



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGGC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCCATGGGTCGGGGGCTGCTCAGGGGCTGTGGCCGCTGCA
NcoI (560)
1 M G R G L L R G L W P L H

MluI (613)
601 CATCGTCTGTGGACGCGTATCGCCAGCACGATCCCACCGCACGTTTCAAGTTCGTTAATAACGACATGATAGTCACTGACAACAACGGTGCAGTCAAG
13 I V L W T R I A S T I P P H V Q K S V N N D M I V T D N N G A V K
PstI (771)
701 TTTCCACAACGTGTAAATTTGTGATGTGAGATTTTCCACCTGTGACAACAGAAATCCTGCATGAGCAACTGCAGCATCACCTCCATCTGTGAGAAGC
47 F P Q L C K F C D V R F S T C D N Q K S C M S N C S I T S I C E K
801 CACAGGAAGTCTGTGGCTGTATGGAGAAAGTACGAGAAACATAACACTAGAGACAGTTTCCATGACCCCAAGCTCCCTACCATGACTTTATTCT
80 P Q E V C V A V W R K N D E N I T L E T V C H D P K L P Y H D F I L
901 GGAAGATGCTGCTTCCAAAGTGCATTATGAAGGAAAAAAAAAGCCTGGTGAAGTCTTCTCATGTGTTCTGTAGCTCTGATGAGTGAATGACAAC
113 E D A A S P K C I M K E K K K P G E T F F M C S C S S D E C N D N
1001 ATCATCTTCTCAGAAGAATATAACACCAGCAATCCTGACTTGTGCTAGTCAATTTCAAGTGACAGGCATCAGCCTCCTGCCACCACTGGGAGTTGCCA
147 I I F S E E Y N T S N P D L L L V I F Q V T G I S L L P P L G V A

HpaI (1132)
1101 TATCTGTCATCATCATCTTCTACTGCTACCGGTTAACCGGCAGCAGAAGCTGAGTTCAACCTGGGAAACCGCAAGACGCGGAAGCTCATGGAGTTCAG
180 I S V I I I F Y C Y R V N R Q Q K L S S T W E T G K T R K L M E F S

BsrBI (1230) 1201 CGAGCACTGTGCCATCATCCTGGAAGATGACCGCTCTGACATCAGCTCCACGTGTGCCAACACATCAACCACAACACAGAGCTGCTGCCATTGAGCTG
BbrPI (1248)
213 E H C A I I L E D D R S D I S S T C A N N I N H N T E L L P I E L

BglII (1391)
1301 GACACCCTGGTGGGAAAGTTCGCTTTGCTGAGGTCTATAAGGCCAAGCTGAAGCAGAACACTTCAGAGCAGTTTGAAGCAGTGGCAGTCAAGATCTTTT
247 D T L V G K G R F A E V Y K A K L K Q N T S E Q F E T V A V K I F

BsrBI (1495)
1401 CCTATGAGGAGTATGCCTCTTGAAGACAGAGAAGGACATCTTCTCAGACATCAATCTGAAGCATGAGAACATACTCCAGTTCCTGACGGCTGAGGAGCG
280 P Y E E Y A S W K T E K D I F S D I N L K H E N I L Q F L T A E E R

PvuII (1587)
1501 GAAGACGGAGTTGGGAAACAATACTGGCTGATCACCGCTTCCACGCCAAGGGCAACCTACAGGAGTACCTGACGCGCATGTCATCAGCTGGGAGGAC
313 K T E L G K Q Y W L I T A F H A K G N L Q E Y L T R H V I S W E D

FspI (1601) 1601 CTGCGCAAGCTGGGCAGCTCCCTCGCCCGGGGATTGCTCACCTCCACAGTATCACACTCCATGTGGGAGGCCAAGATGCCCATCTGCACAGGGACC
XmaI (1625)
347 L R K L G S S L A R G I A H L H S D H T P C G R P K M P I V H R D
BsaBI (1677) 1701 TCAAGAGCTCAATATCCTCGTGAAGAACGACCTAACCTGCTGCTGCTGACTTTGGGCTTCCCTGCGTCTGGACCCTACTCTGTCTGTGGATGACCT
ApaLI (1687)
380 L K S S N I L V K N D L T C C L C D F G L S L R L D P T L S V D D L

XcmI (1856) 1801 GGCTAACAGTGGGAGGTGGAACTGCAAGATACATGGCTCCAGAAGTCTAGAAATCCAGGATGAATTTGGAGAATGTTGAGTCTTCAAGCAGACCGAT
PshAI (1893)
413 A N S G Q V G T A R Y M A P E V L E S R M N L E N V E S F K Q T D

NcoI (1907)
1901 GTCTACTCCATGGCTCTGGTCTGGGAAATGACATCTCGTGAATGCAGTGGGAGAAGTAAAAGATTATGAGCCTCCATTTGGTCCAAGGTGCGGG
447 V Y S M A L V L W E M T S R C N A V G E V K D Y E P P F G S K V R
2001 AGCACCCCTGTGTCGAAAGCATGAAGGACAACGTGTTGAGAGATCGAGGGCGACCAGAAATCCAGCTTCTGGCTCAACCACCAGGGCATCCAGATGGT
480 E H P C V E S M K D N V L R D R G R P E I P S F W L N H Q G I Q M V
2101 GTGTGAGACGTTGACTGAGTGTGGGACCACGACCCAGAGGCCGCTCACAGCCAGTGTGTGGCAGAACGCTTCAAGTGGAGCATCTGGACAGG
513 C E T L T E C W D H D P E A R L T A Q C V A E R F S E L E H L D R

MscI (2291)
2201 CTCTCGGGAGGAGCTGCTCGGAGGAGAAGATTCTGAAGACGGCTCCCTAAACACTACCAAAATAGCTCTTCTGGGGCAGGCTGGGCTAGCTGGCCAGAC
SapI (2265)
547 L S G R S C S E E K I P E D G S L N T T K •
NheI (2285)

2301 ATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAA

HpaI (2423) MfeI (2434)
 2401 CCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTCAATTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAA

EcoRI (2519)
 2501 CCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGG
 2601 CATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGGTTTGAAC

SapI (2701) SspI (2758) SwaI (2772)
 2701 AGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATA
 2801 AATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAAAT
 2901 TGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTTCATCTCAAT
 141 • N R T Y K L P I L E E I T T K V L K G N M E I
 3001 GAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGG
 117 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 S Y P
 3101 TGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCTGCTCACAGCAGACCCAAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGG
 83 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 G I Y A
 3201 CCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGT
 50 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 I K E T
 3301 GCGCACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGC
 17 A V E V L E L D Q Q S I N F T K M
 XmnI (3339)
 3401 CGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTA
 AseI (3405)

SpeI (3560)
 3501 CCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGA
 3601 GACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA
 SnaBI (3688)
 3701 CTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGA
 NdeI (3793)
 3801 TACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCA

PacI (3979) PstI (3972) SdaI (3971) BspLU11I (3989)
 3901 TTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCA
 4001 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAAATCGACGCTCAA
 4101 GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGG
 4201 ATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGC
 4301 TGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAG
 4401 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATT
 4501 TGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGT
 4601 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAG

ApaLI (4303) EagI (4739) PacI (4719) SwaI (4728) NotI (4738)
 4701 GGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGTTTTTGTGTGAATCG
 4801 TAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATC
 4901 GAA