



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTCAACTCTACGCTTTTGTTCGTTT

MluI (558)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGCACGCGTCACCATGGATGTGTGCGCCGCTTGCCTGTGGCT

1 M D V C A R L A L W L
NheI (667)
601 TCTTTGGGGCTCCTTCTGCATCAGGGCCAGAGTCTCAGCCATAGTACAGTGAAGAATAACAGGAGCTAGCTCCGGGGCGACTTCTGAAGAGTCTACC

11 L W G L L L H Q G Q S L S H S H S E K N T G A S S G A T S E E S T
701 GAAGCAGAGTTTTGCCGAATTGACAAGCCCCTGTGCCACAGTGAAGTGAAGCTCAGCTTTGAGGCCGTCGAAACATCCATAAGCTGATGGATGACG

45 E A E F C R I D K P L C H S E D E K L S F E A V R N I H K L M D D
XcmI (803)
801 ATGCCAATGGTGATGTGGATGTGGAAGAAAGTATGAGTTCCTAAGGGAAGACCTCAATTACCATGACCCAACAGTGAACATAGCACCTTCCATGGTGA

78 D A N G D V D V E E S D E F L R E D L N Y H D P T V K H S T F H G E
HindIII (904) **BsrGI (953)** **SnaBI (993)**
901 GGATAAGCTTATCAGCGTGGAGGACCTGTGGAAGGCGTGAAATCATCAGAAGTGTACAAGTGGAGTGTGGATGAGGTGATACAGTGGCTCATTACGTAT

111 D K L I S V E D L W K A W K S S E V Y N W T V D E V I Q W L I T Y
BspEI (1028) **NheI (1065)**
1001 GTGGAGCTGCCACAGTATGAGGAGACCTTCCGGAAGTTGCAGCTTACTGGCCACGCCATGCCAAGGCTAGCAGTAACCAACACCACCATGACAGGGACTG

145 V E L P Q Y E E T F R K L Q L T G H A M P R L A V T N T T M T G T
1101 TACTGAAGATGACAGATCGGAGCCACAGGCAGAAGCTGCAGCTGAAGGCCCTGGACACAGTGTGTTGGCCCTCCTCTTACTGCGCATAATCACCT

178 V L K M T D R S H R Q K L Q L K A L D T V L F G P P L L T R H N H L
XmnI (1200)
1201 GAAGGACTTCATGCTGGTGTCTATCGTTATTGGTGTGGTGGCTGCTGGTTTGCCTATATCCAGAACCGTTACTTAAGGAGCACATGAAGAAAATG

211 K D F M L V V S I V I G V G G C W F A Y I Q N R Y S K E H M K K M
1301 ATGAAGATCTGGAAGGTTACACCGGCTGAGCAGAGTCTGCATGACCTTCAGGAAAGCTGCACAAGGCCAGGAGGAGCACCGAATGTGGAAGTAG

245 M K D L E G L H R A E Q S L H D L Q E R L H K A Q E E H R T V E V
1401 AGAAAAGTCCACCTGGAGAAGAAGCTGCGAGATGAGATCAACCTTGCCAAAGCAGGAAGCTCAGCGGCTGAAGGAGCTGAGGGAGGGTACTGAGAATGAGAG

278 E K V H L E K K L R D E I N L A K Q E A Q R L K E L R E G T E N E R
StuI (1544)
1501 GAGCCGTCAAAAATATGCTGAGGAAGAGCTGGAGCAGGTTCCGGAGGCCCTGAGGAAAGCAGAGAAGGAGCTGGAATCACACAGCTCATGGTATGCTCCT

311 S R Q K Y A E E E L E Q V R E A L R K A E K E L E S H S S W Y A P
ScaI (1646)
1601 GAGGCCCTGCAGAAGTGGCTGCAGTGAACCATGAGGTGGAGGTGCAGTACTACAACATCAAGAAGCAAAAATGCAGAGAGGCAGTGTGGTGGCCAAGG

345 E A L Q K W L Q L T H E V E V Q Y Y N I K K Q N A E R Q L L V A K
Acc65I (1741)
1701 AGGGGGCTGAGAAAATAAAAAAGAAGAGAAACACGCTTTTTGGTACCTTCCATGTGGCCACAGCTTCCCTGGATGATGTGGATCATAAAATCCTAAC

378 E G A E K I K K K R N T L F G T F H V A H S S S L D D V D H K I L T
AgeI (1850) **SgrAI (1849)**
1801 TGCTAAGCAAGCTCTGAGTGAAGTGACAGCGGCACTGAGGGAGCGCTGCACCGGTGGCAGCAGATCGAGATCCTCTGCGGTTCCAGATTGTCAATAAC

411 A K Q A L S E V T A A L R E R L H R W Q Q I E I L C G F Q I V N N
BspHI (1982)
1901 CCCGGCATCCACTCCTTGGTGGCTGCTCTCAACATCGACCCAGCTGGATGGCAGCACCCGCTAACCCCGCCACTTCATCATGACTGACGATGTGG

445 P G I H S L V A A L N I D P S W M G S T R P N P A H F I M T D D V
2001 ATGACATGGATGAGGAGATTGTGTCGCCCTTGTCCATGCAGTCCCCAGCTGCAGAGCAGTGTCCGGCAGCGCTGACGGAGCCACAGCTTGGCCTGGG

478 D D M D E E I V S P L S M Q S P S L Q S S V R Q R L T E P Q L G L G
2101 ATCTCAGAGGATTTGACCCATTCCGATTCCGAGTCTCCCTCCACATGAGTGACCGCCAGCGTGTGGCCCCAAGCCTCCTCAGATGGGCGGTGCTGCA

511 S Q R D L T H S D S E S S L H M S D R Q R V A P K P P Q M G R A A
2201 GATGAAGCTCTCAATGCCATGCCTTCAATGGCAGCCATCGGCTGATTGAGGGGTCCATCCAGGATCTCTGGTGGAGAAACTGCCTGACAGCCCTGCTC

545 D E A L N A M P S N G S H R L I E G V H P G S L V E K L P D S P A
DraIII (2378)
2301 TGGCAAGAAGACATTTATGGCGTTGAACCATGGCCTAGACAAGGCCACAGCCTGATGGAGCTGAACCCCTCAGTCCCACCTGGTGGCTCCCCACTTTT

578 L A K K T F M A L N H G L D K A H S L M E L N P S V P P G G S P L L
EcoRI (2495)
2401 GGATTCTTCCATTCTCTTAGCCCCAGTCCCCAGACCCAGACACACCATCTCCAGTTGGGGACAACCGAGCTCTGCAGGGTAGCCGAAACACACGAATT

611 D S S H S L S P S S P D P D T P S P V G D N R A L Q G S R N T R I

PshAI (2563)
 2501 CCCCACTTGGCTGGCAAGAAGGCAATGGCTGAGGAGGATAATGGTTCCATTGGTGAGGAGACAGACTCCAGTCCAGGCAGGAAGAAGTTTCCTCTCAAAA
 645▶ P H L A G K K A M A E E D N G S I G E E T D S S P G R K K F P L K

AvrII (2658)
 2601 TTTTAAAGAAGCCTCTTAAAGAAGTAGGCAGACTAGGGTGGTAGTGTGAGACAGCCTGCCTAGGACTAGCTGGCCAGACATGATAAGATACATTGATGAG
 678▶ I F K K P L K K •

2701 TTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAC

HpaI (2802) **MfeI (2813)** **EcoRI (2898)**
 2801 AAGTTAACAAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGA
 2901 ATTCTAAAATACAGCATAGCAAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTG
 3001 CCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATATAGTGATTTTTCCCAAGTTTGAAGCTAGCTCTTCATTTCTTTATGTT

SspI (3137) **SwaI (3151)**
 3101 TTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAA
 3201 TCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCT
 3301 TCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGC
 —141◀ • 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
 3401 ATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCAGAGTAGGGGTGCCTGACAGCCACAATGGTG
 110◀ 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 H R V A V I T

StuI (3576)
 3501 TCAAAGTCCCTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGA
 76◀ 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 E I H V A S I
 3601 TGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAG
 43◀ 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 A V E V L E L

XmnI (3718) **AseI (3784)**
 3701 ATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACA
 10◀ D Q Q S I N F T K M ◀
 3801 GCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGG

SpeI (3939)
 3901 GCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGT

SnaBI (4067)
 4001 CAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCA

NdeI (4172)
 4101 TAAGTCACTGACTGGGCATAATGCCAGGCGGGCCATTACCCTGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAG
 4201 TGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATATTGACGTCAATGGGCGGG

PacI (4358) **SdaI (4350)** **BspLU11I (4368)**
 4301 GGTGTTGGGCGTCCAGCAGCGGGCCATTACCCTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGG
 4401 AACCGTAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGA
 4501 CAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCC

ApaLI (4682)
 4601 TTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGCTT
 4701 CAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTA
 4801 GCAGAGCGAGGTATGTAGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA
 4901 GCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACCGCG

PacI (5098)
 5001 AGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTT

EagI (5118)
SwaI (5107) **NotI (5117)**
 5101 AATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCAT
 5201 CAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTATCGAA