



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

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCTGAGGCC
HindIII (245)
Bsu36I (291)
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

KasI (535) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTGAGTGGCCGCCCTTGTCTCTGTCTGTCT
AgeI (552) 1▶ M P R G W A A P L L L L L
601 GCTCCAGGAGGCTGGGGCTGCCCGACCTCGTCTGCTACACCGATTACCTCCAGACGGTCTATCTGCATCCTGAAATGTGGAACCTCCACCCAGCAGC
13▶ L Q G G W G C P D L V C Y T D Y L Q T V I C I L E M W N L H P S T

SphI (560)
701 CTCACCCCTTACCTGGCAAGACCAGTATGAAGAGCTGAAGGACGAGGCCACCTCCTGCAGCCTCCACAGGTGCGCCACAATGCCACCGTCCACCTACA
47▶ L T L T W Q D Q Y E E L K D E A T S C S L H R S A H N A T H A T Y
801 CCTGCCACATGGATGATTCCACTTCATGGCCGACGACATTTTCAGTGTCAACATCACAGACCAGTCTGGCAACTACTCCAGGAGTGTGGCAGCTTTCT
80▶ T C H M D V F H F M A D D I F S V N I T D Q S G N Y S Q E C G S F L
901 CCTGGCTGAGAGCATCAAGCCGGCTCCCTTTCAACGTGACTGTGACCTTCTCAGGACAGTATAATATCTCCTGGCGCTCAGATTACGAAGACCTGCC
113▶ L A E S I K P A P P F N V T V T F S G Q Y N I S W R S D Y E D P A

HindIII (1018)
1001 TTCTACATGCTGAAGGGCAAGCTTCAAGTATGAGCTGCAGTACAGGAACCGGGGAGACCCCTGGGCTGTGAGTCCGAGGAGAAAGCTGATCTCAGTGGACT
147▶ F Y M L K G K L Q Y E L Q Y R N R G D P W A V S P R R K L I S V D

XhoI (1140) 1101 CAAGAAGTGTCTCCTCCTCCCTGGAGTTCGCAAAAGACTCGAGCTATGAGCTGCAGTGCAGTGCAGGCGGGCAGGGCCCATGCCTGGCTCCTCTACAGGGGAC
180▶ S R S V S L L P L E F R K D S S Y E L Q V R A G P M P G S S Y Q G T
1201 CTGGAGTGAATGGAGTGACCCGGTCACTTTTCAGACCCAGTCAAGGAGTAAAGGAAGGCTGGAACCTCACCTGCTGCTTCTCCTCCTGCTTGTCTATA
213▶ W S E W S D P V I F Q T Q S E E L K E G W N P H L L L L L L L V I

Bsp120I (1168)
1301 GTCTTCATCCTGCCTTCTGGAGCCTGAAGACCCATCCATTGTGGAGGCTATGGAAGAAGATATGGGCGTCCCCAGCCCTGAGCGTTCTTCATGCCCC
247▶ V F I P A F W S L K T H P L W R L W K K I W A V P S P E R F F M P

BsrBI (1381)
BsrGI (1400) 1401 TGTACAAGGGCTGCAGCGGAGACTTCAAGAAATGGGTGGGTGCACCCCTCACTGGCTCCAGCCTGGAGCTGGGACCCTGGAGCCAGAGGTGCCCTCCAC
280▶ L Y K G C S G D F K K W V G A P F T G S S L E L G P W S P E V P S T
ApaLI (1439) **XcmI (1457)** **SandI (1470)**

BsrGI (1508) 1501 CCTGGAGGTGTACAGCTGCCACCCACCAGGAGCCCGCAAGAGGCTGCAGCTCACGGAGTACAAGAACCAGCAGAGCTGGTGGAGTCTGACGGTGTG
313▶ L E V Y S C H P P R S P A K R L Q L T E L Q E P A E L V E S D G V
1601 CCCAAGCCAGCTTCTGGCCGACAGCCAGAATCGGGGGGCTCAGCTTACAGTGAAGGAGGGATCGGCCATACGGCCTGGTGTCCATTGACACAGTGA
347▶ P K P S F W P T A Q N S G G S A Y S E E R D R P Y G L V S I D T V

StuI (1797)
1701 CTGTGCTAGATGCAGAGGGGCCATGCACCTGGCCCTGCAGCTGTGAGGATGACGGCTACCCAGCCCTGGACCTGGATGCTGGCCTGGAGCCCAGCCCAGG
380▶ T V L D A E G P C T W P C S C E D D G Y P A L D L D A G L E P S P G

PshAI (1827) 1801 CCTAGAGGACCCACTCTTGGATGCAGGGACCAAGTCTGCTGTGGCTGTGTCTCAGTGGCAGCCCTGGGCTAGGAGGGCCCTGGGAAGCCTCCTG
413▶ L E D P L L D A G T T V L S C G C V S A G S P G L G G P L G S L L
Bsp120I (1879)

BstEII (1964) 1901 GACAGACTAAAGCCACCCCTTGCAGATGGGGAGGACTGGGCTGGGGGACTGCCCTGGGGTGGCCGGTACCTGGAGGGGTCTCAGAGAGTGAAGCGGGCT
447▶ D R L K P P L A D G E D W A G G L P W G G R S P G G V S E S E A G

XmaI (2089) 2001 CACCCTGGCCGGCTGGATATGGACACGTTTACAGTGGCTTTGTGGCTCTGACTGCAGCAGCCCTGTGGAGTGTGACTTACCAGCCCGGGGACGA
480▶ S P L A G L D M D T F D S G F V G S D C S S P V E C D F T S P G D E

NheI (2199) 2101 AGGACCCCCCGGAGCTACCTCCGCCAGTGGGTGGTCACTTCTCCGCCACTTTTCGAGCCCTGGACCCAGCCAGCTAATGAGGCTGACTGGATGTCCAG
513▶ G P P R S Y L R Q W V V I P P P L S S P G P Q A S •

MscI (2205) 2201 CTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTAT

HpaI (2337) 2301 TGCTTTATTTGTAACATTATAAGTGAATAAACAAGTTAAACAACAATTGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTT
MfeI (2348)

EcoRI (2433) 2401 TAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTAAATAACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTG
2501 AGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTC

SspI (2672) 2601 CCAAGTTTGAAGTACTCTTCACTTTTATGTTTTAAATGCACTGACCTCCACATCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCA
SwaI (2686)

2701 TTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAA
2801 CCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTG
141 • N R T Y K L P I L E E I T T K V L K
SacI (2947)
2901 CCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCGACATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCT
121 G 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
3001 CATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGAC
88 D 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
StuI (3111)
3101 CCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCCTCATAGAGCATG
55 R 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
BspHI (3261)
3201 GTGATCTTCTCAGTGGGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTTCATGATGGCCCTCTATAGTGAGTCTGATTATACTATG
21 T I K E T A V E V L E L D Q Q S I N F T K M
XmnI (3253)
3301 CCGATATACTATGCCGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCC
AseI (3319) SacI (3376)
3401 ACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGAC
SpeI (3474)
3501 GTC AATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGTATCCACGCCATTGATGTA CTG CCAAACCGCATCATCATGGTAATAGCGATGACT
SnaBI (3602)
3601 AATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTA CTG GGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCG
NdeI (3707)
3701 TACTTGGCATATGATACACTTGATGTA CTG CCAAGTGGG CAGTTTACCGTAAACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTAT
PacI (3893)
3801 GGG AACATACGT CATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAA GTTATGTAACGCTGCAGGTTAAITTA
SdaI (3885)
3901 AGAACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAA
BspLU11I (3903)
4001 AAATCGAGCTCAAGTCAGAGGTGGCGAAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTCCGACC
4101 CTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCC
ApaLI (4217)
4201 GCTCCAAGCTGGGCTGTGTGCACGAACCCCGTT CAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTT
4301 ATCGCCACTGGCAGCAGCCACTGGAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACT
4401 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCG
4501 GTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGA
EagI (4653)
PacI (4633) SwaI (4642) NotI (4652)
4601 AAACCTCACGTTAAGGGATTTTGGTCA TGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTT
4701 TTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAG
4801 AACATTTCTCTATCGAA