



PvuI (7)
SgfI (6)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **NcoI (568)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTAGGAGGGCCACCATGGTGTTCATGTGACACTGAAGAGA
601 CTAATTCTTATCCTTTTTAACAATAATCCTAATTTCCAAACTCTTGGGCTAGATGGTTTCTAAAACCTGTCCTGTGATGTCACCTGGATGTTCCAA
111 L I L I L F N I I L I S K L L L G A R W F P K T L P C D V T L D V P
701 AGAACCATGTGATCGTGGACTGCACAGACAAGCATTGACAGAAATCCTGGAGGTATCCACGAACACCACGAACCTCACCTCACATTAACCACAT
44 K N H V I V D C T D K H L T E I P G G I P T N T T N L T L T I N H I

ClaI (849) **BspLU11I**
801 ACCAGACATCTCCCAGCGTCTTTACAGACTGGACCATCTGGTAGAGATCGATTTTCAGATGCAACTGTGTACCTATCCACTGGGGTCAAAAAACAAC
77 P D I S P A S F H R L D H L V E I D F R C N C V P I P L G S K N
901 ATGTGCATCAAGAGGCTGCAGATTAACCCAGAAGCTTTAGTGGACTCACTTATTTAAAATCCCTTTACCTGGATGGAACACAGCTACTAGANATCCGC
111 M C I K R L Q I K P R S F S G L T Y L K S L Y L D G N Q L L E I P
1001 AGGGCCTCCCGCTAGCTTACAGCTTCTCAGCCTGAGGCCAACACATCTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCCACATAGAAATACT
144 Q G L P P S L Q L L S L E A N N I F S I R K E N L T E L A N I E I L
1101 CTACCTGGCCAAAACCTGTTATTATCGAAATCCTGTTATGTTTCATATTCAATAGAGAAAAGATGCCTTCTAAACTTGACAAAAGTTAAAAGTCTCTCC
177 Y L G Q N C Y Y R N P C Y V S Y S I E K D A F L N L T K L K V L S
1201 CTGAAAGATAACAATGTCACAGCCGCTCCTACTGTTTTGCCATCTACTTTAACAGAATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATG
211 L K A D N N V T A V P T V L E P S T L T E L Y L Y N N M I A K I Q E D
1301 ATTTAATAACCTCAACCAATTAACAATTTCTGACCTAAGTGGAAATGCCCTCGTTGTATAATGCCCATTTCTTGTGKCCCGTGTAAAATAATTC
244 D F N N L N Q L Q I L D L S G N C P R C Y N A P F P C A P C K N N S
1401 TCCCTACAGATCCCTGTAATGCTTTTGTGCGCTGACAGAATTAAGTTTACGCTACACAGTAACTCTCTCAGCATGTGCCCAAGATGGTTT
277 P L Q I P V N A F D A L T E L K V L R L H S N S L Q H V P P R W F
1501 AAGAACATCAACAACTCCAGGAACTGGATCTGTCCAAAACCTTCTGGCCAAAAGAAATGGGGATGCTAAATTTCTGCATTTTCTCCCAGCCTCATCC
311 K N I N K L Q E L D L S Q N F L A K E I G D A K F L H F L P S L I
1601 AATTGGATCTGTCTTTCAATTTTGAACCTCAGGCTATCGTGCATCTATGAATCTATCACAAGCATTTCTTCACTGAAAAGCCTGAAAATCTCGCGGAT
344 Q L D L S F N F E L Q V Y R A S M N L S Q A F S S L K S L K I L R I
1701 CAGAGGATATGCTTTAAAGAGTTGAAAAGCTTAACTCTCGCCATTACATAATCTTCAAAAATCTTGAAGTCTTGATCTTGGCACTAACTTTATAAAA
377 R G Y V F K E L K S F N L S P L H N L Q N L E V L D L G T N F I K

PmeI (1817) **BglII (1847)**
1801 ATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGACTGAAAGTCATAGATCTTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCT
411 I A N L S M F K Q F K R L K V I D L S V N K I S P S G D S S E V G
1901 TCTGCTCAAATGCCAGAACTTGTAGAAAGTATGAACCCAGGTCCTGGAACAATTACATTTTTCAGATATGATAAGTATGCAAGGAGTTGCAGATT
444 F C S N A R T S V E S Y E P Q V L E Q L H Y F R Y D K Y A R S C R F
2001 CAAAAACAAGAGGCTTCTTTTCAATGCTGTTAATGAAAGCTGTACAAGTATGGGCGACCTTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGTCC
477 K N K E A S F M S V N E S C Y K Y G Q T L D L S K N S I F F V K S
2101 TCTGATTTTTCAGCATCTTTCTTCTCAATGCCTGAATCTGTGAGAAATCTCATTAGCCAAACTCTAATGGCAGTGAATCCAACCTTTAGCAGAGC
511 S D F Q H L S F L K C L N L S G N L I S Q T L N G S E F Q P L A E

XmnI (2256)
SapI (2256)
2201 TGAGATATTTGGACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTTGAAAGAGCTTCAAAAACCTGGAAGTTCTGGATATAAGCAGTAATAG
544 L R Y L D F S N N R L D L L H S T A F E E L H K L E V L D I S S N S

NdeI (2328)
2301 CCATTATTTTCAATCAGAAGGAATTACTCATATGCTAAAATTTACCAAGAACCTAAAGGTTCTGCAGAACTGATGATGAACGACAATGACATCTCTTCC
577 H Y F Q S E G I T H M L N F T K N L K V L Q K L M M N D N D I S S

NcoI (2413)
2401 TCCACCAGCAGGACCATGGAGAGTGTGAGTCTTTAGAATCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTAC
611 S T S R T M E S E S L R T L E F R G N H L D V L W R E G D N R Y L
2501 AATTATCAAGAATCTGCTAAAATAGAGGAATTAGACATCTCTAAAATCCCTAAGTTTCTTGCCTTCTGGAGTTTTGATGGTATGCCTCCAATCT
644 Q L F K N L L K L E E L D I S K N S L S F L P S G V F D G M P P N L
2601 AAAGAATCTCTTTGGCCAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGTCTAAAGAACCTGGAACCTTTGGACCTCAGCCACAACCAA
677 K N L S L A K N G L K S F S W K K L Q C L K N L E T L D L S H N Q

PshAI (2702)
2701 CTGACCACTGTCCCTGAGAGATTATCCAATGTTCCAGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTAC
711 L T T V P E R L S N C S R S L K N L I L K N N Q I R S L T K Y F L

EcoRV (2818)
2801 AAGATGCCTTCCAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCAGAAAATGTCTCAACAATCTGAAGAT
744▶ Q D A F Q L R Y L D L S S N K I Q M I Q K T S F P E N V L N N L K M

ApaLI (2927) **HpaI (2961)**
2901 GTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGGTTAACCATACGGAGGTGACTATTCCTTACCTGGCCACA
777▶ L L L H H N R F L C T C D A V W F V W W V N H T E V T I P Y L A T

BsrGI (3058) **BglIII (3074)**
3001 GATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGCCAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCT
811▶ D V T C V G P G A H K G Q S V I S L D L Y T C E L D L T N L I L F
3101 CACTTCCATATCTGTATCTCTCTTCTCATGGTGTGATGACAGCAAGTCACTCTATTTCTGGGATGTGTGGTATATTTACCATTCTGTAAAGCCAA
844▶ S L S I S V S L F L M V M M T A S H L Y F W D V W Y I Y H F C K A K

NheI (3240)
3201 GATAACGGGGTATCAGCGTCTAATATCACCAGACTGTAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATG
877▶ I T G Y Q R L I S P D C •

HpaI (3378)
3301 CAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAGTTAACAAACAACAAATTGCATTC
3401 ATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAA
3501 CTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAG

SapI (3656)
3601 CCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCAAGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATT

SspI (3713) **SwaI (3727)**
3701 CCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATA
3801 ATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACT
141▶ • N R T Y K

SacI (3988)
3901 TGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCA
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

BstXI (4017)
4001 CATGCCACAGGGGCTGACCACCTGTGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTC
102▶ 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

StuI (4152)
4101 ACAGCAGACCCAATGGCAATGGCTTCCAGCACAGACAGTGACCCTGCCAATGTAGGCCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGA
68▶ V 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

BbsI (4298) **XmnI (4294)**
4201 TGGCCGCCCCGACATGGTGTGTTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGT
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

AseI (4360)
4301 CTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTAT
2▶ K M

SacI (4417)
4401 CTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAA

SpeI (4515)
4501 AAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGA

SnaBI (4643)
4601 TGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATG

NdeI (4748)
4701 CCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCC
4801 ACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTGAGCCAGGGC

PacI (4934) **SdaI (4926)** **BspLU11I (4944)**
4901 GGCCATTTACCGTAAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTG
5001 GCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGT
5101 TTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCA

ApaLI (5258)
5201 TAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCC

5301 GGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTG

5401 CTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT

5501 TGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGAT

EagI (5694)

PacI (5674) SwaI (5683) **NotI (5693)**

5601 CCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCG

5701 CAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAA

5801 CTAGCAAATAGGCTGTCCCAGTGCAAGTGCAAGTGCCAGGTGCCAGAACATTTCTCTATCGAA