ I G T G S T K Q E A K Q L A A K L A Y L Q I L S E E T S V K S D Y L

1101 GTCCTCTGGTTCTTTTGTACTACTGTGAGTCCCAAAGCAACTCTTGTAGTACCAGCACACTCGCTTCTGAATCATCATCTGAAGGTGACTTCTCAGCA

177▶ S S G S F A T T C E S Q S N S L V T S T L A S E S S S E G D F S A

PmeI (1231) **BglII (1290)**
1201 GATACATCAGAGATAAATTTAAACAGTACAGTTTAAACAGTCTTCTGTTGCTTATGAATGGTCTCAGAAAATAATCAAAGGAAGGCAAAAAGATCTTTGG

211▶ D T S E I N S N S D S L N S S S L L M N G L R N N Q R K A K R S L

Bst1107I (1337)
1301 CACCCAGATTTGACCTTCTGACATGAAAGAAACAAAGTATACTGTGGACAAGAGGTTTGGCATGGATTTTAAAGAAATAGAATTAATTGGCTCAGGTGG

244▶ A P R F D L P D M K E T K Y T V D K R F G M D F K E I E L I G S G G

MscI (1403)
1401 ATTTGGCCAAAGTTTTCAAAGCAAAACACAGAATTGACGAAAGACTTACGTTATTAACGTTAAATATAAATACGAGAAGCGGAGCGTGAAGTAAAA

277▶ F G Q V F K A K H R I D G K T Y V I K R V K Y N N E K A E R E V K

SspI (1524)
1501 GCATTGGCAAAACTTGATCATGTAATATTGTTCACTACAATGGCTGTTGGGATGGATTTGATTATGATCCTGAGACCAGTGAATCTCTTGGAGCA

311▶ A L A K L D H V N I V H Y N G C W D G F D Y D P E T S D D S L E S

1601 GTGATTATGATCCTGAGAACAGCAAAAATAGTTCAAGGTCAAAGACTAAGGAATCTGTGATAAAGGGACCTTGAACAATGGATTGAAAAAGAAGAGG

344▶ S D Y D P E N S K N S S R S K T K E F C D K G T L E Q W I E K R R G

BglII (1790)
1701 CGAGAACTAGACAAAGTTTTGGCTTTGGAACCTTTGAACAAATAACAAAAGGGTGGATTATACATTCAAAAAATTAATTCATAGAGATCTTAAG

377▶ E K L D K V L A L E L F E Q I T K G V D Y I H S K K L I H R D L K

1801 CCAAGTAATATATTCTAGTAGATACAAAACAAGTAAAGATTGGAGACTTTGGACTTTGAACTCTGAAAAATGATGAAAAGCAACAAGGAGTAAGG

411▶ P S N I F L V D T K Q V K I G D F G L V T S L K N D G K R T R S K

1901 GAACCTTTCGATACATGAGCCCAGAACAGATTTCTCGCAAGACTATGGAAAGGAAGTGGACCTCTACGCTTTGGGGCTAATCTTGTGAACCTTCTCA

444▶ G T L R Y M S P E Q I S S Q D Y G K E V D L Y A L G L I L A E L L H

2001 TGTATGTGACACTGCTTTTGAACATCAAAGTTTTTACAGACCTACGGGATGGCATCATCTCAGATATATTTGATAAAAAAGAAAAACTCTTCTACAG

477▶ V C D T A F E T S K F F T D L R D G I I S D I F D K K E K T L L Q

Bsu36I (2118) **BspLU11I (2199)**
2101 AAATTACTCTCAAAGAAACCTGAGGATCGACCTAACACATCTGAAATACTAAGACCTTGACTGTGTGGAAGAAAAGCCAGAGAAAAATGAACGACACA

511▶ K L L S K K P E D R P N T S E I L R T L T V W K K S P E K N E R H

MscI (2257) **NheI (2251)**
2201 CATGTTAGAGCCCTTCTGAAAAAGTATCCTGCTTCTGATATGCAGTTTTCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCA

544▶ T C •

HpaI (2389)
2301 CAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACA

2401 CAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGGTATGGAATTCATAAATACA

2501 GCATAGCAAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTA

SapI (2667)

2601 GCTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGA

SspI (2724) SwaI (2738)

2701 CCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAA

2801 GGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTT

141 • N
SacI (2999)

2901 CCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGAGCATAGTCAGAGATG
139 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 D P A Y D S I

BstXI (3028)

3001 AGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCT
105 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 I T D F D K Q

StuI (3163)

3101 GCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGT
72 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 A S I I E G T

3201 CTTGGTCTGATGGCCGCCGACATGGTGTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAG
39 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 L E L D Q Q S

BbsI (3309)

3301 ATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGT
5 I N F T K M

SacI (3428)

3401 CTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTAC

SpeI (3526)

3501 GACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCC

SnaBI (3654)

3601 ACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAAAGTCATGTAC

NdeI (3759)

3701 TGGCATAATGCCAGGCGGGCCATTTACCGTCAATGACGTCAATAGGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGAGTTTACC

3801 GTAAATACTCCACCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATATTGACGTCAATGGGCGGGGCTGTTGGGCGG

PacI (3945)

PstI (3938)
SdaI (3937) BspLU11I (3955)

3901 TCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGACAGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG

4001 CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAG

4101 ATACCAGGCGTTTCCCCGGAAGTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG

ApaLI (4269)

4201 GCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGCT

4301 GCGCCTTATCCGTAACATATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA

4401 TGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC

4501 GGAAAAAGAGTTGGTAGCTCTTGTATCCGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTGAAGCAGCAGATTACGCGCAGAAAAAAGGAT

PacI (4685) SwaI (4694)

4601 CTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAA

EagI (4705)
NotI (4704)

4701 ATCAGCGCGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAACGA

4801 AACAAACAAACTAGCAAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA