



PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
EcoNI (287)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCATCATGAGCTCTCCGCCGCCGCCGCGAGTGGCTTTTACCG
1 M S S P P P A R S G F Y R

BstEII (606) **BssHII (630)** KasI (667)
601 CCAGGAGGTGACCAAGACGCCTGGGAGGTGCGCGCCTGTACCGGGACTGCAGCCCGTGGGCTCGGGCGCTACGGCGCGGTGTGCTCGGCCGTGGAC
13 Q E V T K T A W E V R A V Y R D L Q P V G S G A Y G A V C S A V D

SgrAI (705) **BssHII (768)**
701 GGCCGACCGGCGCTAAGGTGGCCATCAAGAAGCTGTATCGGCCCTTCCAGTCCGAGCTGTTCCGCAAGCGCGCTACCGCGAGCTGCGCCTGCTCAAGC
47 G R T G A K V A I K K L Y R P F Q S E L F A K R A Y R E L R L L K
801 ACATGCGCCACGAGAACGTGATCGGGCTGCTGGACGTATTCACTCCTGATGAGACCCTGGATGACTTACGACTTTTACCTGGTGTGATGCCGTTTCATGG
80 H M R H E N V I G L L D V F T P D E T L D D F T D F Y L V M P F M G

BamHI (947)
901 CACCGACCTGGGCAAGCTCATGAAACATGAGAAGCTAGGCGAGGACCGGATCCAGTTCCTCGTACCAGATGCTGAAGGGGCTGAGGTATATCCACGCT
113 T D L G K L M K H E K L G E D R I Q F L V Y Q M L K G L R Y I H A

NgoMIV (1000)
NaeI (1000) **BbsI (1048)**
1001 GCCGGCATCATCCACAGAGACCTGAAGCCCGCAACCTGGCTGTGAACGAAGACTGTGAGCTGAAGATCCTGGACTTCGGCCTGGCCAGGCAGGCAGACA
147 A G I I H R D L K P G N L A V N E D C E L K I L D F G L A R Q A D

Asp718I (1130)
BstEII (1119) **Acc65I (1130)**
1101 GTGAGATGACTGGGTACGTGGTACCCGGTGGTACCGGGCTCCCGAGGTCATCTTGAATTGGATGCGCTACACGCAGACGGTGGACATCTGGTCTGTGGG
180 S E M T G Y V V T R W Y R A P E V I L N W M R Y T Q T V D I W S V G

BspHI [m] (1272)
1201 CTGCATCATGGCGGAGATGATCACAGGCAAGACGCTGTTCAAGGGCAGCGACCACCTGGACCAGCTGAAGGAGATCATGAAGGTGAGGGGACGCCTCCG
213 C I M A E M I T G K T L F K G S D H L D Q L K E I M K V T G T P P
1301 GCTGAGTTTGTGACGCGGTGCAGAGCGATGAGGCCAAGAAGTACATGAAGGGCTCCCGAATTGGAGAAGAAGGATTTGCGCTTATCTGACCAATG
247 A E F V Q R L Q S D E A K N Y M K G L P E L E K K D F A S I I L T N
1401 CAAGCCCTTGGCTGTGAACCTCCTGGAGAAGATGCTGGTGTCTGGACGCGGAGCAGCGGGTGACGGCAGGCGAGGCGCTGGCCATCTACTTTCGAGTC
280 A S P L A V N L L E K M L V L D A E Q R V T A G E A L A H P Y F E S
1501 CCTGCACGACACGGAAGATGAGCCCGAGTCCAGAAGTATGATGACTCCTTTGACGACGTTGACCGCACACTGGATGAATGGAAGCGTGTACTTACAAA
313 L H D T E D E P Q V Q K Y D D S F D D V D R T L D E W K R V T Y K

BglII (1666) **NheI (1682)**
1601 GAGGTGCTCAGCTTCAAGCTCCCGGAGCTGGGGGCCAGGCTCCTCAAGGAGACGCCTCTGTGAAGATCTCTGGCTCCGGCTAGCTGGCCAGACATG
347 E V L S F K P P R Q L G A R V S K E T P L •

1701 ATAAGATACATTGATGAGTTTGGACAAACCAACTAGAATGCAGTGAATAAATGCTTTATTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCA

HpaI (1820) MfeI (1831)
1801 TTATAAGCTGCAATAAACAAAGTTAAACAACAATTGCATTCTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCT

EcoRI (1916)
1901 CTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCAT
2001 AGGCATCAGGGGCTGTTGCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACG

SspI (2155) **Swal (2169)**
2101 TCTTCATTTCTTTATGTTTTAAATGCAGTACCTCCACATTCCTTTTATGATAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAAT
2201 GTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATGG
2301 ACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAG
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

BstXI (2459)
2401 CACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGC
116 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 H

StuI (2594)
2501 CTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACGACAGACAGTACCTGCCAATGTAGGCCT
82 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 E
2601 CAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTGTTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGC
49 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 A

BbsI (2740)
XmnI (2736)

2701 GACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGA
16 V E V L E L D Q Q S I N F T K M

AseI (2802)

2801 TGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCG

SpeI (2957)

2901 CCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGA

SnaBI (3085)

3000 CTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACT

NdeI (3190)

3100 GCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATA

3200 CACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATT

SdaI (3368) PacI (3376) BspLU11I (3386)

3300 ATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCA
3398 AAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAA
3498 GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGG
3598 ATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGGTGAGGTGTTTCGCTCCAAGCTGGCC

ApaLI (3700)

3698 TGTGTGCACGAACCCCCGTTGAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAG
3798 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATT
3898 TGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTT
3998 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAG

PacI (4116) SwaI (4125) NotI (4135)

4098 GGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCG
4198 TAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATC
4298 GAA