



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCGCCCTACCTGAGGGC
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTACCATTGGAACATTTTATCCCTGGGTTTCAACCTAAAAAGA
1 M E H F D P L G F N L K D

XmnI (630)
601 CGTCCTGAGAAAGCTGGACAAGACTGAGTTGAACAATTTCAAGAGAACATTGAGGAGCTGTTCTCTGCCAGATACAATGAAACAGATCAACAAGCTGACA
13 V L R K L D K T E L N N F K R T L R S C S L P D T M K Q I N K L T

NheI (723)
701 ATGGACCTGGCTAATGGAGCTCAGTAGCAGAAATTCACAGACCACTGCCCGAGTCTGGATAAAGAGAGTCACCGTCCAGATCTTAGAGGAAATAA
47 M D L A N G A Q L A E I L T D H C P S A W I K R V T V Q I L E E I

Bsu36I (859)
Acc65I (855)
801 ACCGTGTAGATCTAGCTGAGTTAGTAGTAAAGCAAATCGAAGAAGCAGTATTAAGGTACCTGAGGAAAAGGTTTCTTCTAAACCAAGAGAACCCTCGGG
80 N R V D L A E L V V K Q I E E A V L K V P E E K V S S K P R E P S G
901 GACACTAACTTTCCCATGGAATTTGTTCAAGGAGCTAAAAGGCCAGAGGACAAGCAAAAAGAGGAATGGAAGACTAGATACACAGCTAAATGGAAGCAG
113 T L T F P W N F V Q G A K R P E D K Q K E E W K T R Y T A K W K Q
1001 AACTTCTGGCCTAAATGCAATAAAGAAATCTATGTGGTTACCGAGAGCTACAAGACACTCCTGGCATTGTGTAACCCAAAGATAGAAACCCCATTTGCTC
147 N F W P K C N K E I Y V V T E S Y K T L L A L C N P K I E T P F A
1101 ATGCAATTGTGCTGCATGGCCCTCCAGGCTCTGGGAAAACCACAATGGCAAAGCAGCTAATGTTAGAATGGTCAGAGAGTAAGCAGGCCAGATTTTCTC
180 H A I V L H G P P G S G K T T M A K Q L M L E W S E S K Q A Q I F S

PvuII (1215)
1201 ATGTGCCTTCTACATCAGCTGCAGGGAAGTAATAATACTAAACCTTGCACTTTTCCCACCTCCTCTCCATGGACAATCCCTCCTGGAGGGACTGTGTG
213 C A F Y I S C R E V N N T K P C T F A H L L S M D N P S W R D C V
1301 ATTCGAGATCTAATCCTGGGAAAGGAATTTCTATTTGTGGTAGATGGTTTTGATGAGCTGACATTCACGAGGAGCTCTGATCCGTGACCTTTGTGGTG
247 I R D L I L G K E F L F V V D G F D E L T F P A G A L I R D L C G

BstXI (1469) **Tth11I (1491)**
1401 ACTGGAACACAGTGAAGCCTGTAGAGGTCTTACTGGGCAGTTTGTGAAGAGGAAGATGGCACCTCATGCCACCTGTGGTAACCACACGGACACAGTC
280 D W N T V K P V E V L L G S L L K R K M A P H A T L L V T T R T Q S

BspHI (1517) **SpeI (1536)** **ScaI (1577)**
1501 TTTGCACCAAATCTTTGTCATGATGGATCAGCCACTACTAGTAGAAACTCTGGGCTTCTGGAGCAAGAAAAGCAGGAGTACTTTAGAAAATCTTTGAA
313 L H Q I F V M M D Q P L L V E T L G F L E Q E K Q E Y F Q K Y F E
1601 GATGAGGAGGGTGAAGGAGGATAAAGGTGAGGAAAAGGCACCTAGAGCTCTCAAGGAAGTGAAGTGAATGCTGATCTATACCAATGGCCTCACTTC
347 D E E G E E E D K G E G K A L R A L K E V R C N A D L Y Q M A S L

BspLU11I (1768)
1701 CTAATGATGTGGGATATTCTGCCTCTGTCTGGAGCTAAGGATGAAGAAGGGGAAGACCTGTCTCTGACATGTCAGACATACACCTCTATGTTCTGAA
380 P T A C G I F C L C L E L R M K K G E D L S L T C Q T Y T S M F L N

XcmI (1892)
1801 CTTCTGTGCGAAGTCTTCTCATCAGAAACCTGTGAGGACCATCTCAATGAGGAATCCAAATCTTATTCAAGAAAATATGTATCCTGGCTGCCAATAGT
413 F L C E V F S S E T C E D H L N E E F Q I L F K K I C I L A A N S
1901 CTCTTGGAAACAGGTGCCATACTCTGTGAAGAAGACTTCTTGACATTAATAATGAACCTAAACAATTTGCATCCCATGGTGTGAGGACATCCTCTTTA
447 L L E Q V P I L C E E D F L T L K L N L N N L H P M V C R H I L F
2001 AGGACAGTTCCAGTACACACTGTCTCTTTTCTGCTCGGTATCCAGCAACTCCTGGCTGCAATAATATTTGTTGAGGAGCTTGACAGGAAAAGCAA
480 K D S S S T H C L S F I C L G I Q Q L L A A I I F V Q E L G Q E S K

Bst1107I (2117)
2101 GGGTGTCTCTAAATATAGTATACAGAACATGCTTTCAAGGGAAGCAAGATTAATAAACCTGACCTGTCTGGGCTGCTGCCATTTGTATTTGGCTCCTG
513 G V S K Y S I Q N M L S R E A R L K N P D L S G L L P F V F G L L
2201 AATGAGACTCGTATTCAAGAGTTGAAGACTACTTTTGGCTGCCAAATATCAACTGAGGTCAAGAGAAAATTCCTGGAGTGTGAGTCAAGGAAAATAAAC
547 N E T R I Q E L K T T F G C Q I S T E V K R K F L E C E S G E N K
2301 CCTTACTATTACTGATGAATATGCAAGAAATCTTGTCTGTCTATGAATCTCAGGAGGAGGGGTTTGTGAAGGAAGCCATGGTCTCTTTGAGGACAT
580 P L L L L M N M Q E I L S C L Y E S Q E E G F V K E A M V L F E D I

Tth11I (2472)
2401 CTCCTTGCAATTTGAAAACAGCACTGACCTCATTATGCTTCTGCTCAAGAACTCTCAGAAGTTCAGACAATGTCCCTGAAAGTAGAAAAGGGC
613 S L H L K T S T D L I H A S F C L K N S Q N L Q T M S L K V E K A

2501 GTCTTTCCAGAGAATGTTGCTGCACTAGAGTCCACAGCTAAGCATCAAAGGTCCCGGATGAACAACGCATGTTAACTTTCTGGACAGACTTTTGTGACA
647▶ V F P E N V A A L E S T A K H Q R S P D E Q R M L T F W T D F C D
XbaI (2628) HindIII (2643)

2601 CATTAAATCAAATAAGAACTGGTATTCTAGACATCCATGAAAGCTTCTCAACAGCTCTGCACTGGAGATTCTTTGTGAAAAGCTGCCCTCTGCTTC
680▶ T F N S N K K L V F L D I H E S F L N S S A L E I L C E K L P S A S
2701 CTGTTGTCTCCAGAAAGTGGTCTCAAAAATATTTCCAGATGATGCCTACGAGAAATTGTGCCTCATTTTTAATGGTTATAAAACCATCTCACATCTG
713▶ C C L Q K V V L K N I S P D D A Y E K L C L I F N G Y K T I S H L
NsiI (2827)

2801 ATCCTGCAAGGTGGCAACCTGGACAGCATGCATCACTCACTGTGTGAGTTCTGAAAAATCCAGCCTGCAACCTGAAGTTTCTCAGCCTGGGATCTTGTT
747▶ I L Q G G N L D S M H H S L C E V L K N P A C N L K F L S L G S C
SphI (2825) DraIII (2837)

2901 CTACTGCTGCTCAGAAATGGGATGACTTCTCCAGTCTGAAAGTCAATCAATCCCTGATATTTCTGGATCTCACAGACAACAGTCTCTGGACAAAAG
780▶ S T A A Q K W D D F F P V L K V N Q S L I F L D L T D N S L L D K S
3001 TGCTAAGCTCCTATGTAATATTTGGAAGGAACCAAAGTGCATACTGCAGAGGGTATCGTTGGAGAAGTGTGAGCTCACTGAAGCCTGTGCAAGGACCTC
813▶ A K L L C N I W K E P K C I L Q R V S L E N C Q L T E A C C K D L
PshAI (2977)

