



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

Psp1406I (203)
HindIII (245)
Bsu36I (291)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTCTGCCGCTCCCGCCTGTGGTGCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCACCATGGCTATTGCTCTGCAGCCAGTGTCTGGTCTTCGA
1▶ M A I A L Q P S D L V F E

EcoRV (622)
PvuII (631)
601 GTTTGAAGCAACGGGATGGATGATATCCACCAGCTGGAAGACCCCTTCACTGTTCCAGCCGTGATCGTGAACAGGTCCTATCCTGAATTAGTGCAT
13▶ F A S N G M D D I H Q L E D P S V F P A V I V E Q V P Y P E L V H
701 CTGTGCTCAGGACTGGATCTGGATGAGGTCCACAATGGCATCATAAGGACAGGACCTTGTGCATGACACAGGATCAGATTTTAGAAGGCAGTATTTTGC
47▶ L C S G L D L D E V H N G I I R D R T L C M T Q D Q I L E G S I L

BglII (893)
801 TGACAGATGATGATGATCCACCTCAAATAACGTGTATCCACTGAAGTCTATTCAATGTGGCAACTCCCAGTGTGCTGGATGAGAAGCAGATCCT
80▶ L T D D D V S T S N N V S S T E V L F N V A T P S D V L D E K Q I F
901 CAGCTACCGGAAGTCTTTCAGACTCCAACCTGTTCAGGCCATCAATCTACCCTGCTCTACCCCTGAACCTGATGACCTGAAGCAAGACCA
113▶ S S P E V L S D S N S V Q A I N L P N F L L S T P E P D D L K K T

BstEII (1009)
1001 AGTGATGCTGGTGACCAGAAGGAGCATTCTGAGGAGGAGAAGGCTCCAGAGAGGAAAATCTTAGGAAGATGGGAAGGCACGGAAGAGAAACCGAAAAGA
147▶ S D A G D Q K E H S E E E K V S R E E N L R K M G K A R K R N R K

SphI (1139)
1101 CCAAGAACAACCGAAGTACCTCACCTGTCAGTACCCTAGCATGCCTATACGGAAGAAATCAAAGATGGCAAAGGCAGCACCATTATCTGTGGGAGTT
180▶ T K N N R S T S P V T D P S M P I R K K S K D G K G S T I Y L W E F

SapI (1207)
1201 CCTCTGGCTCTTCTGCAAGACAGAAAACCTGCCCAAGTACATTAAGTGGACGAGAGAGAAGGCATCTTCAAGTTGGTGGACTCCAAGGCTGTG
213▶ 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 V

NcoI (1349)
MscI (1391)
1301 TCCAAGCTGTGGGCAAGCAGAAAAACAACTGACATGAACTACGAGACCATGGGGCGAGCCCTGAGATATTATTATCAAAGAGGAATCCTGGCCAAAG
247▶ 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 K

Bst1107I (1417)
Bsu36I (1438)
1401 TGGAAGGGCAGAGGCTGGTATACCAGTTCAGGAGATGCCTAAGGACTTGGTGGTGATTGATGATGAAGAAGAGACCCTGAGACACCAGAAGACTCTTC
280▶ V E G Q R L V Y Q F K E M P K D L V V I D D E E E S P E T P E D S S

StuI (1502)
BspEI (1538)
1501 CCAGGCTCGACTTCTCCACACCTCGACCAGTACCACCGGAGAGCCAGCTCCAGGGTGGAAACCAGAGCCTCCCCGAGGACAAGGATAGCCCTCCC
313▶ Q A S T S S T P S T S T I R R A S S R V G T R A S P E D K D S P P
1601 TGGGAGAAGCCAAAAGTCCAACACTGGTCTCCAGCCATCTGCAAGCCTGGAGTTAGGATTGCTGTGGATGAGGAGTTCCACCACCTCCACCATGC
347▶ W E K P K V Q H T G L Q P S A S L E L G L S V D E E V P T T S T M

AvrII (1773)
1701 TTGCCAGCCACTACAGAGCCAGGCCAGGCTCACAAAACCTGTGAGTCTTCTCCAGCACCCAGTAACATCCACCTAGGAGTAGCCCTGTGGGGCCTGG
380▶ L A S P L Q S Q A R L T K T V S S S P A P S N I H L G V A P V G P G

ScaI (1861)
1801 CTCCACTGTACCCTGCAGACCATCCCGCTGACTACGGTGTGACCAATGGGCTCCTGCCAGTACTACTGCTCCAACCTCAACTCGTTCTTTCAGAGTGT
413▶ S T V 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 V
1901 CCGCAGGTGCAACATTCAGGACACCTTCACTTTGCAGACCTCCTTCCCCCTGAACCAATTTGCAAGAGAACCAGGTGGCAACCCAAAGGGCCCCAC
447▶ P Q V S T F K D T F T L Q T S F P L N T N L Q E N Q V A T Q G A P
2001 TGATCCTCAGTGGTCTCCCCCAACTTCTGGCTGGGGCCAAACCCTCAGAGCAACCAGCTCCATCCCAGGTGATAGGTGCTGGGTGAGGAGGCTAGCTC
480▶ L I L S G L P Q L L A G A N P Q S N P A P S Q V I G A G S A G P S S

NdeI (2192)
2101 TCAGCCCCCTGGGACTGTGATTGCTGCCTTTATCAGGACTTCCAGTGGCACATCAGTGCCTGTGGTAAAGGAGGGGCCCTTGGAGTCTCTTTCATATGTTG
513▶ Q P P G T V I A A F I R T S S G T S V P V V K E G P L R S S S Y V
2201 CAGGGTGTGGTACTGGGGCACCCGTGGAGGGGCTGTTGGTTCCTGAAGAGACCTGAGAGAGCTCCTGAGAGATCAGGGTCACTTTCAGCCACTTCCGA
547▶ Q G V V T G A P V E G L L V P E E T L R E L L R D Q G H L Q P L P
2301 GTCAGGTGCTCTCAAGGGTTCCATAACCTGAGCCTTGTGGGGAACCAAGTCTCTCCCCCTAGCCACCCACTGTTGGGCTAACCCAGTGGCTGA
580▶ S Q V L L S R G S H N L S L V G N Q T L S P P S H P T V G L T P V A E

XhoI (2401)
2401 GCTCGAGCTCTGTCAGGCTCAGGGCCCTGTTTCGTAACCTGAGCCTAGTGTGACCAGATCCCCAACCCAGGCCCTTTCTCCCATTCATCCCACTTCC
613▶ L E L S S G S G P L F V T E P S V T R S P T Q A P F S P F N P T S

MscI (2545)
NheI (2539)
2501 CTCATTAAGATGGAACCCCAAGATATATAAACAAGGGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGC
647▶ L I K M E P Q D I •

2601 **HpaI (2677)** MfeI (2688)
AGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCA

2701 **EcoRI (2773)**
TTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAAATTCTAAAATACAGCATAGCAAAC

2801
TTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGC

2901 **SapI (2955)**
CTCACCTTCTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGTTTGAAC TAGCTCTTCATTCTTTATGTTTTAAATGCACTGACCTCCCACATTC

3001 **SspI (3012)** **SwaI (3026)**
CCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAA

3101
TATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTT

3201 GAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCAC
135 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 I L E R C

3301 ATGCCACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCA
101 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 Q G N S V

3401 **StuI (3451)**
CAGCAGACCAATGGCAATGGCTT CAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGAT
68 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 T K T R I

3501 **XmnI (3593)**
GGCCGCCCGACATGGTGTCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTC
35 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 S I N F T

3601 **AseI (3659)**
TTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATC
14 K M

3701 TGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTGGAA

3801 **SpeI (3814)**
AGTCCCGTTGATTTACTAGTCAAACAACCTCCATTGACGTCAATGGGGTGGAGACTGGAAATCCCGTGAGTCAAACCGTATCCACGCCATTGAT

3901 **SnaBI (3942)**
GTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCATGTACTGGGCATAATGC

4001 **NdeI (4047)**
CAGGCGGGCCATTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTATGTA CTGCAAGTGGGCAGTTTACCGTAAATACTCCA

4101
CCCATTGACGTCAATGAAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGG

4201 **PacI (4233)** **SdaI (4225)** **BspLU11I (4243)**
GCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAAAAGCCGCGTTGCTGG

4301
CGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATC GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTT

4401
TCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCAT

4501 **ApaLI (4557)**
AGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGCTGCGCCTTATCCG

4601
GTAACATCGTCTTGAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGC

4701
TACAGAGTCTTGAAGTGGTGGCCTAACGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGAGTT

4801
GGTAGCTCTTGATCCGGCAAACAACCCGCTGGTAGCGGTGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATC

4901 **EagI (4993)** **PacI (4973)** **SwaI (4982)** **NotI (4992)**
CTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGC

5001
AATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAAACAAAACGAAACAAAACAAC

5101
TAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTATCGAA