



PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGTGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
 EcoNI (287)
 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

XcmI (560)
 NcoI (560)
 BstEII (555)
AgeI (552)
 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGAGTCTGTGGAGCCCCGGTCAAAGACGGCATCCT
 1 M E S V E P P V K D G I L

BstAPI (623)
 601 CTACCAGCAGCAGTAAAGTTTGGCAAGAAATGCTGGCGCAAAGTGTGGGCTCTGCTGTATGCGGGAGGCCATCAGGGGTAGCTCGGCTAGAAAAGCTGG
 13 Y Q Q H V K F G K K C W R K V W A L L Y A G G P S G V A R L E S W
 701 GACGTGCGTGTGGTGGCCTGGGACCAGCAGGCAGGTCACAGGCCAGCCGTCGAGGGGAACGCCGGTACATCGCTTGGCTGACTGTGTATCTG
 47 D V R D G G L G P A G D R S T G P S R R G E R R V I R L A D C V S
 801 TCCTGCTGCGGATGGGAGAGCTGTCCAGGGACACTGGTGCCTTCTGATTACCACACTGAGCGAAGCCACTGTTGGCTGCACAGCACCGCCAGTC
 80 V L P A D G E S C P R D T G A F L I T T T E R S H L L A A Q H R Q S

Acc65I (934)
 XcmI (911) XmaI (930) NcoI (995)
 901 CTGGGTGGACCCCATCTGTCAGCTGGCCTTCCCGGTTACCGGAGAATGTTGTCAGGATCAGGACAGGCTGAGAGTCCAAAAGGGGCTTTGTTCCCATG
 113 W V D P I C Q L A F P G T G E C S S G S G Q A E S P K R G F V P M
 1001 GAGGAAAACCTCTATCTACTCCTCCTGGCAGGAAGTGACCGAGTTTCCGGTGATCGTGACAGAGGACAGAGGCCACTCCCGCTGCCAGCTGAAAGGACCCT
 147 E E N S I Y S S W Q E V T E F P V I V Q R T E A T S R C Q L K G P

StuI (1154) **FspI (1184)**
 1101 ACCTCCTGGTGTGGCCAAAGTGCATCCAAGTGAAGGAGACATCCAAGCCCCAGGCTGTTTTAGCTGGCCCTACCGTTTCTGCGCAAGTACGGCTC
 180 Y L L V L G Q D D I Q L R E T S K P Q A C F S W P Y R F L R K Y G S

NdeI (1287)
 1201 TGACAAGGGTGTGTTCTCGTTTGAAGCTGGCCGCGCTGTGACTCAGGTGAGGCCTTTTTCCTTTCAGTAGCCCGCTGCCAGACATATGTGGGGTT
 213 D K G V F S F E A G R R C D S G E G L F A F S S P R A P D I C G V

BbsI (1331) MscI (1343)
 1301 GTGGCTGCCGCCATTGCCCGCCAGCGGGAGCGTCTTCCAGAGCTGGCCATGTCCCCACCTGCCCCCTGCCTCGGGCCCTCCTCCTGCCCTCCCTAGAGC
 247 V A A A I A R Q R E R L P E L A M S P P C P L P R A L S L P S L E

XmaI (1471)
 1401 CCCCTGGAGAGCTTCGGGAGGTGGCCCCAGGATTTGAGCTGCCACTCCAGAAAAGTGCCTCTAACTGATCCCGGCCCTCAAAGCCTACCACTGCTGCT
 280 P P G E L R E V A P G F E L P T P R K L P L T D P G P Q S L P L L L
 1501 CAGCCCCACACAAGAAGGACCGCATCCGGTCTCTATGCGTCCGTGTGCAAGCAGACCAGCAAGCACACAGGCACGGCGGAGCATCTCTATGAGAAGCTG
 313 S P T Q E G P A S G L Y A S V C K Q T S K H T G T A E H L Y E N V

SphI (1601)
 1601 TGCATGCTGGAGGCCAGCCCTGGGCTGACCAATGGGGTCTGAAGCCAAAGAGGGCCCCCTGGTGGCCGAGCCCCCTGGGACGCCCTATCTACCATA
 347 C M L E A S P G L T N G G P E A Q E G P P G G R S P L G S P I Y H

NgoMIV (1798)
 1701 ACACTGAGGATCTGAGTTGGCCGGGCTCGGCCAGGACAGCAATCTGGAAGCCAGTACCGGAGGCTGCTGAACTGGAGCTGGATGAGCGCGGAAGCGC
 380 N T E D L S W P G S A Q D S N L E A Q Y R R L L E L E L D E A G S A

BsrBI (1803)
 EagI (1800) BstEII (1839) **NheI (1899)**
 1801 CGGCCGCTCTGGAGCGCAGGCAGGCATCAAGGCCAAGCTGGTACCCTGCTGACCCGTGAACGGAAGAAGGGCCCCGCCCTGTGACCGGCCCTGAAGG
 413 G R S G A Q A G I K A K L V T L L T R E R K K G P A P C D R P •

MscI (1905)
 1901 CTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAAGTGCAGTGAAGAAAAATGCTTTATTTGTGAAATTTGTGATGCTAT

HpaI (2037) MfeI (2048)
 2001 TGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTT

EcoRI (2133)
 2101 TAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCTAAATACAGCATAGCAAACTTTAACTCAAATCAAGCCTCTACTTGAATCCTTTTCTG
 2201 AGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTT

SapI (2315) **SspI (2372)** SmaI (2386)
 2301 CCAAGTTTGAAGTAGCTCTTCAATTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTATGATAAATATTCAAATAATTAAATACATCA
 2401 TTGCAATGAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAA

2501 CCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTG
141 • N R T Y K L P I L E E I T T K V L K
SacI (2647) BstXI (2676)
2601 CCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCT
121 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 I S R D V E
2701 CATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGAC
88 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 A C V T V
StuI (2811)
2801 CCGCCAATGTAGGCCTCAATGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATAGAGCATG
55 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 D E Y L M
BbsI (2957)
2901 GTGATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCTGCTGAGAGATGTTGAAGGTCCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATG
21 T I K E T A V E V L E L D Q Q S I N F T K M
XmnI (2953)
3001 CCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCC
AseI (3019) SacI (3076)
3101 ACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGAC
SpeI (3174)
3201 GTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACT
SnaBI (3302)
3301 AATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGTGCATGTAAGTGGGCATAATGCCAGGCGGGCCATTTACCGTATTGACGTCAATAGGGGGCG
NdeI (3407)
3401 TACTTGGCATATGATACACTTGATGTAAGTGGCAGTTTACCGTAAACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTAT
PacI (3593)
3501 GGGACATACGTCAATTATTGACGTCAATGGGGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAAGCCTGCAGGTTAATTA
PstI (3586)
SdaI (3585)
3601 AGAACATGTGAGCAAAAGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAA
BspLU11I (3603)
3701 AAATCGACGCTCAAGTCAAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCTGGAAGTCCCTCGTGGCTCTCCTGTTCCGACC
3801 CTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT
ApaLI (3917)
3901 GCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTT
4001 ATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACT
4101 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCG
4201 GTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGA
EagI (4353)
4301 AAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTGGTT
PacI (4333) SwaI (4342) NotI (4352)
4401 TTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAG
4501 AACATTTCTCTATCGAA