3101 TCTTCCGTTTTGATGGTCAGCCGAACCTGACACACCTCAGCCTGGCCAACAATAAATTGGGGATAACGGAGTGAAAAACCTGTGTGAAAGCATAAGCT
847▶ S S V L M V S R T L T H L S L A N N K L G D N G V K N L C E S I S
MscI (3143)

3201 GCACGGAGTGCAATCTACAGACCTGGTGTGTGGTCTGTAACATCACCAACGCTGGTTGCCACTATCTCTCAAAGATGCTCAAACAAACACTGAGCCT
880▶ C T E C N L Q T L V L W S C N I T N A G C H Y L S K M L K Q T L S L
3301 GAAACACTTGGATCTGGGGCTAAATCGCATCGGAACCAAAGGAGCAAAGTTTCTGTGTGAGGCTTTGAAGAACCCCAAGAGTAAATGAAAAGTCTGTGG
913▶ K H L D L G L N R I G T K G A K F L C E A L K N P K S K L K S L W
DraIII (3201)

3401 CTGTGTGGATGCTCCATCACTCCACTGCAAGACTTCTGTGAGACTCTTAGAAGCAACAAGAGCCTGAACACTCTAGACCTGTCTCAGAAGCTCC
947▶ L C G C S I T P L N C Q D F S E T L R S N K S L N T L D L S Q N V
3501 TGGAACTGATGCCATAAAGACATTCTGTGAAGCCTTGAACCTTCAAGATTTGCCCCCTGCAAAATGCTTAGATTGAAATTTGATGAAGCTAAACCTAGTAT
980▶ L G T D A I K T F C E A L K L Q I C P L Q M L R L K F D E A K P S I
3601 CCAGAAGCTGATCAAGAGATGAAGGTGAGCCATCCACAAGTGAAGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
1013▶ Q N L I Q E M K V S H P Q L R I S S D Q V D L K N P P L P H F I F
AvrII (3703) MscI (3715)

3701 TGACCTAGGACTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAACCCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTT
1047▶ •

3801 GTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACACAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGGGAGGTGTG
HpaI (3847)

3901 GGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAA
4001 TCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTAAGATATA

4101 GTGTATTTTCCAAGGTTTGAAGTAGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTATAGTAAATATTCAGAAATAATTT
SapI (4125) SmaI (4196)

4201 AAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGG
4301 AACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTT
141▶ • N R T Y K L P I L E E I T T K
BstXI (4486)

4401 GACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGAT
125▶ V L K G N M E 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
4501 CTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCAC
91▶ R D V E D S Y 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
StuI (4621)

4601 AGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGTCTC
58▶ V T V R G I 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
XmnI (4763)

4701 ATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTA
25▶ Y L M T I K E T A V E V L E L D Q Q S I N F T K M

4801 TTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATA
AseI (4829)

4901 TAGACCTCCCACGTTACACGCCTACCGCCATTTGCGTCAATGGGGGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGGATTTACTAGTCAAAAACAAC
SpeI (4984)

5001 TCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAAT

SnaBI (5112)

5101 AGCGATGACTAATACGTAGATGTAAGTCCATAAAGTCTGACTGGGCATAATGCCAGGCGGGCCATTACCGTCATTGACGTCA

NdeI (5217)

5201 ATAGGGGGCGTACTTGGCATATGATACACTTGATGTAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTG

SdaI (5395)

5301 GCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTACCGTAAGTTATGTAACGCCCTGC

PacI (5403) BspLU11I (5413)

5401 AGGTTAAITAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACG

5501 AGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCC

5601 TGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTG

ApaLI (5727)

5701 TAGGTCGTTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAA

5801 GACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTA

5901 CGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACACC

6001 GCTGGTAGCGGTGGTTTTTTTGGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTC

EagI (6163)

PacI (6143) SwaI (6152) NotI (6162)

6101 AGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAGCGGCCGCAATAAAAATATCTTTATTTTCATTACATCTG

6201 TGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTG

6301 CAGGTGCCAGAACATTTCTATCGAA