



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
 301 GCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552)
BspHI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCATCAGGGTCTGGGTGGGCGCTCGGGGGCGCTGCTGGC
 601 GTGTCTCCTCCTAGTCTCCGCTCTCAGAGGCAAACCTTTTTGTCAAAGCAACAGGCTTCAAAAGTCTGGTTAGGAAGCGTCTGCAAATCTTTACTT
 13▶ C L L L V L P V S E A N F L S K Q Q A S Q V L V R K R R A N S L L

NsiI (732)

701 GAAGAAACCAAACAGGGTAATCTTAAAGAGAATGCATCGAAGAACTGTGCAATAAAGAAGAAGCCAGGGAGGTCTTTGAAAATGACCCGAAACGGATT
 47▶ E E T K Q G N L E R E C I E E L C N K E E A R E V F E N D P E T D
 801 ATTTTTATCCAAAATACTTAGTTGTCTTCGCTTTTTCAAACCTGGGTTATCACTGCTGCACGTGAGTCAACTAATGCTTATCCTGACCTAAGAAGCTG
 80▶ Y F Y P K Y L V C L R S F Q T G L F T A A R Q S T N A Y P D L R S C

HindIII (974)

901 TGTCATGCCATTCCAGACCAGTGTAGTCTCTGCCATGCAATGAAGATGGATATATGAGCTGCAAAGATGGAAAAGTCTTTTACTTGCACCTGTAAA
 113▶ V N A I P D Q C S P L P C N E D G Y M S C K D G K A S F T C T C K
 1001 CCAGGTTGGCAAGGAGAAAAGTGTGAATTTGACATAAATGAATGCAAAGATCCCTCAAATATAAATGGAGGTTGCAGTCAAATTTGTGATAATACACCTG
 147▶ P G W Q G E K C E F D I N E C K D P S N I N G G C S Q I C D N T P
 1101 GAAGTTACCACTGTTCTGTAAAAATGGTTTTGTTATGCTTTCAAATAAGAAAAGATTGTAAGATGTGGATGAATGCTTTTGAAGCCAAGCATTGTGG
 180▶ G S Y H C S C K N G F V M L S N K K D C K D V D E C S L K P S I C G

PvuII (1202)

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

BspLU11I (1310)

1301 TGCTCTGAGAACATGTGCTCAGCTTTGTGCAATTACCCTGGAGGTTACACTTGTCTATTGTGATGGGAAGAAGGATTCAAACCTGCCAAGATCAGA
 247▶ C S E N M C A Q L C V N Y P G G Y T C Y C D G K K G F K L A Q D Q
 1401 AGAGTTGTGAGGTTGTTTCAGTGTGCCCTCCCTTGAACCTTGACACAAAGTATGAATTACTTTACTTGGCGGAGCAGTTTGACGGGTTGTTTATATTT
 280▶ K S C E V V S V C L P L N L D T K Y E L L Y L A E Q F A G V V L Y L

NdeI (1553)

BspEI (1547)
ClaI (1591)

1501 AAAATTCGTTTCCAGAAATCAGCAGATTTTTCAGCAGAAATTTGATTTCCGGACATATGATTGAGAAGGCGTGACTGTACGCAGAATCTATCGATCAC
 313▶ K F R L P E I S R F S A E F D F R T Y D S E G V I L Y A E S I D H

DraIII (1619)

1601 TCAGCGTGGCTCCTGATTGCACCTCGTGGTGGAAAGATTGAAGTTCAGCTTAAAGATGAACATACATCCAAAATCACAACCTGGAGGTGATGTTATTAATA
 347▶ S A W L L I A L R G G K I E V Q L K N E H T S K I T T G G D V I N
 1701 ATGGTCTATGGAATATGGTGTCTGTGGAAGAATTAGAACATAGTATTAGCATTAAAATAGCTAAAGAAGCTGTGATGGATATAAATAAACCTGGACCCCT
 380▶ N G L W N M V S V E E L E H S I S I K I A K E A V M D I N K P G P L

XbaI (1896)

