



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGGAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)** **BspLU11I (560)**
501 TCTGTTTGTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTTGCTAGTGTGCTGATCTTGGCTGCATCGTGCAG
1 M L L V L L I L A A S C R

XhoI (611) **XcmI (649)**
601 GAGCGCCCTGCCTCGAGAGCCGACTATTCAAGTGTGGCTCTGAGACAGGCGCATCTCCAGAGTGGATGGTCCAACACACACTCACTCCAGGAGACTTGAGG
13▶ S A L P R E P T I Q C G S E T G P S P E W M V Q H T L T P G D L R
701 GACCTCCAAGTGGAACTCGTCAAGACAAGTGTGGCAGCAGAGGAGTTTCAATTTTGATGAACATAAGCTGGATACTCCGGGAGAGCCAGCATCCGCT
47▶ D L Q V E L V K T S V A A E E F S I L M N I S W I L R A D A S I R

BglIII (815) **EcoRI (843)** **StuI (878)**
801 TGTTGAGGCGCCAAAGTCTGCGTGTGGCAAAAACAACATGAATTCATACAGTGTGTGAGGTGCAACTACACAGAGGCTTCCAAAGCCAGACCAG
80▶ L L K A T K I C V S G K N N M N S Y S C V R C N Y T E A F Q S Q T R
901 ACCTTCCGGCGGCAAATGGACATTCTCCTATGTAGGCTTCCCTGTGGAGCTGAGCACTCTCTATCTCATCAGCGCCATAACATCCCCAATGTAATATG
113▶ P S G G K W T F S Y V G F P V E L S T L Y L I S A H N I P N A N M

ApaLI (1077)
1001 AATGAGGACAGCCCTTCTTGTCTGTGAACCTCACCTCGCCAGGCTGCCTAAACCACGTAATGAAATATAAAAAGCAGTGCAGTGGGCGGGAAGCCTGT
147▶ N E D S P S L S V N F T S P G C L N H V M K Y K K Q C T E A G S L

SmaI (1100)
1101 GGGACCCAGACATCACTGCTTGTAAAAAGAACGAGAAGATGGTTGAAGTGAATTTCAACCAATCCCCTTGGAAACAGATACACGATTCTCATTCAACG
180▶ W D P D I T A C K K N E K M V E V N F T T N P L G N R Y T I L I Q R

XbaI (1219)
1201 GGACACGACATTGGGGTTTTCTAGAGTGTGGAGAATAAACTGATGAGGACGCTGTAGCCATCCCGGTGACTGAGGAGAGTGAAGGTGCGGTGGTTGAG
213▶ D T T L G F S R V L E N K L M R T S V A I P V T E E S E G A V V Q
1301 CTGACCCCATATTTACATACCTGCGGCAATGACTGCATCCGACGCGAAGGGACAGTTGTGCTTTGCTCAGAGACAAGTGTCCATCCCTCCAGATGACA
247▶ L T P Y L H T C G N D C I R R E G T V V L C S E T S A P I P P D D

SphI (1406)
1401 ACAGACGATGCTGGGAGGCTGGCTGCCTCTTCTTCTGGTGTGCTGGTGGCTGTGTTGGTGTGGCAGCTGGGATCTACCTAATTGGAGGCAAGGAAG
280▶ N R R M L G G W L P L F L V L L V A V W V L A A G I Y L T W R Q G R
1501 GAGCAGGAAGACGCTCTTCTTCTTCCACCATGCTCCTGCCCTCATTAAGTCTGGTGGTTATCCTTCTGAGATATGTTCCATCACACCGTCTGT
313▶ S T K T S F P I S T M L L P L I K V L V V Y P S E I C F H H T V C

PstI (1626)
1601 CGTTCACTGACTTTCTTCAAACTACTGCAGAAGTGGGTCATCCTTGA AAAATGGCAGAAAAGAAAATCGCCGAGATGGGGCCGGTACAGTGGCTGA
347▶ R F T D F L Q N Y C R S E V I L E K W Q K K K I A E M G P V Q W L

MscI (1776)
1701 CCACTCAGAAGCAAGCGGAGATAAAGTGGTCTTCTTCTTCCAGTGCAGTCCCGACCTTTGTGACAGTGCCTGTGGCCACAATGAGGGCAGCGCCAG
380▶ T T Q K Q A A D K V V F L L P S D V P T L C D S A C G H N E G S A R
1801 GGAGAACTCTCAGGATCTGTTCCCTCTTGCCTTAACTCTTTGTAGTGTATTCAGCAGCCAGCGCATCTGCACAAATACCTGGTGGTCTATCTTGGG
413▶ E N S Q D L F P L A F N L F C S D F S S Q T H L H K Y L V V Y L G

BspHI (1955)
1901 GGAGCAGACCTCAAAGGCGACTATAATGCCTGAGTGTCTGCCCAATATCATCTCATGAAGGACGCCACAGCTTCCACACAGAATTCTCAAGGCTA
447▶ G A D L K G D Y N A L S V C P Q Y H L M K D A T A F H T E L L K A

XmaI (2066) **NheI (2096)**
2001 CGCAGAGCATGTCAGTGAAGAAACGCTCACAAGCCTGCCATGATAGCTGTTACCCCTTGTAGTCCACCCGGGGGAATAGAGACTCTGAAGCCTCCGCTA
480▶ T Q S M S V K K R S Q A C H D S C S P L •

MscI (2102)
2101 GCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAAGTGAAGTGAAGGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGC

HpaI (2234) **MfeI (2245)**
2201 TTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCTATTTATGTTTCAGGTTTTCAGGGGAGGTGTTGGGAGGTTTTTAA

EcoRI (2330)
2301 AGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGG
2401 GATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAAGATATAGTATTTTCCCA

SspI (2569) **SwaI (2583)**
2501 AGGTTTGAAGTACTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTG
2601 CAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCAATATCCCCAGTTAGTGTGGACTTAGGGAACAAAGGAACCT

2701 TTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCA
141 • N R T Y K L P I L E E I T T K V L K G
2801 TTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCAT
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
2901 CAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCT
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
3001 GCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATAGAGCATGGTG
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
3101 ATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCG
20 I K E T A V E V L E L D Q Q S I N F T K M
3201 ATATACTATGCCGATGATTAATTGTCAAACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACC
3301 GTACACGCCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGT
3400 CAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCGCAAAACCGCATCATCATGGTAATAGCGATGACTAA
SnaBI (3499)
3500 TACGTAGATGTACTGCCAAGTAGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTA
3600 CTTGGCATATGATACACTTGATGTACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGG
NdeI (3604)
3700 GAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTG C A G G T T A A T T A
PstI (3783) SdaI (3782) PacI (3790)
3798 AGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAA
BspLU11I (3800)
3898 AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAAGTCCCTCGTGCCTCTCTGTCCGACC
3998 CTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT
4098 GCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTT
ApaLI (4114)
4198 ATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACT
4298 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCG
4398 GTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAACGA
4498 AAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTGGTT
PacI (4530) SmaI (4539) EagI (4550) NotI (4549)
4598 TTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAG
4698 AACATTTCTCTATCGAA