



PvuI (7) SgfI (6) MfeI (82)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGTGCCTA
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) Psp1406I (203) PvuII (239) Bsu36I (291)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGACAGTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCTGTGGTGCCTCTGAACTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555) AgeI (552) NeoI (560) SgrAI (570)
501 TCTGTTTGTGCGCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATGGAGGGCGCCGCGCGAACGACAAGAAAAAGAT
1 M E G A G G A N D K K K I

XhoI (626) BglII (640)
601 AAGTTCTGAACGTCGAAAAGAAAAGTCTCGAGATGCAGCCAGATCTCGGCGAAGTAAAGAATCTGAAGTTTTTATGAGCTTGCTCATCAGTTGCCACTT
13 S S E R R K E K S R D A A R S R R S K E S E V F Y E L A H Q L P L

StuI (728)
701 CCACATAATGTGAGTTCCGATCTTGATAAGGCCTCTGTGATGAGGCTTACCATCAGCTATTTGCGTGTGAGGAACTTCTGGATGCTGGTATTGGATA
47 P H N V S S H L D K A S V M R L T I S Y L R V R K L L D A G D L D
801 TTGAAGATGACATGAAAGCACAGATGAATTGCTTTTATTTGAAAGCCTGGATGGTTTTGTTATGTTTCTCACAGATGATGGTACATGATTTACATTT
80 I E D D M K A Q M N C F Y L K A L D G F V M V L T D D G D M I Y I S

DraIII (949)
901 TGATAATGTGAACAAATACATGGGATTAACCTAGTTTGAACCTGACAGTGTGTTTACTCATCCATGTGACCATGAGGAAATGAGAGAA
113 D N V N K Y M G L T Q F E L T G H S V F D F T H P C D H E E M R E

HindIII (1056)
1001 ATGCTTACACACAGAAATGGCCTTGTAAGAAAGGTAAGAACAACACACAGCGAAGCTTTTCTCAGAATGAAGTGTACCTAACTAGCCGAGGAA
147 M L T H R N G L V K K G K E Q N T Q R S F F L R M K C T L T S R G

XcmI (1179)
1101 GAACTATGAACATAAAGTCTGCAACATGGAAGGTATTGCACTGCACAGGCCACATTCACGTATATGATACCAACAGTAACCAACTCAGTGTGGGTATAA
180 R T M N I K S A T W K V L H C T G H I H V Y D T N S N Q P Q C G Y K

XmnI (1234) Sall (1292)
1201 GAAACCACCTATGACCTGCTTGGTGTGATTTGTGAACCCATTCTCACCATCAAATATTGAAATTCCTTTAGATAGCAAGACTTTCTCAGTCGACAC
213 K P P M T C L V L I C E P I P H P S N I E I P L D S K T F L S R H

BsrBI (1377)
1301 AGCCTGGATATGAAATTTCTTATTGTGATGAAAGAATTACCGAATTGATGGGATATGAGCCAGAAGAACTTTTAGGCCGCTCAATTTATGAATATTATC
247 S L D M K F S Y C D E R I T E L M G Y E P E E L L G R S I Y E Y Y

BspHI (1434)
1401 ATGCTTTGGACTCTGATCATCTGACCAAACTCATGATGTTTACTAAAGGACAAGTCACCACAGGACAGTACAGGATGCTTGCCAAAAGAGGTGG
280 H A L D S D H L T K T H D M F T K G Q V T T G Q Y R M L A K R G G
1501 ATATGCTGGGTTGAAACTCAAGCAACTGTCATATATAACACCAAGAATTCTCAACCACAGTGCATTGTATGTGTAATTACGTTGTGAGTGGTATTATT
313 Y V W V E T Q A T V I Y N T K N S Q P Q C I V C V N Y V V S G I I

AgeI (1647)
1601 CAGCAGACTTGATTTTCTCCCTTCAACAAACAGAATGTGTCCTTAAACCGGTTGAATCTTCAGATATGAAAATGACTCAGCTATTACCAAAGTTGAAT
347 Q H D L I F S L Q Q T E C V L K P V E S S D M K M T Q L F T K V E
1701 CAGAAGATAACAAGTAGCCTCTTTGACAACTTAAAGAAGAACCTGATGCTTTAACTTTGCTGGCCCCAGCCGCTGGAGACACAATCATATCTTTAGATTT
380 S E D T S S L F D K L K K E P D A L T L L A P A A G D T I I S L D F
1801 TGGCAGCAACGACACAGAAACTGATGACCAGCAACTTGAGGAAGTACCATTATATAATGATGTAATGCTCCCCTACCCAACGAAAAATTACAGAATATA
413 G S N D T E T D D Q Q L E E V P L Y N D V M L P S P N E K L Q N I

BstBI (1946) Bsp119I (1946)
1901 AATTTGGCAATGTCTCCATTACCCACCGCTGAAACGCCAAAGCCACTTCGAAGTAGTGCTGACCTGCACTCAATCAAGAAGTTGCATTAATAATAGAAC
447 N L A M S P L P T A E T P K P L R S S A D P A L N Q E V A L K L E
2001 CAAATCCAGAGTCACTGGAACCTTTCTTTTACCATGCCAGATCAGACACCTAGTCCCTCCGATGGAAAGCACTAGACAAAGTCCACTGAGCC
480 P N P E S L E L S F T M P Q I Q D Q T P S P S D G S T R Q S S P E P
2101 TAATAGTCCCAGTGAATATTGTTTTATGTGGATAGTATGGTCAATGAATCAAGTTGGAATTTGGTAGAAAACTTTTGTGTAAGACACAGAAGCA
513 N S P S E Y C F Y V D S D M V N E F K L E L V E K L F A E D T E A
2201 AAGAACCATTCTTACTCAGGACACAGATTTAGACTTGGAGATGTTAGCTCCCTATATCCCAATGGATGATGACTTCCAGTTACGTTCTTCCGATCAGT
547 K N P F S T Q D T D L D L E M L A C P Y I P M D D D F Q L R S F D Q
2301 TGTACCATTAGAAAAGCAGTTCCGCAAGCCCTGAAAGCGCAAGTCTCAAAGCACAGTTACAGTATTCCAGCAGACTCAAATACAAGAACCTACTGCTAA
580 L S P L E S S S A S P E S A S P Q S T V T V F Q Q T Q I Q E P T A N
2401 TGCCACCCTACCCTGACCACCCTGATGAATTAACCAAGTACAGCAAGACCGTATGGAAGACATTAATAATTTGATTGCATCTCCATCTCCTACCCAC
613 A T T T T A T T D E L K T V T K D R M E D I K I L I A S P S P T H

SpeI (2515)
2501 ATACATAAAGAACTACTAGTGCACATCATCACCATATAGAGATACTCAAAGTCGGACAGCCTACCAAAACAGAGCAGGAAAAGGAGTCATAGAACAGA
647 I H K E T T S A T S S P Y R D T Q S R T A S P N R A G K G V I E Q

Bsu36I (2665)
2601 CAGAAAAATCTCATCAAGAAGCCCTAACGTGTTATCTGTGCTTTGAGTCAAAGAAGTACAGTTCTGAGGAAGAACTAAATCAAAGATACTAGCTTT
680 T E K S H P R S P N V L S V A L S Q R T T V P E E E L N P K I L A L
2701 GCAGAATGCTCAGAGAAAGCGAAAAATGGAACATGATGGTTCACTTTTCAAGCAGTAGGAATGGAACATTATTACAGCAGCCAGACGATCATGCGACT
713 Q N A Q R K R K M E H D G S L F Q A V G I G T L L Q Q P D D H A A

BsaBI (2831)
 2801 ACTACATCACTTTCTTGAAACGTGAAAAGGATGCAAATCTAGTGAACAGAATGGAATGGAGCAAAAGACAATTATTTAATACCTCTGATTTAGCAT
 747▶ T T S L S W K R V K G C K S S E Q N G M E Q K T I I L I P S D L A

PvuII (2941) **PstI (2998)**
 2901 GTAGACTGCTGGGCAATCAATGGATGAAAGTGGATTACCACAGCTGACCAGTTATGATTGTGAAGTTAATGCTCCTATACAAGGCGAGCAGAACTACT
 780▶ C R L L G Q S M D E S G L P Q L T S Y D C E V N A P I Q G S R N L L

MscI (3049)
 3001 GCAGGGTGAAGAATTACTCAGAGCTTTGGATCAAGTTAACTGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACACTAGA
 813▶ Q G E E L L R A L D Q V N •

HpaI (3181) **MfeI (3192)**
 3101 ATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAATTGCA
 3201 TTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCA
 3301 AAACTTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTG

SapI (3459)
 3401 CAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCAAGGTTTGAAGTACTAGCTCTTCATTCTTTATGTTTAAATGCACTGACCTCCAC

Swal (3530) **EcoO109I (3591)**
 3501 ATTCCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTC
 3601 ATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGT
 141▶ • N R T Y

SacI (3791)
 3701 ACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCT
 136▶ K L P I L 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

BstXI (3820)
 3801 GCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTG
 103▶ C 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

StuI (3955)
 3901 CTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCC
 69▶ S 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

XmnI (4097)
 4001 TGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAA
 36▶ I 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

AseI (4163)
 4101 GGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCT
 3▶ T K M

SacI (4220)
 4201 IATCTGACGGTTCACTAAACGAGCTCTGTTATATAGACCTCCCACCGTACACGCTACCGCCAATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTT

SpeI (4318)
 4301 GGAAAGTCCCCTGTTGATTTACTAGTCAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCCAT

SnaBI (4446)
 4401 TGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCCATAGGTCATGTAAGTGGGCATA

NdeI (4551)
 4501 ATGCCAGGCGGGCATTACCGTCAATGACGTCAATAGGGGGTACTTGGCATATGATACACTTGTACTGCAAGTGGGAGTTTACCGTAAATAC
 4601 TCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGAAACATACGTCAATATTGACGTCAATGGGCGGGGCTGTTGGCGGTGAGCCAG

PacI (4737)
PstI (4730) **SdaI (4729)** **BspLU11I (4747)**
 4701 GCGGGCATTACCGTAAGTTATGTAACGCTGCAAGTTAAATTAAGAACAATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAGGCCGCGTTG
 4801 CTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGGTGGCAAACCCGACAGGACTATAAAGTACCAGG
 4901 CGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCGCTTCTCCCTTCGGGAAGCGTGGCGCTTTC

ApaLI (5061)
 5001 TCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGGCTGTTCCGCTCCAAGTGGGCTGTGTCACGAACCCCGTTCAGCCCGACCGCTGCGCTTA
 5101 TCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGG
 5201 GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAG
 5301 AGTTGGTAGCTCTTGTATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAA

EagI (5497)
PacI (5477) **Swal (5486)** **NotI (5496)**
 5401 GATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGG

5501 CCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAAC
 5601 AAACCTAGCAAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA