



PvuI (7)
SgfI (6)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTAGGAGGGCCACCATTGGTGGTATCTTTCAGCAGGTTTCTTC

AgeI (552) **NcoI (568)**
1► M A G D L S A G F F

ScaI (638)
601 ATGGAGGAACTTAATACATACCGTCAGAAGCAGGGAGTAGTACTTAAATATCAAGAACTGCCTAATTCAGGACCTCCACATGATAGGAGGTTTACATTTCC

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 AAGTTATAATAGATGGAAGAGAATTTCCAGAAGGTGAAGGTAGATCAAAGAAGGAAGCAAAAAATGCCGACGCAAAATAGCTGTTGAGATACTTAATAA

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 GAAAAAGAAGGCAGTTAGTCCTTATTATTGACAACAACGAATTCCTCAGAAGGATTATCCATGGGAATTACATAGGCCCTTATCAATAGAATTGCCAG

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 TTGGTACAGGTTCTACTAAACAGGAAGCAAAACAATTGGCCGCTAAACTTGCATATCTCAGATATTATCAGAAGAACTCAGTAAATCTGACTACCT

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 GATACATCAGAGATAAATTCTAACAGTGACAGTTTAAACAGTCTTCTGTTGCTTATGAATGGTCTCAGAAAATAATCAAAGGAAGGCAAAAAGATCTTTGG

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 ATTTGGCCAAAGTTTTCAAAGCAAAACACAGAATTGACGGAAAGACTTACGTTATTAACAGTGTAAATATAATAACGAGAAGCGGAGCGTGAAGTAAAA

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 GCATTGGCAAAACTTGATCATGTAATATTGTTCACTACAATGGCTGTGGGATGGATTTGATTATGATCCTGAGACCAGTGATGATTCTCTTGGAGCA

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 GTGATTATGATCTGAGAACAGCAAAAATAGTTCAGGTCAAAGACTAAGTGCCTTTTCATCAAATGGAATCTGTGATAAAGGGACCTTGAACAATG

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

1701 GATTGAAAAAAGAAGAGGCGAGAAACTAGACAAAGTTTTGGCTTGGAACTCTTGAACAAATAACAAAAGGGGTGGATTATATACATTCAAAAAAATTA

377► I E K R R G 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

BglIII (1808)
1801 ATTCATAGAGATCTTAAGCCAAGTAATATATTCTTAGTAGATACAAAACAAGTAAAGATTGGAGACTTTGGACTTGTAAACATCTCTGAAAAATGATGGAA

411► I H R D L K 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

1901 AGCGAACAAAGGAGTAAGGGAACTTTGCATACATGAGCCAGAACAGATTTCTCGCAAGACTATGGAAGGAAGTGGACCTCTACGCTTTGGGGCTAAT

444► K R T R S K 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

2001 TCTTGCTGAACCTCTTATGATGTGACTGCTTTTGAACATCAAAGTTTTTACAGACCTACGGGATGGCATCATCTCAGATATATTTGATAAAAAA

477► L A E L L H 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

Bsu36I (2136)
2101 GAAAAAATCTTCTACAGAAATTAATCTCAAAGAAACCTGAGGATCGACTTAACATCTGAAATACTAAGGACCTTACTGTGTGGAAGAAAAGCCAG

511► E K T L L Q 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

MscI (2275)
BspLU11I (2217) **NheI (2269)**
2201 AGAAAAATGAACGACACACATGTTAGAGCCCTTCTGAAAAAGTATCCTGCTTCTGATATGCAGTTTTCCGCTAGCTGGCCAGACATGATAAGATACATTG

544► E K N E R H T C •

2301 ATGAGTTTGGACAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAA

HpaI (2407)
2401 TAAACAAGTTAAACAACAATTCATTTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGT

2501 ATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGC
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2601 TGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTAGCTCTTCAATTTCTTT
 SapI (2685)

2701 ATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGG
 SspI (2742) SwaI (2756)

2801 CAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGC

2901 GAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTCTCAATGAGCACAAAGCAGTCA
 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 D
 SacI (3017) BstXI (3046)

3001 GGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAA
 111 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 I
 StuI (3181)

3101 TGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGC
 78 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 A

3201 AGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGC
 45 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 L
 BbsI (3327)

3301 TCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTGTATTATACTATGCGGATATACTATGCGGATGATTAATTGTCA
 11 E L D Q Q S I N F T K M ←

3401 AAACAGCTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCA
 ←
 SacI (3446)

3501 ATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGG
 SpeI (3544)

3601 TGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAG
 SnaBI (3672)

3701 TCCATAAGTTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTG
 NdeI (3777)

3801 CCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGG

3901 GCGGGGTCGTTGGGCGTCAAGCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAITAAAGAACATGTGAGCAAAAGGCCAGCAAAAGG
 PacI (3963)
 PstI (3956) SdaI (3955) BspLU11I (3973)

4001 CCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCGAAA
 ←

4101 CCCGACAGGACTATAAAGATACCAGGCTTTCCCCTGGAAGTCCCTCGTGCCTCTCTGTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTT

4201 CTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCC
 ApaLI (4287)

4301 CCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAG

4401 GATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTG

4501 CTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTA

4601 CGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGC

4701 TAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTAATCGTAACTAACATACGCTC
 PacI (4703) SwaI (4712) EagI (4723) NotI (4722)

4801 TCCATCAAACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA