



125

PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGTGGCGGGGTAAGTGGAAAGTGTGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245) **EcoNI (287)**

201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535)
AgeI (552) **BspLU11I (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCAACATGTCAGGGTGGGAGTCATATTACAAAACCGAGGGCGA
 601 TGAAGAAGCAGAGGAAGAACAAGAAGAGAACCTGAAGCAAGTGGAGACTATAAATATTCAGGAAGAGATAGTTTGTATTTTTTGGTTGATGCCTCCAAG
 13▶ E E A E E E Q E E N L E A S G D Y K Y S G R D S L I F L V D A S K

BsrGI (770) **BsaBI (796)**

701 GCTATGTTTGAATCTCAGAGTGAAGATGAGTTGACACCTTTTGCATGAGCATCCAGTGTATCCAAAGTGTGTACATCAGTAAGATCATAAGCAGTGTATC
 47▶ A M F E S Q S E D E L T P F D M S I Q C I Q S V Y I S K I I S S D

BglII (801)
Acc65I (826)

801 GAGATCTTTGGCTGTGGTGTCTATGGTACCGAGAAAGACAAAAATTCAGTGAATTTAAAAATTTTACGTTTACAGGAGCTGGATAATCCAGGTGC
 80▶ R D L L A V V F Y G T E K D K N S V N F K N I Y V L Q E L D N P G A

XbaI (909)
EcoRI (905) **Psp1406I (947)** **DraIII (986)**

901 AAAACGAATTCAGAGCTTGACCAGTTTAAAGGGGAGCAGGGACAAAAACGTTTCCAAGACATGATGGCCACGGATCTGACTACTCAGTGAAGTGC
 113▶ K R I L E L D Q F K G Q Q G Q K R F Q D M M G H G S D Y S L S E V

NcoI (1086)

1001 CTGTGGGTCTGTGCCAACCTCTTAGTGATGTCCAATTCAGATGAGTCATAAGAGGATCATGCTGTTCCACCAATGAAGACAACCCCATGGCAATGACA
 147▶ L W V C A N L F S D V Q F K M S H K R I M L F T N E D N P H G N D
 1101 GTGCCAAAGCCAGCCGGCCAGGACCAAAGCCGGTGATCTCCGAGATACAGGCATCTTCTTGAFTTGTGACCTGAAGAAACCTGGGGGCTTTGACAT
 180▶ S A K A S R A R T K A G D L R D T G I F L D L M H L K K P G G F D I

EcoRV (1216)

1201 ATCCTTGTCTCAGAGATATCATCAGCATAGCAGAGGATGAGGACCTCAGGGTTCACTTTGAGGAATCCAGCAAGCTAGAAGACCTGTTGCGGAAGGTT
 213▶ S L F Y R D I I S I A E D E D L R V H F E E S S K L E D L L R K V
 1301 CGCGCAAGGAGACCAAGGAGCGAGCACTCAGCAGGTTAAAGCTGAAGCTCAACAAAGATATAGTGATCTCTGTGGGATTTATAATCTGGTCCAGAAGG
 247▶ R A K E T R K R A L S R L K L K L N K D I V I S V G I Y N L V Q K
 1401 CTCTCAAGCTCCTCCAATAAAGCTCTATCGGAAACAAATGAACAGTGAACCAAGACCCGGACCTTAAACAAGTACAGGCGGTTTGTCTCTGCC
 280▶ A L K P P P I K L Y R E T N E P V K T K T R T F N T S T G G L L L P

BglII (1520)

1501 TAGCGATACCAAGAGGTCTCAGATCTATGGGAGTCGTGAGATTACTGGAGAAAGAGGAAACAGAAGAGCTAAAACGGTTTGTGATCCAGGTTTGTGAT
 313▶ S D T K R S Q I Y G S R Q I I L E K E E T E E L K R F D D P G L M
 1601 CTCATGGGTTTCAAGCCGTTGGTACTGCTGAAGAAACACCATTACCTGAGGCCCTCCCTGTTCTGTGATCCAGAGGAGTGCCTGGTATTGGGAGCTCAA
 347▶ L M G F K P L V L L K K H H Y L R P S L F V Y P E E S L V I G S S
 1701 CCCTGTTCAAGTGTCTGCTCATCAAGTGTCTGGAGAAGGAGGTTGCAGCATTGTGAGATACACACCCCGAGGAACATCCCTCTTATTTTGTGCTTT
 380▶ T L F S A L L I K C L E K E V A A L C R Y T P R R N I P P Y F V A L

PvuII (1858)

1801 GGTGCCACAGGAAGAAGAGTTGGATGACCAGAAAATTCAGGTGACTCCTCCAGGCTTCCAGCTGGTCTTTTTACCCTTTGCTGATGATAAAAGGAAGATG
 413▶ V P Q E E E L D D Q K I Q V T P P G F Q L V F L P F A D D K R K M

HindIII (1963)

1901 CCCTTACTGAAAAATCATGGCAACTCCAGAGCAGGTGGGCAAGATGAAGGCTATCGTTGAGAAGCTTCGTTTACATACAGAAGTGCAGCTTTGAGA
 447▶ P F T E K I M A T P E Q V G K M K A I V E K L R F T Y R S D S F E

PstI (2008)

2001 ACCCCGTGCTGCAGCAGCACTTCAGGAACCTGGAGGCCTTGGCCTTGATTTGATGGAGCCGGAACAAGCAGTGGACCTGACATTGCCAAGGTTGAAGC
 480▶ N P V L Q Q H F R N L E A L A L D L M E P E Q A V D L T L P K V E A

BsaBI (2158)

2101 AATGAATAAAAGACTGGGCTCCTTGGTGGATGAGTTTAAAGGAGCTTGTATCCACCAGATTACAATCCTGAAGGGAAAGTTACCAAGAGAAAAACAGAT
 513▶ M N K R L G S L V D E F K E L V Y P P D Y N P E G K V T K R K H D
 2201 AATGAAGTTCTGGAAGCAAAAGCCAAAGTGGAGTATTCAGAAAGAGGAGCTGAAGACCCACATCAGCAAGGATACGCTGGGCAAGTTCAGTGTGCCCA
 547▶ N E G S G S K R P K V E Y S E E E L K T H I S K G T L G K F T V P

NheI (2398) **XcmI (2392)**

2301 TGCTGAAAGAGGCTGCCGGCTTACGGGCTGAAGAGTGGGCTGAAGAAGCAGGAGCTGCTGGAAGCCCTCACCAAGCACTTCCAGGACTGACCAGAGGC
 580▶ M L K E A C R A Y G L K S G L K K Q E L L E A L T K H F Q D •

MscI (2404)

2401 TAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATT

HpaI (2536)
MfeI (2547)

2501 GCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTAAACAACAACATTCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTT

EcoRI (2632)
2601 AAAGCAAGTAAAACCTCTACAAATGTGGTATGGAAATCTAAAATACAGCATAGCAAACCTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGA
2701 GGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCC

SwaI (2885)
2801 CAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCAT
2901 TGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAAC
3001 CTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGC
141 • N R T Y K L P I L E E I T T K V L K G

BstXI (3175)
3101 CATTCACTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCCCTGATGGATCTGTCCACCTC
121 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 R D V E
3201 ATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAAGCAGACAGTGAAC
88 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 V T V
3301 CTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTGGTCTGATGGCCGCCGACATGGTGCCTGTTGTCTCATAGAGCATGG
54 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 Y L M T

BspHI (3460)
XmnI (3452)
3401 TGATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGC
21 I K E T A V E V L E L D Q S I N F T K M

AseI (3518)
3501 CGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCC

SpeI (3673)
3600 ACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTACTAGTCAAAAACAACTCCCATTGA
3699 CGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAACCGCATCATCATGGTAATAGCGATGAC

SnaBI (3801)
3799 TAATACGTAGATGTAAGTCCAGTAGGAAAGTCCATAAGGTCATGTAAGTCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGC

NdeI (3906)
3899 GTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTA

PstI (4085)
SdaI (4084) PacI (4092)
3999 TGGGAACATACGTCATTATTGACGTCAATGGGCGGGGCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCCTGCAGGTTAA

BspLU11I (4102)
4097 TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCA
4197 CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCG
4297 ACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGC

ApaLI (4416)
4397 TTCGCTCAAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCGTAAGACACGA
4497 CTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTAC
4597 ACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGMAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTA
4697 GCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAA

EagI (4852)
PacI (4832) SwaI (4841) NotI (4851)
4797 CGAAAACCTACGTTAAGGGATTTGGTCAATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTG
4897 GTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGC
4997 CAGAACATTTCTCTATCGAA