



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGGGGTAAGTGGAAAGTGTGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGCTCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
XcmI (560)
BstEII (555)
KasI (535) **AgeI (552)** **XmaI (586)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTACCATGGAGCCCGTGGAGGCTGGACCCCGGAAGGTGGC
1▶ M E P V E A W T P G K V A

XhoI (697)
601 AGCTTGGCTGAGAGGCCTTGATGATGCCCTACAGACTATCCCTTCGAGGACTGGCAGCTGCCTGGAAAGTACCTGCTGCAGCTCTGTCCCAAAGCCTC
13▶ A W L R G L D D A L Q D Y P F E D W Q L P G K Y L L Q L C P Q S L
XmnI (733) **XbaI (741)**
701 GAGGCTGACTGTGTGGCCTTTGGGCCACGGAACCTATTCTAGATGGGTGGAACAACCTCCGGGCCCTGGGCTCTAATCTACAGACAGAGAACCCTGC
47▶ E A L T V W P L G H Q E L I L D G V E Q L R A L G S N L Q T E N L
HindIII (843)
801 AGAGCCTGGCTCAGGGGCTGCTGGAAGGACCCAGGCCTTCCAAGCTTGGTCCAAGGCTCTCTGGCAACTGTGCTGAGACACCGGCTGACGTCTCAA
80▶ Q S L A Q G L L E R T Q A F Q S L V Q G S L G N C A E T P A D V L K
901 GGCTGCGGTGGAGCTGGTGGGGAAGCCATGCCCTCCTCTCTGGCTCAACGGGTACCTTCTCTCACTTAAATGACTTCTCTGCCTGCCAGGAGATT
113▶ A A V E L V R E A H A L L S W L N G Y L F S H L N D F S A C Q E I
SdaI (1029) **Bsu36I (1071)** **BbrPI (1087)**
1001 GCGTGTGTGCGGGGAGCTGGGCCAAGTCTCGAGGAGGACTGCCAGAGGCTGAGAAGGAACGAAACATCTGAGGATTTGGCGCCACGTGGCTGGGA
147▶ G V L C G E L G Q V L Q E D C P E A E K E R N I L R I C G H V A G
XbaI (1188)
1101 TCTGTCAACATCCTGAGCTGCAGCCAGAGGAGCTGCTGGAACAGAAGGCCGTGCTGGAGTCGGTGCAGGTGGACGACCCTCCGGTCTAGAAATTCA
180▶ I C H N I L S C S P E E L L E Q K A V L E S V Q V D D P S G L E I H
DraIII (1219)
1201 CACCACCAGCAACTGCCTGCACTTTGTGTCGCCGAGTAGGGTTTCAAGGCTGCCACCAGCTCCAGATCCTGCCAGGAGACGAGATTGTCCAGGTCAATGAG
213▶ T T S N C L H F V S R V G V Q A A T S S Q I L P G D E I V Q V N E
1301 CAGGTGGTGGTGGGCTGGTCCATAAGAACATGCTGAGGAGCTGCTGAGGGAACAGCAAGGTCAGCCTGGTACTGAAGAAGATTCCCGTGCCAGAGA
247▶ Q V V V G W S H K N M L R K L L R E P A K V S L V L K K I P V P E
1401 CCCCTCACAGAGCTCCCTGGACTCTCCTCACCTGCTAAGCCAACTCGTCCCTGAACCCAGCTCTCCAGGTTCCATCTGAAGGCTTTTAGCAGA
280▶ T P S Q T S L D S P H L L S Q S L P L N P P S P R V P S E G L L A D
1501 TGGAACTCTGGACCCAGCCTGCTTGGACAGACTCTACTCCCTTGGAGCTCAGTCCCCGCCACTCCCCTGGACCACCAGGCTACTTCCAGAAGAA
313▶ G T P G P S P A W T D S T S L D A Q S P P T P P G P P G V L P E E
PshAI (1633)
1601 ACAGCAGAACCTCTGAGTCTTCCGGACACCCTGACAAGATCCATCCTTGGTCCGGAAGAACTAAAGGTATAGCCACGAGGCTGAGCCGCCCGCCGGG
347▶ T A E P L E S S G H P D K S P I L G R K K S K G I A T R L S R R R
KasI (1784)
1701 TGTCTGCCGAGAGTTGGGCTGCGCGGATTGTGATGGATGGCTTCTACTGCGGAAGTACCCGGTGGCTTTATGGGCCACGCTGGCCCGCTGCTGGTT
380▶ V S C R E L G L P D C D G W L L L R K V P G G F M G P R W R R C W F
1801 TGTGCTCAAGGGACACACCTATACTGGTACCGCAACCCAGGATGAAAAGGCCAAGGCTTATCAATCTCTCAACTACAGCCTAGAGAGTGGACAT
413▶ V L K G H T L Y W Y R Q P Q D E K A E G L I N L S N Y S L E S G H
BsrGI (1940) **Tth111I (1968)**
1901 GACCAGAAGAAAAATATGTGTTCCAGCTGACCCATGATGTGTAACAAGCCCTTCTTTGCTGCCGAGACCCTGTCTGATCTGAGCAAGTGGGTGCGAC
447▶ D Q K K K Y V F Q L T H D V Y K P F I F A A E T L S D L S K W V R
2001 ATCTCATTACCTGCATTTCCAAGTACCAGGCTCAAGGCCGGGCCCCCTCTCTGCCAGAGAGGAACTGCTACAGTGAAGCAGAAGCAGAAGACCCCGA
480▶ H L I T C I S K Y Q A Q G R A P S S A R E E D C Y S E T E A E D P D
BsrBI (2115) **XcmI (2134)**
2101 TGAGGAGGTGGGTCGCCCTCCGCTTCTCTGGCCAGCTCAAGCGTGGAGTGACACATCACCCGTGGCTTACCCTGCAGAGTCCGAGAACTCCTTT
513▶ E E V G S R S A S P G P A Q A W S D T S P V A S P L Q S P R T S F
2201 AACTCTTACCAGACAGCAGTGACAGAGCCCTGGAAGGAATGGTACAGGGGCTGAGGCAGGGAGGGGTGTCCCTCTGGGCCAGCCCCAGCCCCTGACC
547▶ N S S P D S S D R A L E G M V Q G L R Q G G V S L L G Q P Q P L T
BspHI (2321) **ApaLI (2357)**
2301 ATGAACAATGGCGGAGTTCTTTTATGAGGCGCAACCGTGACCCTCATCTCAATGAGCGTGCACACCGTATCCGGGCACTCCAGAGCACCTCAAGGCAAA
580▶ H E Q W R S S F M R R N R D P H L N E R A H R I R A L Q S T L K A K
2401 GCTGCAGGAAGTGCAGGCCCTGGAGGAAGTGTGGGTGATCCTGAECTCACAAGTGAAGGTTCCGACAGTGAAGGAACAGAACCAGGAGCTATACTCA
613▶ L Q E L Q A L E E V L G D P E L T S A K F R Q W K E Q N Q E L Y S
2501 GAGGCCTGAGAACCCTGGGAGGACGTGGGCCAGCAGCTCCTCAGACCTCAAACTGACTCCAGGGCTCATTTCCACAGCCCTCCCTTTGATC
647▶ E G L R T W G G T W A Q T S S S D P N S D S R A H S P Q P L P F D

MscI (2695)

2601 CTGAAGAGCCTCCAGCTTTTTCCCTTAACCCAGAGAAGACCTGCCAACCTCTGACCTCTGACCCTGGCTGAGGACTACTTCATTCCGCTAGCTGGCC
680▶ P E E P S Q L F P L T P E N S C Q P P D L •

2701 AGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTT

HpaI (2827) MfeI (2838)

2801 GTAACCATATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGT

EcoRI (2923)

2901 AAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAAT

3001 AAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTG

SspI (3162) SwaI (3176)

3101 AACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAA

3201 AATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAG

3301 AAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTTCATCT

• N R T Y K L P I L E E I T T K V L K G N M E

3401 CAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTA

118▶ 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 D S Y

3501 GGGTGCCTGACAGCCACAAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCTGCCAATG

85▶ 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 R G I

3601 TAGGCCTCAATGTGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTGCTCATAGAGCATGGTATCTTCT

51▶ 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 T I K E

BspHI (3751)

XmnI (3743)

3701 CAGTGGGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACT

18▶ T A V E V L E L D Q Q S I N F T K M

AseI (3809) SacI (3866)

3801 ATGCCGATGATTAATTGTCAAACACGCTGGATGGCGTCTCCAGCTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCACCGTACAC

SpeI (3964)

3900 GCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGG

SnaBI (4092)

3999 GGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCAGCCCATTTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTA

NdeI (4197)

4099 GATGTAAGTCCAAGTAGGAAAGTCCCATAAAGTTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCAATGAGGGGCGTACTTGGC

4199 ATATGATACACTTGATGTAAGTGGCAGTTTACCCTAAATACTCCACCATTTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACAT

SdaI (4375) PacI (4383) BspLU11I

4299 ACGTCAATTATTGACGTCAATGGGCGGGGCTGTTGGGCGGTACAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTG C A G T T A A T T A A G A A C C A

4397 TGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCG

4497 ACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCG

4597 CTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGTTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCCA

ApaLI (4707)

4697 AGCTGGGCTGTGTCACGAACCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCC

4797 ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA

4897 ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCGCTGGTAGCGGTGTT

4997 TTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACTC

EagI (5143) NotI (5142)

PacI (5123) SwaI (5132)

5097 ACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGTTTTTGT

5197 GTGAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATT

5297 TCTCTATCGAA