1801 TTTAAGCCGGAAAATGGATTGCTGAAACCAAAGTATACTTTGCAGGATCCCTCGGAAAAGTGGAAAAGTGAACCTATAAACCGATTAACCCCTGCTCA
 413▶ F K P E N G L L E T K V Y F A G F P R K V E S E L I K P I N P R L
 1901 GATGGATGTATACGAAGCTGGAATTTGATGAAGCAAGGAGCTTCTGGAATAAAGGAAATTTCAAGAAAAACAAAATAAGCATTGCCTGGTACTGTGG
 447▶ D G C I R S W N L M K Q G A S G I K E I I Q E K Q N K H C L V T V
 2001 AGAAGGGCTCCTACTATCCTGGTCTGGAATTGCTCAATTTACATAGATTATAAATAATGTATCCAGTGTGAGGGTTGGCATGTAATGTGACCTTGAA
 480▶ E K G S Y Y P G S G I A Q F H I D Y N N V S S A E G W H V N V T L N
 2101 TATTCGTCACACGGGCACTGGTGTATGCTTGCCTTGGTTCGTAACAACACAGTGCCTTTGCTGTGTCCTTGGTGGACTCCACCTCGAAAAA
 513▶ I R P S T G T G V M L A L V S G N N T V P F A V S L V D S T S E K
 2201 TCACAGGATATTCTGTGTTGAAAATACTGTAATATATCGGATACAGGCCCTAAGTCTATGTTCCGATCAACAATCTCATCTGGAATTTAGAGTCA
 547▶ S Q D I L L S V E N T V I Y R I Q A L S L C S D Q Q S H L E F R V

SalI (2319)

2301 ACAGAAACAATCTGGAGTTGTGCACACCACTTAAAATAGAAACCATCTCCCATGAAGACCTTCAAAGACAACCTGCGCTCTTGACAAAAGCAATGAAAGC
 580▶ N R N N L E L S T P L K I E T I S H E D L Q R Q L A V L D K A M K A

BstXI (2408)
BsrGI (2499)

2401 AAAAGTGGCCACATACCTGGGTCCTCCAGATGTTCCATTGAGTGCACACCAAGTGAATGCCTTTTATAATGGCTGCATGGAAGTGAATATTAATGGT
 613▶ K V A T Y L G G L P D V P F S A T P V N A F Y N G C M E V N I N G

EcoRI (2583)

2501 GTACAGTTGGATCTGGATGAAGCCATTTCTAAACATAATGATATTAGAGCTCACTCATGTCCGTCAGTTTGGAAAAAGACAAAAGATTCTTAAGGCATCT
 647▶ V Q L D L D E A I S K H N D I R A H S C P S V W K K T K N S •

2601 TTTCTCTGCTTATAATACCTTTTCCTTGTGTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAA

NheI (2631)

2701 AAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACCAAGTTAACAAACAATTGCATTCAATTTATGT

HpaI (2769) MfeI (2780)

2801 TTCAGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCT

EcoRI (2865)

2901 CCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTT

SapI (3047)

3001 CTTTCATGGAGTTTAAGATATAGTGATTTTTCCAAGGTTTGAAGTACTCTTCTATTCTTTATGTTTTAAATGACTGACCTCCACATTCCCTTTTTTA

SwaI (3118)

3101 GTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCC

3201 AGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGA

BstXI (3408)

3301 TGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACA

132 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 M G C

BstXI (3408)

3401 GGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGAC

99 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 A S

StuI (3543)

3501 CCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCC

65 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 A A G

3601 CGCATGGTGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGT

32 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 K M

3701 GGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTT

3801 CACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGT

SpeI (3906)

3901 TGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCC

SnaBI (4034)

4001 AAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTGGCATAATGCCAGGCGGG

NdeI (4139)

4101 CCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGA

4201 CGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTA

PacI (4325)

PstI (4318)

SdaI (4317)

BspLU11I (4335)

4301 CCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCGGAACCGTAAAAAGGCCGCTTGTGGCCTTTTTC

4401 CATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTG

4501 GAAGTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGG

ApaLI (4649)

4601 CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTCACGAACCCCGTTCAGCCCAGCCGCTGCGCTTATCCGGTAACTAT

4701 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGT

4801 TCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTC

4901 TTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATC

EagI (5085)

PacI (5065) SwaI (5074) NotI (5084)

5001 TTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAAT

5101 ATCTTTATTTTTCATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAA

5201 TAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA