



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGC
PvuII (239)
301 GCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
Bsu36I (291)

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **SphI (560)**
501 TCTGTTCTGCCGCTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTGAGTGCCTGGGGTCCAGGAGTCTCCAAGCTCTGCCTGC
1► M P G G P G V L Q A L P A
601 CACCATCTTCTCTCTCTCTGCTGTCTGCTGTCTACCTGGCCCTGGGTGCCAGGCCCTGTGGATGCACAAGTCCAGCATCATTGATGGTGAAGCTG
13► T I F L L F L L S A V Y L G P G C Q A L W M H K V P A S L M V S L

BbsI (703) **DraIII (753)** **BbrPI (783)**
701 GGGGAAGACGCCCACTTCCAATGCCCGACAATAGCAGCAACAACGCCAACGTACCTGGTGGCGCTCCTCCATGGCAACTACACGTGGCCCCCTGAGT
47► G E D A H F Q C P H N S S N N A N V T W W R V L H G N Y T W P P E

XmaI (807) **SrfI (806)**
801 TCTTGGGCGCGGAGGACCCCAATGGTACGCTGATCATCCAGAATGTGAACAAGAGCCATGGGGGCATATACGTGTGCCGGTCCAGGAGGCAACGA
80► F L G P G E D P N G T L I I Q N V N K S H G G I Y V C R V Q E G N E

XcmI (950)
901 GTCATACCAGCAGTCTGCGGCACCTACCTCCGCTGCGCCAGCCGCCAGGCCCTTCTGGACATGGGGGAGGGACCAAGAACCGAATCATCACA
113► S Y Q Q S C G T Y L R V R Q P P P R P F L D M G E G T K N R I I T
1001 GCCGAGGGGATCATCCTCCTGTTCTGCGCGGTGGTGCCTGGGACGCTGCTGCTTTCAGGAAACGATGGCAGAACGAGAAGCTCGGGTTGGATGCCGGGG
147► A E G I I L L F C A V V P G T L L L F R K R W Q N E K L G L D A G

StuI (1128) **XmaI (1169)**
1101 ATGAATATGAAGATGAAAACCTTTATGAAGGCCTGAACCTGGACGACTGCTCCATGTATGAGGACATCTCCGGGGCTCCAGGGCACCTACCAGGATGT
180► D E Y E D E N L Y E G L N L D D C S M Y E D I S R G L Q G T Y Q D V

MscI (1259)
1201 GGGCAGCCTCAACATAGGAGATGTCCAGCTGGAGAAGCCGTGACACCCTACTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAA
213► G S L N I G D V Q L E K P •

HpaI (1391)
1301 CACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA

MfeI (1402) **EcoRI (1487)**
1401 AACCAATTGCATTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCATAAATA
1501 CAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCAT

SapI (1669)
1601 TAGCTGTTTCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTGTGAAGTACTAGCTCTTCATTTCTTTATGTTTTAAATGCAT

SspI (1726) **SwaI (1740)**
1701 GACCTCCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTC
1801 AAGGCCCTCATAATATCCCCAGTTTGTAGTGTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAG
1901 TTCCTGGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGA
139► 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 P A Y D S I

SacI (2001) **BstXI (2030)**
2001 TGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTT
106► 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

StuI (2165)
2101 CTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCA
73► 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 S I I E G
2201 GTCTTGGTCTGATGGCCGCCGACATGGTGTCTGTTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAG
39► 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 E L D Q Q S

BbsI (2311) **XmnI (2307)** **AseI (2373)**
2301 AGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGC
6► I N F T K M

2401 GTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTT
 SacI (2430)

2501 ACGACATTTTGGAAAGTCCCCTTGATTTACTAGTCAAAAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTAT
 SpeI (2528)

2601 CCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGT
 SnaBI (2656)

2701 ACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTA
 NdeI (2761)

2801 CCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTGGGGC

2901 GGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAA
 PacI (2947)
 PstI (2940)
 SdaI (2939)
 BspLU11I (2957)

3001 GGCCGCTTGTGCGGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA
 BspLU11I (2957)

3101 AGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCG

3201 TGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCG
 ApaLI (3271)

3301 CTGCGCTTATCCGGTAACTATCGTCTTGAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG

3401 TATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT

3501 TCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGG

3601 ATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTT
 PacI (3687) SwaI (3696)

3701 AAATCAGCGGCGCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAC
 EagI (3707)
 NotI (3706)

3801 GAAACAAAACAACTAGCAAAATAGGCTGTCCCGAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA