



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **BstEII (555)** **NcoI (560)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATTGGCTATTACCTACAGCCAGTGACCTGATCTTTGA
1▶ M A I T L Q P S D L I F E

EcoRV (625) **Acc65I (678)**
601 GTTCGAAGCAACGGGATGATGATATCCACAGCTGGAAGACCCCTCTGTGTTCCAGCTGTGATCGTGAGCAGGTACCCTACCTGATTACTG
13▶ F A S N G M D D D I H Q L E D P S V F P A V I V E Q V P Y P D L L

701 CATCTGTACTCGGACTGGAGTTGGACGACGTTCAATGGCATATAACAGACGGGACCTTGTGCATGACGCAGGATCAGATCCTGGAAGGCAGTTTTT
47▶ H L Y S G L E L D D V H N G I I T D G T L C M T Q D Q I L E G S F

SacII (842) **EcoRV (877)** **BglII (896)**
801 TGCTGACAGATGACAATGAGGCCACCTCGCACACCATGTCAACCGGGAAGTCTTACTCAATATGGAGTCTCCAGCGATATCCTGGATGAGAAGCAGAT
80▶ L L T D D N E A T S H T M S T A E V L L N M E S P S D I L D E K Q I

XmnI (913)
901 CTTCACTACCTCCGAAATGCTTCCAGACTCGGACCCCTGCACCAGCTGTCACTCTGCCAACTACCTGTTTCTGCCTCTGAGCCCGATGCCCTGAACAGG
113▶ F S T S E M L P D S D P A P A V T L P N Y L F P A S E P D A L N R

SpeI (1009) **BspEI (1094)**
1001 GCGGGTGACACTAGTGACCAGGAGGGCATTCTCTGGAGGAGAAGGCCTCCAGAGAGGAAAGTCCAAGAAGACTGGGAAATCAAAGAAGAGAATCCGGA
147▶ A G D T S D Q E G H S L E E K A S R E E S A K K T G K S K K R I R

1101 AGACCAAGGGCAACCGAAGTACCTCACCTGTCACTGACCCAGCATCCCATTAGGAAGAAATCAAAGGATGGCAAAGGCAGCACCATCTATCTGTGGGA
180▶ K T K G N R S T S P V T D P S I P I R K K S K D G K G S T I Y L W E

1201 GTTCTCTGGCTCTTCTGCAAGACAGAAACACCTGTCCAAAGTACATCAAGTGGACCCAGCAGAGAGAAAGGCATCTTCAAAGTGGTGGACTCCAAAGCT
213▶ F L L A L L Q D R N T C P K Y I K W T Q R E K G I F K L V D S K A

MscI (1394)
1301 GTGTCCAAGCTGTGGGGGAAGCAGAAAAACAAGCCTGACATGAACATGAGACAATGGGGCGGGCACTAAGATACTACTACCAAAGAGGCATACTGGCCA
247▶ V S K L W G K Q K N K P D M N Y E T M G R A L R Y Y Y Q R G I L A

BstXI (1442)
1401 AAGTGAAGGGCAGAGGCTGGTGTACCAGTTTAAAGGAGATGCCCAAGGACCTGGTGGTCAATTGAAGATGAGGATGAGAGCAGCGAAGCCACAGCAGCCCC
280▶ K V E G Q R L V Y Q F K E M P K D L V V I E D E S S E A T A A P

SfiI (1506) **SfiI (1515)** **BglII (1570)**
1501 ACCTCAGGCCTCCACGGCCTCTGTGGCCTCTGCCAGTACCACCCGGCGAACCAGCTCCAGGGTCTCATCCAGATCTGCCCCCAAGGGCAGGCTCT
313▶ P Q A S T A S V A S A S T T R R T S S R V S S R S A P Q G K G S S

1601 TCTTGGGAGAAGCCAAAATTCAGCATGTCGGTCTCCAGCCATCTGCGAGTCTGGAATTGGGACCGTCTGCTAGACGAGGAGATCCCCACTACCTCCACCA
347▶ S W E K P K I Q H V G L Q P S A S L E L G P S L D E E I P T T S T

AvrII (1776)
1701 TGCTCGTCTCCAGCAGAGGGCCAGGTCAGCTACCAAAGCTGTGAGTGCATCTTCAAGTGGCCAGCAACATCCACCTAGGAGTGGCCCCCGTGGGGTC
380▶ M L V S P A E G Q V K L T K A V S A S S V P S N I H L G V A P V G S

PstI (1816) **ScaI (1864)**
1801 GGGCTCGGCCTGACCCTGCAGACGATCCCACTGACCACGGTGTGACCAATGGGCTCCTGCCAGTACTACTGCTCCCACTCAGCTCGTTCTCCAGAGT
413▶ G S A L T L Q T I P L T T V L T N G P P A S T T A P T Q L V L Q S

1901 GTTCCAGCGGCCTCTACTTTCAAGGACACCTTCACTTTGACGGCTCTTTCCCTGAAAGCAGTTTCAAGACAGCAGGTTGACGCCCCAGGGGCTC
447▶ V P A A S T F K D T F T L Q A S F P L N A S F Q D S Q V A A P G A

KasI (2058) **Bsp120I (2092)**
2001 CACTGATTCTCAGTGGCCTCCCAACTTCTGGCTGGGGCCAACCGTCCGACCAACCCGGCGCCACCCACGGTACAGGGGCTGGACCAGCAGGCCCCAG
480▶ P L I L S G L P Q L L A G A N R P T N P A P P T V T G A G P A G P S

AvrII (2161)
2101 CTCTCAGCCCCCTGGGACTGTCATTGCTGCCTTCACTCAGGACTTCTGGCACTACAGCAGCCCCTAGGGTCAAGGAGGGGCCACTGAGGTCTCTCTCTAT
513▶ S Q P P G T V I A A F I R T S G T T A A P R V K E G P L R S S S Y

NcoI (2225) **Bsp120I (2219)**
2201 GTTCAGGGTATGGTGACGGGGGCCCCATGGAGGGGCTGCTGGTTCCTGAAGAGACCCCTGAGGGAGCTCCTGAGAGATCAGGCTCATCTTCAGCCACTTC
547▶ V Q G M V T G A P M E G L L V P E E T L R E L L R D Q A H L Q P L

Tth111I (2352)
2301 CAACCCAGGTGGTTTCCAGGGGTTCCACAATCCGAGCCTTCTGGGCAACCAGACTTTGTCTCTCCAGCCGCCCACTGTTGGGCTGACCCCAAGTGGC
580▶ P T Q V V S R G S H N P S L L G N Q T L S P P S R P T V G L T P V A

SmaI (2425)
2401 TGAACCTGAGCTCTCTCAGGCTCAGGTCCTGCTGATGGCTGAGCCTAGTGTGACCACATCTGGGAGCCTTCTGACAAGATCCCCACCCAGCCCCCT
613▶ E L E L S S G S G S L L M A E P S V T T S G S L L T R S P T P A P

MscI (2560)

2501 TTCTCCCCATTCAACCTACTTCCCTCATTAAAGATGGAGCCCCATGACATATAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAA
647▶ F S P F N P T S L I K M E P H D I •

HpaI (2692)

2601 CCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA

MfeI (2703) EcoRI (2788)

2701 CAACAATTGCATTCAATTTATGTTTCAGGTTCCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATCTAAAAT

2801 ACAGCATAGCAAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCA

2901 TTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTTAAATGCAC

SspI (3027) SwaI (3041)

3001 TGACCTCCACATTCCCTTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCT

3101 CAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAATTGGACAGCAAGAAAGCAGCTTCTAGCTTTA
141▶ •

3201 GTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAG
140▶ N R T Y K L P I L E E I T T K V L K G N M E I L V F C D P A Y D S

BstXI (3331)

3301 ATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTC
106▶ I L E R C M G C P S V V R I S R D V E D S Y P H R V A V I T D F D K

3401 TCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCC
73▶ Q G N S V A S G I A I A E A C V T V R G I Y A E I H V A S I I E G

3501 AGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCCTCATAGAGCATGGTGTATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGTGTGA
40▶ T K T R I A A G V H H K N D E Y L M T I K E T A V E V L E L D Q Q

XmnI (3608) AseI (3674)

3601 GAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGG
6▶ S I N F T K M

3701 CGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGT

SpeI (3829)

3801 TACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTA

SnaBI (3957)

3901 TCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCATG

NdeI (4062)

4001 TACTGGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTT

4101 ACCGTAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATATTGACGTCAATGGGGGGGGTCTTGGG

PacI (4248)

PstI (4241) SdaI (4240) BspLU11I (4258)

4201 CGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGAGGTTAAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAA
▶

4301 AGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACGACTATA

4401 AAGATACCAGGCGTTTCCCTGGAAGTCCCTCGTGGCTCTCTGTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGC

ApaLI (4572)

4501 GTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACC

4601 GCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCACTGGCAGCAGCCACTGTAACAGGATTAGCAGAGCGAG

4701 GTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC

4801 TTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAG

PacI (4988) SwaI (4997)

4901 GATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATT

EagI (5008) NotI (5007)

5001 TAAATC AGCGGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTTTGTGTAATCGTAACATAACGCTCTCCATCAAAACAAA
5101 CGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA