



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCCGCCGCCCTACCTGAGGCC
PvuII (239)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
Bsu36I (291)

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCCCTACCTGAGATCACCGGTCACCATGGGCTGTGATCGAACTGTGGGCTCATTGCTGGAGC
601 TGTATTGGTGCAGTCTGGCTGTGTTGGAGGCATTCTATGCCAGTCCGAGACATGCTTATTGAGAAGACAATAAAAGGGAAGTTGCTCTGAAGAA
1 M G C D R N C G L I A G A
13 V I G A V L A V F G G I L M P V G D M L I E K T I K R E V V L E E
701 GAAACCACTGCTTTCAAAAAGTGGTTAAAACAGGCACCCTGTGTACAGACAGTTTTGGATCTTTGATGTGCAAAACCCAGATGACGTGGCAAAGAACA
47 G T T A F K N W V K T G T T V Y R Q F W I F D V Q N P D D V A K N
801 GCAGCAAAATCAAGGTTAAACAAAGAGGTCCTTACACATACAGAGTTCGTTATCTAGCCAAGGAAAATATAACTCAGGACCCCGAGGACCACACTGTGC
80 S S K I K V K Q R G P Y T Y R V R Y L A K E N I T Q D P E D H T V S
DraIII (889)
901 TTTTGTACAGCCCAATGGAGCCATCTTTGAGCCTTCACTGTCTGTTGGAACAGAGGATGACAACTTACAGTTCTGAATCTGGCTGTAGCAGCTGCACCA
113 F V Q P N G A I F E P S L S V G T E D D N F T V L N L A V A A A P
PvuII (989)

BglIII (1078)
1001 CATATCTACAAAATTCATTTGTTCAAGTTGTGCTCAACTCTTATAAAAAAGTCCAAGTCTTCTATGTTCCAAACAAGATCTTTGAAAGAAGCTTTGT
147 H I Y Q N S F V Q V V L N S L I K K S K S S M F Q T R S L K E L L
1101 GGGTTACAAAGATCCATTCCTCAGTTTGGTTCCATATCCTATAAGTACCACAGTTGGTGTGTTTTATCCTTACAATGACACTGTAGATGGAGTTTATAA
180 W G Y K D P F L S L V P Y P I S T T V G V F Y P Y N D T V D G V Y K

MscI (1276) 1201 AGTTTTCAATGAAAAGGATAACATAAGCAAAGTTGCCATAATTGAGTCCATAAAGGGAAAAGGAATTTGTCCTATTGGCCAAGCTATTGCGACATGATT
213 V F N G K D N I S K V A I I E S Y K G K R N L S Y W P S Y C D M I
AseI (1297)
1301 AATGGCACAGACGCGCCCTCTTCCACCTTTTGTGAAAAGTCTCGGACATTGAGATTCTTTTCTCTGACATTTGCAGGTCTATCTACGCTGTGTTG
247 N G T D A A S F P P F V E K S R T L R F F S S D I C R S I Y A V F
1401 GATCTGAAATCGACCTTAAAGGAATCCCGTGTACAGATTTGTTCTTCCAGCAATGCCTTTGCATCACCCCTCCAGAATCCAGACAACCATTGTTTCTG
280 G S E I D L K G I P V Y R F V L P A N A F A S P L Q N P D N H C F C
1501 CACTGAAAAGTAATCTCCAATAACTGTACATCTTATGGTGTGCTAGACATTGGCAAATGCAAAGAAGGAAAGCTGTGTATATTCCGTTCCACATTT
313 T E K V I S N N C T S Y G V L D I G K C K E G K P V Y I S L P H F
1601 CTACATGCAAGTCCAGATGTTTTCAGAACCATTGAAGCTTACATCCAATGAAGATGAGCATAGGACATACTTAGATGTGGAACCCATAACTGGATTC
347 L H A S P D V S E P I E G L H P N E D E H R T Y L D V E P I T G F

PstI (1720) 1701 CTCTACAATTTGCAAAACGACTGCGAGTCAACATATTGGTCAAGCCAGCTAGAAAAATAGAAGCATTAAAGAATCTGAAGAGACCTTACATTGTACCTAT
380 T L Q F A K R L Q V N I L V K P A R K I E A L K N L K R P Y I V P I
1801 ACTGTGGCTAAATGAGACTGGGACCTTGGTGATGAAAAGCAGAAATGTTCAAAAACCAAGTACTGGGAAAATCAAGCTCCTTGGCATGGTAGAGATG
413 L W L N E T G T I G D E K A E M F K T Q V T G K I K L L G M V E M
NheI (1996)

MscI (2002) 1901 GCCTTACTTGGGATTGGAGTGGTGTGTTTGTGCTTTTATGATTTTATATTGTGCTTGCAAATCCAAGAATGGAAAATAAGTAGTGGATGAGCCTGCTA
447 A L L G I G V V M F V A F M I S Y C A C K S K N G K •

2001 GCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAAGTGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGC

HpaI (2134) 2101 TTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATAATTGCATCTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTAA
MfeI (2145)

EcoRI (2230) 2201 AGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGG
2301 GATGAATAAGGCATAGGCATCAGGGGCTTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATATAGTATTTTCCCA

SapI (2412) 2401 AGGTTTGAAGTACTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTGAGAAATAATTTAAATACATCATTG
SspI (2469) 2501 CAATGAAAATAAATGTTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCT
Swal (2483)
2601 TTAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCA
1+1 N R T Y K L P I L E E I T T K V L K G
SacI (2744) 2701 TTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCAT
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
BstXI (2773)

2801 CAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCT
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 (2908)

2901 GCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTG
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
XmnI (3050)

3001 ATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCG
20 I K E T A V E V L E L D Q Q S I N F T K M
AseI (3116) SacI (3173)

3101 ATATACTATGCCGATGATTAATTGTCAAACACAGCTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACC
SpeI (3271)

3201 GTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTACTAGTCAAAAACAACTCCCATTGACGTC
SnaBI

3301 AATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAAT
3401 ACGTAGATGTACTGCCAAGTAGGAAAGTCCCAT AAGGT CATGTACTGGGCATAATGCCAGGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTAC
NdeI (3504)

3501 TTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGG
PacI (3690)
PstI (3683)
SdaI (3682)

3601 AACATACGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGT CAGCCAGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGA
BspLU11I (3700)

3701 ACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAA
3801 TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCCTG
3901 CCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGGTAGGTCGTTCCGCT
ApaLI (4014)

4001 CCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC
4101 GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGA
4201 AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG
4301 GTTTTTTTGTGGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAA
EagI (4450)
PacI (4430) SwaI (4439) NotI (4449)

4401 CTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTT
4501 TGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAAC
4601 ATTTCTCTATCGAA