



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82) **EcoNI (96)**
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC
EcoNI (287)
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **BspLU11I (560)**
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCAACATGTCTCGGATCGAATCCCTCACGGGGCGCGGATCGA
1 M S R I E S L T R A R I D
601 CCGGAGCAGAGAGCTGGCGAGCAAGACCCGGGAAAAGGAGAAGATGAAGGAAGCCAAGGATGCCCGCTATACCAATGGGCACCTCTTACCACCATTTCA
13 R S R E L A S K T R E K E K M K E A K D A R Y T N G H L F T T I S
701 GTTTCAGGCATGACCATGTGCTATGCTGTAAACAAGAGCATCACAGCCAAGGAAGCCCTCATCTGCCAACCTGCAATGTGACTATCCACAACCGCTGTGA
47 V S G M T M C Y A C N K S I T A K E A L I C P T C N V T I H N R C

BstBI (890) **Bsp119I (890)**
801 AAGACACCCTCGCCAAGTGTACCAAGGTCAAGCAGAAGCAACGAAAGCGGCCCTGCTGAAGAACAACACCGCCTTGCAGTCCGTTTCTTCCGAAGTAA
80 K D T L A N C T K V K Q K Q Q K A A L L K N N T A L Q S V S L R S K
901 GACAACCTACCGGAGCGGCAAGCTCGGCCATCTACCCCTCCGACAGCTTCCGGCAGTCCCTCTGGGCTCCCGCGGTGGCCGCTCCTCTTGTCTTTA
113 T T I R E R P S S A I Y P S D S F R Q S L L G S R R G R S S L S L
1001 GCCAAGAGTGTCTTACCACCAACATTGCTGGACATTTCAATGATGAGTCTCCCTGGGGCTGCGCCGGATCCTCTCACAGTCCACAGACTCCCTCAACA
147 A K S V S T T N I A G H F N D E S P L G L R R I L S Q S T D S L N
1101 TGCGGAACCGAACCTATCCGTGGAATCCCTCATTGACGAAGCAGAGGTAATCTACAGTGAAGTGTGAGTGAAGTGTGAGTGGATGAGAAGGACTTTGC
180 M R N R T L S V E S L I D E A E V I Y S E L M S D F E M D E K D F A
1201 AGCTGACTTTGGAGTCTTGTGTGGACAGCAGCTTCCGAGCAGCATAAAAAGGAGGTGATGAAGCAGCAAGATGTATGAGCTAATCCAGACA
213 A D S W S L A V D S S F L Q Q H K K E V M K Q Q D V I Y E L I Q T

DraIII (1306) **BspHI [m] (1326)**
1301 GAGCTGCACCATGTGAGGACACTGAAGATCATGACCCGCTCTTCCGCACGGGATGCTGGAAGAGCTACACTTGAGCCAGGAGTGGTCCAGGGGCTGT
247 E L H H V R T L K I M T R L F R T G M L E E L H L E P G V V Q G L
1401 TCCCTGCGTGGACGAGCTCAGTGACATCCATACAGCTTCTCAGCCAGCTATTAGAAGCAGCCGACGCGCAGGCGCTGTGCCCTGGCAGCAGCCGGA
280 F P C V D E L S D I H T R F L S Q L L E R R Q A L C P G T R N F
1501 TGTATCCATCGCTTGGTGTATGCTCATCAGCCAGTCTCAGTCCAGTGTAGTGGAGCAGATGTGTAAGACCTACTCGGAGTCTGACGAGCCGACAGC
313 V I H R L G D L L I S Q F S G P S A E Q M C K T Y S E F C S R H S

StuI (1601) **BspEI (1658)**
1601 AAGGCCTTAAAGCTTATAAGGAGCTGTACGCCGAGACAAACGCTTCCAGCAATTCATCCGAAAGTGAACCCCGCCGCTGCTCAAGCGGCACGGGG
347 K A L K L Y K E L Y A R D K R F Q Q F I R K V T R P A V L K R H G
1701 TACAGGAGTGCATCCTGCTGGTGAATCAGCGCATCACCAGTACCCGTTACTCATCAGCCGATCCTGCAGCATTCCACGGGATCGAGGAGGAGCGCCA
380 V Q E C I L L V T Q R I T K Y P L L I S R I L Q H S H G I E E E R Q

BglII (1892)
1801 GGACCTGACCACAGCACTGGGGCTAGTGAAGGAGCTGCTGTCCAATGTGGACGAGGGTATTTATCAGCTGGAGAAAGGGCCCGTCTGCAGGAGATCTAC
413 D L T T A L G L V K E L L S N V D E G I Y Q L E K G A R L Q E I Y

SfiI (1942)
1901 AACCGCATGGACCCTCGGGCCAAACCCAGTGCCTGGCAAGGCCCCCTTTGGCCGAGAGAACTTCTGAGGCCAAACCTCATCCACGATGGTGCCTGC
447 N R M D P R A Q T P V P G K G P F G R E E L L R R K L I H D G C L

BbsI (2004)
2001 TCTGGAAGACAGCAGCGGGGCGCTTCAAAGATGTGCTAGTGTGCTGATGACAGATGACTGGTGTCTCCAGGAAAAGGACCAGAAGTACATCTTTCC
480 L W K T A T G R F K D V L V L L M T D V L V F L Q E K D Q K Y I F P

BsiWI (2142)
2101 TACCCTGGACAAGCCTTCAAGTGTGCTGCGAGAACTAATCGTACGAGACATTGCCAACAGGAGAAAGGATGTTTCTGATCAGCGAGCCCCACCT
513 T L D K P S V V S L Q N L I V R D I A N Q E K G M F L I S A A P P

FspI (2270)
2201 GAGATGTACGAGGTGCACACAGCATCCCGGATGACCGGAGCACCTGGATCCGGGTCATTGACGAGCGTGGCAGCATGCCATCCAGGGAGGACTTCC
547 E M Y E V H T A S R D D R S T W I R V I Q Q S V R T C P S R E D F
2301 CCCTGATTGAGACAGAGGATGAGGCTTACCTGCGGCGAATTAAGATGGAGTTGCAGCAGAAGGACCGGCACTGGTGGAGCTGCTGCGAGAGAAGGTCGG
580 P L I E T E D E A Y L R R I K M E L Q Q K D R A L V E L L R E K V G
2401 GCTGTTTGTGATGACCCATTTCCAGGCCAAGAGGATGGTGGCAGTGGGATGGCCCTGCCACCCTGCCAGGGGCTTTTCCGCTCTGAGTCCCTT
613 L F A E M T H F Q A E E D G G S G M A L P T L P R G L F R S E S L

XcmI (2534)
2501 GAGTCCCCTCGTGGCGAGCGGCTGCTGCAGGATGCCATCCGTGAGGTGGAGGGTCTGAAAGACCTGCTGGTGGGGCCAGGAGTGGAACTGCTCTTGACAC
647 E S P R G E R L L Q D A I R E V E G L K D L L V G P G V E L L L T
2601 CCCGAGAGCCAGCCCTGCCCTTGAACACAGACGCGGTGGTAACACAGTCTCTGGGTCAGTCCCAATGGTGAAGCCAGAACCTTCAATGGCTCCATTGA
680 P R E P A L T P L E P D S G G N T S P G V T A N G E A R T F N G S I E
2701 ACTCTGCAGAGCTGACTCAGACTTAGCCAGAGGGATGCAAAATGAAATCAGCTGAGATCACCAGGAGGAGGCTTACAGCGATTGGTCAATCTCTAT
713 L C R A D S D S S Q R D R N G N Q L R S P Q E E A L Q R L V N L Y

2801 GGACTTCTACATGGCCTACAGGCAGCTGTGGCCAGCAGGACACTCTGATGGAAGCCCGTTCCTGAGGGCCCTGAGCGGGGAGAAGCTGTGCCGAG
747▶ G L L H G L Q A A V A Q Q D T L M E A R F P E G P E R R E K L C R
2901 CCAACTCTCGGGATGGGAGGCTGGCAGGGCTGGGGCTGCCCTGTGGCCCTGAAAAGCAGGCCACGGAACTGGCATTACTGCAGCGGCAACATGCGCT
780▶ A N S R D G E A G R A G A A P V A P E K Q A T E L A L L Q R Q H A L

NgoMIV (3023) SrfI (3094)

3001 GCTGCAGGAGGAGCTACGGCGCTGCCGGCGGCTAGGTGAAGAACGGGCAACCGAAGCTGGCAGCCTGGAGGCCCGGCTCCGGGAGAGTGAGCAGGCCCGG
813▶ L Q E E L R R C R R L G E E R A T E A G S L E A R L R E S E Q A R

SfiI (3177)

3101 GCACTGCTGGAGCGTGAGGCCGAAGAGGCTCGAAGGCAGCTGGCCGCCCTGGCCAGACCGAGCCACTCCCAGCTGAGGCCCTGGGCCCGCAGACCTG
847▶ A L L E R E A E E A R R Q L A A L G Q T E P L P A E A P W A R R P

BstAPI (3226)

3201 TGGATCCTCGGCGCGCAGCCTCCCCGAGGCGATGCCCTGTACTTGAGTTTCAACCCCCACAGCCAGCCGAGGCACTGACCGCTGGATCTACCTGT
880▶ V D P R R R S L P A G D A L Y L S F N P P Q P S R G T D R L D L P V
3301 CACTACTCGCTCTGTCCATCGAACTTTGAGGACCGAGAGAGGCAAGAACTGGGAGCCCGAAGAGCGGCTGCAAGACAGCAGTGACCTGACACTGGC
913▶ T T R S V H R N F E D R E R Q E L G S P E E R L Q D S S D P D T G
3401 AGCGAGGAGGAAGGTAGCAGCCGTCTGTCTCCGCCACAGTCCACGAGACTTACCAGAATGCAGGACATCCCGGAGGAGACGGAGACCGCGACGGGG
947▶ S E E E G S S R L S P P H S P R D F T R M Q D I P E E T E S R D G

MscI (3537) NheI (3531)

3501 AGGCTGTAGCCTCCGAGAGCTAAGGGGCCCGTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAA
980▶ E A V A S E S •

HpaI (3669) MfeI (3680)

3601 AAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTTCATTTATGT

EcoRI (3765)

3701 TTCAGGTTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCTAAAATACAGCATAGCAAACTTTAACCT
3801 CCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTGGCAATGTGCATTAGCTGTTTGCAGCCTCACCT
3901 CTTTCATGGAGTTAAGATATAGTGATTTTTCCAAGTTTGAAGTAGCTCTTCATTTCTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTA

SspI (4004) SwaI (4018)

4001 GTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCC
4101 AGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGA
4201 TGAGTTCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACA
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
4301 GGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGCTCGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGAC
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 (4443)

4401 CCAATGGCAATGGCTTCCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCC
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

BbsI (4589) XmnI (4585)

4501 CGACATGGTGCTTGTTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGT
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

AseI (4651)

4601 GGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTT
4701 CACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGT

SpeI (4806)

4801 TGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCCTATCCACGCCATTGATGTACTGCC

SnaBI (4934)

4901 AAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTGATGACTGGGCATAATGCCAGGGGG

NdeI (5039)

5001 CCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGAGTTTACCCTAATACTCCACCATTGA
5101 CGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGCGGGCCATTTA

PacI (5225) SdaI (5217) BspLU11I (5235)

5201 CCGTAAGTTATGTAACCGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTC
5301 CATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTTTTCCCTCG
5401 GAAGCTCCCTCGTGCCTCTCTGTTCCGACCTCGCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACG

ApaLI (5549)

5501 CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAACTAT

5601 CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGT
5701 TCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTC
5801 TTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATC

EagI (5985)
PacI (5965) SwaI (5974) NotI (5984)

5901 TTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAAAT
6001 ATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAA
6101 TAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA