



PvuI (7)
SgfI (6)
 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGGCC
 301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGCTCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)** **BspHI (560)** **BspLU11I (576)**
 501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCATCATGAAATTCAGTTACATGTGAATTCGCCAGGCAATA
 1 M K F K L H V N S A R Q Y

MscI (657)
 601 CAAGGACCTGTGGAATATGAGTGATGACAAACCTTTCTATGTACTGCGCCTGGATGTGGCCAGCGTTTTACCAACGAGGATCATTGGCTGTCCATAAA
 13 K D L W N M S D D K P F L C T A P G C G Q R F T N E D H L A V H K

Tth111I (742)
 701 CATAAACATGAGATGACACTGAAATTTGGTCCAGCAGCTAATGACAGTGTCTTGTGGCTGATCAGACCCCAACACCAACAAGATTCTTGAAAACTGTG
 47 H K H E M T L K F G P A R N D S V I V A D Q T P T P T R F L K N C

XmnI (840) **HindIII (854)** **XbaI (885)**
 801 AAGAAGTGGGTTTGTAAATGAGTTGGCGAGTCCATTTGAGAATGAATCAAGAAAGCTTCAGAAGATGACATTAATAAATGCCTCTAGATTTATCCCC
 80 E E V G L F N E L A S P F E N E F K K A S E D D I K K M P L D L S P
 901 TCTTGCAACCTATCATAAGAAGCAAAATTTGAGGAGCCTTCTGTTGTAGAAACAACCTACCAGGATAGTCTTTACCTACCCAGAGTCTACTACCAGT
 113 L A T P I I R S K I E E P S V V E T T H Q D S P L P H P E S T T S
 1001 GATGAGAAGGAAGTACCATTGGCACAACTGCACAGCCACATCAGCTATTGTTCTCCAGCATCATTACAGGTTCCCAATGTGCTGCTTACAAGTCTCTG
 147 D E K E V P L A Q T A Q P T S A I V R P A S L Q V P N V L L T S S

ScaI (1144)
 1101 ACTCAAGTGAATTATTTCAGCAGGCAGTACCTTACCACCTCAAGTCTGTAATCACCCAGGCACCATCCTCTAACAGGCCAATTGTCCCTGTACCAGG
 180 D S S V I I Q Q A V P S P T S S T V I T Q A P S S N R P I V P V P G
 1201 CCCATTTCTCTTCTGTTACATCTTCTAATGGACAAACCATGCCTGTTGCTATTCTCGCATCAATTACAAGTTCTAATGTGCATGTTCCAGCTGCAGTC
 213 P F P L L L H L P N G Q T M P V A I P A S I T S S N V H V P A A V

NcoI (1319)
 1301 CCACTCGTTCCAGCAGTACCATGGTGCCTAGTGTCCAGGAATCCCAGGTCCTTCTCTCCCAACCAGTACAGTCAGAAGCAAAAATGAGATTAAG
 247 P L V R P V T M V P S V P G I P G P S S P Q P V Q S E A K M R L K

Tth111I (1473) **PshAI (1493)**
 1401 CTGCTTTGACCCAGCAACATCCTCCAGTTACCAATGGTGATACTGTCAAAGGTCATGGTAGCGGATTGGTTAGGACTCAGTCAGAGGAATCTCGACCCGA
 280 A A L T Q Q H P P V T N G D T V K G H G S G L V R T Q S E E S R P Q

XcmI (1569)
 1501 GTCATTACAACAGCCAGCCACATCCACTACAGAACTCCGGCTTCTCCAGCTCACACAACCTCCACAGACCCAAAGTACAAGTGGTCGTCGGAGAAGAGCA
 313 S L Q Q P A T S T T E T P A S P A H T T P Q T Q S T S G R R R R A
 1601 GCTAACGAAGATCCTGATGAAAAAGGAGAAAAGTTTTAGAGCGAAATAGAGCAGCAGCTTCAAGATGCCGACAAAAAGGAAAGTCTGGGTTAGTCTT
 347 A N E D P D E K R R K F L E R N R A A A S R C R Q K R K V W V Q S
 1701 TAGAGAAGAAAGCTGAAGACTTGAGTTCAATTAAGTGCAGTGCAGAGTGAAGTCACTGCTGAGAAATGAAGTGGCACAGCTGAAACAGCTCTCTTCT
 380 L E K K A E D L S S L N G Q L Q S E V T L L R N E V A Q L K Q L L L
 1801 GGCTCATAAAGATTGCCCTGTAACCGCCATGCAGAAGAAATCTGGCTATCATACTGCTGATAAAGATGATAGTTTCAAGACATTTTCAAGTCCGAGTAGT
 413 A H K D C P V T A M Q K K S G Y H T A D K D D S S E D I S V P S S
 1901 CCACATACAGAAGCTATACAGCATAGTTCCGGTCAAGCAGTCAATGGAGTCAAGTCAACTCCAAGGCAGAAGCTGTAGCCACTTCAAGTCCACCCAGA
 447 P H T E A I Q H S S V S T S N G V S S T S K A E A V A T S V L T Q

Bsu36I (2066) **NheI (2086)** **MscI (2092)**
 2001 TGGCGGACCAGAGTACAGAGCCTGCTCTTTACAGATCGTTATGGCTCCTTCTCCAGTCACAGCCCTCAGGAAGTTGATTAAGTAAAGCTAGCTGGCCAGA
 480 M A D Q S T E P A L S Q I V M A P S S Q S Q P S G S •

2101 CATGATAAGATACATTGATGAGTTTGGACAAACCAACAAGTGAAGTGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTA

HpaI (2224)
 2201 ACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAA
 2301 ACCTCTACAAATGTGGTATGGAATTTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAG
 2401 GCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTATTTTCCCAAGGTTTGAAC

SspI (2559) **Swal (2573)**
 2501 TAGCTCTTCAATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAT
 2601 AAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAA
 2701 TTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAA
 141 • N R T Y K L P I L E E I T T K V L K G N M E I

2801 TGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGG
117 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 S Y P

2901 GTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGTCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAG
84 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 G I Y

3001 GCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAG
50 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 I K E T

SacI (2834) BstXI (2863) StuI (2998)

3101 TGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATG
17 A V E V L E L D Q Q S I N F T K M

AseI (3206) BspHI (3148) SacI (3263)

3201 CCGATGATTAATTGTCAAACACAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCT

3301 ACCGCCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTG
SpeI (3361)

3400 GAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATG
SnaBI (3489)

3500 TACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATAT
NdeI (3594)

3600 GATACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGT

3700 CATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTG
SdaI (3772) PacI (3780) BspLU11I (3790)

3798 AGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGC

3898 TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAAGTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGTTA

3998 CCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCT

ApaLI (4104)

4098 GGGCTGTGTGCACGAACCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAAGACACGACTTATCGCCACTG

4198 GCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAG

4298 TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCCGCTGGTAGCGGTGTTTTTT

4398 TGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGT

EagI (4540)

4498 TAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGTTTTTGTGTGA
PacI (4520) SmaI (4529) NotI (4539)

4598 ATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTC
4698 TATCGAA