



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)

101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTATGTCGTGACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACACGCCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCCGCTTAGGTAAGTTTAAAGCTCAGGTCGAGACC
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (566)
BspEI (558) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGCTCCGGACACCATGGCGGCTGCGCTGTTCTGCTGCTGGGATT
▶
1▶ M A A A L F V L L G F

601 CGCGCTGCTGGGCACCCACGGAGCCTCCGGGGCTGCCGGCACAGTCTTCACTACCGTAGAAGACCTTGGCTCCAAGATACTCCTCACCTGCTCCTGAAT
 11▶ A L L G T H G A S G A A G T V F T T V E D L G S K I L L T C S L N
 701 GACAGCGCCACAGAGTACAGGGCACCCTGGCTGAAGGGGGCGTGGTGTGAAGGAGGACGCGCTGCCCGCCAGAAAACGGAGTTCAAGGTGGACT
 45▶ D S A T E V T G H R W L K G G V V L K E D A L P G Q K T E F K V D

ScaI (818)
NcoI (845)
 801 CCGACGACAGTGGGGAGTACTCCTGCGTCTTCTCCCGAGCCATGGGCACCGCAACATCCAGCTCCACGGGCTCCAGAGTGAAGGCTGTGAA
 78▶ S D D Q W G E Y S C V F L P E P M G G T A N I Q L H G P P R V K A V K
 901 GTCGTGAGAACACATCAACGAGGGGAGACGGCCATGCTGGTCTGCAAGTCAAGTCCGTGCCACCTGCTACTGACTGGGCTGGTACAAGATCACTGAC
 111▶ S S E H I N E G E T A M L V C K S E S V P P V T D W A W Y K I T D

BspHI (1016)
EcoO109I (1010) 1001 TCTGAGGACAAGGCCCTCATGAACGGCTCCGAGAGCAGTTCTTCGTGAGTTCCTCGAGGGCCGGTCAGAGCTACACATTGAGAACCTGAACATGGAGG
 145▶ S E D K A L M N G S E S R F F V S S S Q G R S E L H I E N L N M E

AgeI (1115)
FspI (1172)
 1101 CCGACCCCGCCAGTACCGGTGCAACGGCACCAGCTCAAGGGCTCCGACCAGGCCATCATCACGCTCCGCGTGCAGCCACCTGGCCGCCCTTGCC
 178▶ A D P G Q Y R C N G T S S K G S D Q A I I T L R V R S H L A A L W P

BstEII (1233)
 1201 CTTCTGGGCATCGTGGCTGAGGTGCTGGTACCATCATCTTACGAGAAGCGCCGGAAGCCGAGGACGCTCCTGGATGATGACGACGCC
 211▶ F L G I V A E V L V L V T I I F I Y E K R R K P E D V L D D D A

SapI (1314)
Bsu36I (1373)
NheI (1396)
 1301 GGCTCTGCACCCCTGAAGAGCAGCGGGCAGCACCAGAATGACAAAGGCAAGAAGCTCCGCCAGAGAACTCTTCTGAGGCAGGTGGCCCGAGGACGCTA
 245▶ G S A P L K S S G Q H Q N D K G K N V R Q R N S S •

MscI (1402) 1401 GCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAAGTGAAGGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGC

HpaI (1534)
MfeI (1545)
 1501 TTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAACAACAATTGCATTCTTTATGTTTCAGGTTGAGGGGAGGTGTTGGAGGTTTTTTAA

EcoRI (1630)
 1601 AGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGG
▶
◀

1701 GATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCA

SapI (1812)
SspI (1869)
Swal (1883)
 1801 AGGTTTGAAGTACTCTTCTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTATGAAAATATTGAGAAATAATTTAAATACATCATTG

EcoO109I (1944)
 1901 CAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCT

2001 TTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCCA
141▶ • N R T Y K L P I L E E I T T K V L K G

SacI (2144)
BstXI (2173)
 2101 TTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCAT
 120▶ 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 D
 2201 CAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCAGACAGCAGTGACCT
 87▶ 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 R

StuI (2308) 2301 GCCAATGTAGGCCTCAATGTGGACAGCAGATGATCTCCCGCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTTGCTCATAGAGCATGGTG
 54▶ 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 T

2401 ATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCG
20 I K E T A V E V L E L D Q Q S I N F T K M ←

XmnI (2450)

2501 ATATACTATGCCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACC
←

AseI (2516) **SacI (2573)**

2601 GTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCC GTT GATTTACTAGTCAAACAAACTCCCATTGACGTC
←

SpeI (2671)

2701 AATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAAT
←

SnaBI (2799)

2801 ACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTAC
←

NdeI (2904)

2901 TTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGG
←

PacI (3090)

3001 AACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAG
←

PstI (3083)
SdaI (3082)

3101 ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAA
←

BspLU11I (3100)

3201 TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTG
←

3301 CCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCT
←

ApaLI (3414)

3401 CCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC
←

3501 GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGA
←

3601 AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG
←

3701 GTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAA
←

EagI (3850)

3801 CTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTT
←

PacI (3830) **SwaI (3839)** **NotI (3849)**

3901 TGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAAC
4001 ATTTCTCTATCGAA