



PvuI (7)
SgfI (6)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203)
PvuII (239)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCATCATGAAGAACCAAGACAAAAAAGTGGCCTGCCAAACA
1 M K N Q D K K N G P A K H

XmaI (618)
601 CTCCAACCTGAAGGGCAGCCCGGGCAACGGGAAGCAGGACCGGAGGGAGCCATGGACGACCAGACAGACAGCTCTGGGGCGGAAGCCGAAGTTCC
13 S N S K G S P G Q R E A G P E G A H G R P R Q T A P G A E A E G S

NcoI (651)
701 ACAAGCCAGGCTCCTGGGAAGACCGAGGGGGCTCGAGCTAAAGCAGCTCAGCCTGGGGCCTCTGTGACGCTCTGAGGAGCTGAGCCGGCAGTTGGAAG
47 T S Q A P G K T E G A R A K A A Q P G A L C D V S E E L S R Q L E

BstXI (705) **XhoI (731)** **Bsp120I (755)** **NgoMIV (785)**
801 ACATCCTGAGTACATACTGTGTGGACAACAATCAGGGAGGCCGGCTGAGGAGGGAGCACAGGGTGGAGCCACTGAGCCGGAAGACACGGAGAAGTCCCG
80 D I L S T Y C V D N N Q G G P A E E G A Q G E P T E P E D T E K S R
901 AACCTATGCAGCCAGGAATGGGGAGCCTGAACCAGGCATTCCAGCTGTCACGCGGAGAAGGAGACCTTAAGGGAGAGCCTGGAACAGAGGAGATCCGA
113 T Y A A R N G E P E P G I P V V N G E K E T S K G E P G T E E I R
1001 GCAAGTGTGAGGTTGGAGACCGAGACCATCGGAGGCCACAGGAGAAGAAGAAAGCAAGGGTCTAGGGAAGGAGTACTCTGCTGATGCAGACACTGA
147 A S D E V G D R D H R R P Q E K K K A K G L G K E I T L L M Q T L

DraIII (857)
1101 ACACGCTGAGTACCCAGAGGAGAAGCTGGCTGCAGTGTGCAAGAAGTATGCTGAGCTGCTGGAAGAGCATCGGAACCTGCAGAAGCAGATGAAGCTCCT
180 N T L S T P E E K L A A L C K K Y A E L L E E H R N S Q K Q M K L L

SapI (1162)
1201 GCAGAAGAAGCAGAGCCAGCTCGTGCAGGAGAAGGACCATCTGCGAGGGGAACACAGCAAGGCTGCTCTGGCCGAAGCAAGCTTGAAGTCTGTGCCGG
213 Q K K Q S Q L V Q E K D H L R G E H S K A V L A R S K L E S L C R

AgeI (1316)
1301 GAGCTGCAACGGCACAACCGGTCCCTGAAGGAAGAAGCGTGCAGCGAGCCGAGAGGAGGAGAAGCGCAAGAAGTACTTCACTTCCAGGTGA
247 E L Q R H N R S L K E E G V Q R A R E E E E K R K E V T S H F Q V

PvuII (1414) **NheI (1473)**
1401 CACTGAATGACATTGAGTGCAGATGGAACAGCATAACGAGCGAAACTCCAAGCTGCGCCAGGAGAATATGGAGCTAGCCGAGAGGCTCAAGAAGTTGAT
280 T L N D I Q L Q M E Q H N E R N S K L R Q E N M E L A E R L K K L I

Tth111I (1531)
1501 CGAGCAATACGAGCTTGTGAGGAGCATATCGACAAAGTCTTCAAACATAAGGACCTGCAGCAGCAGTGTGAGGAGCAAGCTCCAGCAGGCCAGGAG
313 E Q Y E L R E E H I D K V F K H K D L Q Q Q L V D A K L Q Q A Q E

BsrBI (1618)
1601 ATGCTGAAGGAGGAGGAGGAGCGGCACAGCAGAGAGAAGGAGTTTCTCCTGAAGGAAGCGGTGGAGTCCCAGAGGATGTGCGAGCTGATGAAGCAGCAGG
347 M L K E A E E R H Q R E K E F L L K E A V E S Q R M C E L M K Q Q

BsrGI (1727)
1701 AGACCCACCTAAAGCAGCAGCTCGCCCTGTACACGGAGAAGTTTGGAGGTTCCAGAACACACTTTCCAAAAGCAGTGAAGTGTCCACACGTTCAAACA
380 E T H L K Q Q L A L Y T E K F E E F Q N T L S K S S E V F T T F K Q

ClaI (1856)
1801 GGAGATGGAAGATGACAAAGAAGATCAAGAAGCTGGAGAAAGAAACCACCATGTATCGATCCAGGTGGGAAAGCAGCAACAAGGCTCTGCTGGAGATG
413 E M E K M T K K I K K L E K E T T M Y R S R W E S S N K A L L E M

SdaI (1938)
1901 GCTGAAGAGAAAACCGTCCGGGACAAAAGAGCTGGAGGGCCTGCAGGTGAAAATCCAGCGGCTGGAGAAGCTGTGCCGAGCACTGCAGACTGAGCGCAATG
447 A E E K T V R D K E L E G L Q V K I Q R L E K L C R A L Q T E R N

BsrBI (2056)
2001 ACCTCAACAAGAGGGTACAGGACCTGACTGCAGGGGCATCACTGACATTGGCTCTGAGCGGAGGCCAGAGGCCACCACTGCCTCCAAGGAACAAGGGGT
480 D L N K R V Q D L T A G G I T D I G S E R R P E A T T A S K E Q G V

XcmI (2187)
2101 TGAAGTCTGGGGCTCAACCAGCCAGCTCTCAAGGGCCACAGACGCTCCTTGTGCTCGGGAGCCCGAGCACAGGAACAGCAGGCCAGGCCAGGGCCT
513 E S P G A Q P A S S P R A T D A P C C S G A P S T G T A G Q T G P

SphI (2243) **StuI (2273)** **EcoRI (2295)**
2201 GGAGAGCCACCCCTGCCACTGCCTAGAGATCACGGTCTTGGGCATGCTGGACAGGAGCAGCAGCCAGTCAAGGCTCTGCATGAAGGCTTGAATT
547 G E P T P A T A •

NheI (2301)
2301 CGCTAGCTCGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTG

HpaI (2464) MfeI (2475)
2401 CTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTGTGAACCATTATAAGCTGCAATAAACCAAGTTAACAAACAATTGCATTCATTTTATGTTTCAG

EcoRI (2560)
2501 GTTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAA
2601 TCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTC

SapI (2742) SspI (2799)
2701 ATGGAGTTTAAGATATAGTGATTTTTCCCAAGGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAA

SwaI (2813)
2801 ATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTT
2901 AGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGT
141 • N R T Y K L P I L

SacI (3074)
3001 TCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGC
130 E E I T T K V L K 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

BstXI (3103)
3101 TGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAT
97 V V R I S R D V E D S Y P H R V A V I T D F D K Q G N S V A S G I

StuI (3238)
3201 GGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGTATGGCCGCCCGACA
64 A I A E A C V T V R G I Y A E I H V A S I I E G T K T R I A A G V

XmnI (3380)
3301 TGGTGCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCC
30 H H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M

AseI (3446)
3401 TCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTA

SacI (3503)
3501 AACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTGATT

SpeI (3601)
3601 TACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAAC

SnaBI (3729)
3701 CGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAAGGTGATGACTGGGCATAATGCCAGGCGGGCCATT

NdeI (3834)
3801 TACCGTCATTGACGTCAATAGGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCA
3901 ATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTACCGTA

SdaI (4012) PacI (4020) BspLU11I (4030)
4001 AGTTATGTAACGCCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGCTGGCGTTTTCCATAG
4101 GCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGC
4201 TCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCGCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTA

ApaLI (4344)
4301 GGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCT
4401 TGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGATTCTTG
4501 AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGAGTTGGTAGCTCTTGAT
4601 CCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC

EagI (4780)
4701 TACGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTGGTATGGCTAGTGAATTAACATTTAAATCAGCGGCCGAATAAAATATCTT
PacI (4760) SwaI (4769) NotI (4779)

4801 TATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGC
4901 TGTCACCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA