



125

PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGACAGTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCGCCGCCCTACCTGAGGCC
PvuII (239)
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
Bsu36I (291)

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTGTTTCGTTT

AgeI (552) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCAACATGTCTCGGATCGAATCCCTCACTCGCGCGGATCGA
BssHIII (587)
601 CCGGAGCAAGGAGCAGGCAACCAAGACCCGGAAAAGGAGAAGATGAAGGAAGCTAAAGATGCCCGCTATACCAACGGCCACCTTTCCACCACCATCTCC
13> R S K E Q A T 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 GTCTCCGGCATGACCATGTGCTATGCCTGTAACAAGAGCATCACAGCAAGGAAGCCCTCATTGTCTACATGTAACGTGACCATCCACAACCGCTGTA
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)
801 AAGACACCCTGGCCAACGTACCAAGGTCAAGCAGAAGCAACGAAAGCTGCACTGCTGAGGAACAACACTGCTTTGCACTGTCTCCCTTCGAAGTAA
80> K D T L A N C T K V K Q K Q Q K A A L L R N N T A L Q S V S L R S K
901 GACGACCACAGAGCGGCCAACCTGTCATTTACCTTCCGACAGTCCCGGCGAGTCCCTCCTGGGTTCTCGGGGGGCTCTCCCTTATCTTTG
113> T T T R E R P T S A I Y P S D S F R Q S L L G S R R G L S S L S L
1001 GCCAAAAGTGTTCCTACCAACATTGCTGGACATTTCAATGATGAGTCTCCTCTGGGGTGCCTGAGATCCTCTCCAGTCCACAGACTCCCTCAACA
147> A K S V S T T N I A G H F N D E S P L G L R Q I L S Q S T D S L N
1101 TGCGGAACCGAACCTGTCCGTGGAATCCCTTATTGATGAAGTGTAGAAGTGTCTACAATGAGCTGATGAGCGACTTTGAGATGGATGAGAAGGACTT
180> M R N R T L S V E S L I D E G V E V F Y N E L M S D F E M D E K D F
1201 TGAGGCGGATTCTTGAGCCTTGGCGTGGACAGCAGCTTCTGCGAGCAGCACAAGGAAGATGTAAGAAGCAAGATGTCATCTATGAGCTGATCCAG
213> E A D S W S L A V D S S F L Q Q H K K E V M K K Q D V I Y E L I Q

BbrPI (1312)
DraIII (1309) 1301 ACAGAGCTGCACCACGTGAGAACCTTGAAGATTATGACCCGCCTTTTCGCACTGGGATGCTGGAAGATTGCGAGATGGAGCCAGAAGTGGTCCAGGGCC
247> T E L H H V R T L K I M T R L F R T G M L E E L Q M E P E V V Q G
1401 TGTTCCCTGCGTGGATGAACCTCAGTGACATTCACACAGCTTTCCTTAATCAGCTTCTGGAACGGCGGCCAGGCTCTATGTCAGGCAGCACCAGGAA
280> L F P C V D E L S D I H T R F L N Q L L E R R Q A L C P G S T R N

FspI (1565)
1501 CTTTGTATCCATCGTTTGGGTGACTTGTCTCATCAGTCAAGTCTCAGGTTTCAATGCTGAGCAGATGCGCAAGACTACTCAGAGTTCTGCGAGCCGCCAC
313> F V I H R L G D L L I S Q F S G S N A E Q M R K T Y S E F C S R H

XhoI (1634) 1601 ACCAAGGCCTTAAAGCTCTATAAGGAGCTGTATGCTCGAGACAAACGCTTCAACAGTTCATCCGGAAAATGACCCGCTCAGCTGTGTTGAGCGGCATG
BspEI (1661) 347> T K A L K L Y K E L Y A R D K R F Q Q F I R K M T R S A V L K R H
PvuII (1679)

NsiI (1710) 1701 GAGTTCAGGAATGCATTCTCCTGGTGACTCAGCGGATCACAAATACCCTGTGCTCATCAACC GAATCCTGCAGAATCCACGGGGTTGAAGAAGAGTA
XmnI (1708) 380> G V Q E C I L L V T Q R I T K Y P V L I N R I L Q N S H G V E E E Y
EcoRI (1773)

SpeI (1824) 1801 CCAAGACTTGGCGTCAGCCCTAGGACTAGTGAAGGAGTTGTTGTCCAATGTGGACCAGGATGTGCACGAGCTGGAGAAAGAGGCCCGCTGCAGGAGATT
AvrII (1818) 413> Q D L A S A L G L V K E L L S N V D Q D V H E L E K E A R L Q E I
ApaLI (1861)

BamHI (1911) 1901 TACAACCGAATGGATCCCGGGCTCAGACCCCGTACCTGGCAAGGGCCCTTCGCGCCGAGATGAACCTTTACGGAGAAAACCTTATCCACGAAGGCTGCC
SfiI (1945) 447> Y N R M D P R A Q T P V P G K G P F G R D E L L R R K L I H E G C
EagI (1953)

BbsI (2007) 2001 TGCTCTGGAAGACAGCCACAGGCGCTTCAAAGATGTCCTGTTGCTGCTGATGACAGAGCTGCTCGTGTCTTCCAGGAAAAGGACCAGAAATACATTTT
BstAPI (2265) 480> L L W K T A T G R F K D V L L L L M T D V L V F L Q E K D Q K Y I F
2101 CACATCCCTGGACAAGCCCTCAGTGGTGTCTTGCAGAACCTCATCGTAAGAGACATAGCCAACAGGCGAAAGGGATGTTTCTGATTAGTTCTGGACC
513> T S L D K P S V V S L Q N L I V R D I A N Q A K G M F L I S S G P

BspEI (2333) 2200 GCCTGAGATGATGAGGTAATGCGCGCTCCCGAGACGACCGGACTACCTGGATCCGTGTCTCCAGCAGAGTGTGCGCTGTGCCGCTCCAGGGAGGA
546> P E M Y E V H A A S R D D R T T W I R V I Q Q S V R L C P S R E D

2299 CTTTCTCTGATCGAGACAGAGGATAAGCGTATCTCCGGAGGATCAAGACGAAACTGCAGCAGAAAAACAGGCGCTAGTGGAGCTGTACAGAAGAAT
579> F P L I E T E D K A Y L R R I K T K L Q Q K N Q A L V E L L Q K N
2399 GTTGAGCTGTTTGGCAGATGGTCCACTTCCAGGCCTTAAAGGCTGGCTTCTGTTGGAATGCCCCACCCGCTGCCAGGGGTCTTTCCGCTTGTGAGT
613> V E L F A E M V H F Q A L K A G F V G M P P P A L P R G L F R L E
2499 CCTTTGAGTCCCTCCGAGGCGAGCCTGCTAAAGGATGCCCTCCGTGAAGTGAAGGCTGAAAGACCTGCTGTTGGGCCATGTGTGGACCTGCCAA
646> S F E S L R G E R L L K D A L R E V E G L K D L L G G P C V D L P
2598 CGACATCCCGAGAACCAGCCTTACCCTTGGACTCTGACAGCGGTAGCTGTCTGGGGTACTGCCAATGGAGAGGCCAGAACCTTCAATGGCTCCATTGA
679> T T S R E P A L P L D S D S G S C P G V T A N G E A R T F N G S I E

2698 ACTCTGTAGAGCAGACTCGGATTCCAGCCAGAAGGATCGGAATGGAAATCAGTTGAGGTCACCCAGGAGGAGGTGTACAGCCATTGATCAATCTTTAT
712▶ L C R A D S D S S Q K D R N G N Q L R S P Q E E V L Q P L I N L Y
BstEII (2753)
Bsu36I (2860)
2798 GGACTTCTACATGGCCTGCAGGCTGTTGTGGTCCAGCAGGAAAGACTGATGGAAGCCCTGTTCCCTGAGGGCCCTGAACGGTGGGAAAAGCTATCCCGAG
746▶ G L L H G L Q A V V V Q Q E R L M E A L F P E G P E R W E K L S R
BstXI (2960)
2898 CCAACTCTCGGGATGGTGAAGCTGGCCGGGCTGCGGTTGCTTCTGTAACCTCTGAGAAGCAGGCCAGGACTGGCACTACTGCAGAGGCAACACACCCT
779▶ A N S R D G E A G R A A V A S V T P E K Q A T E L A L L Q R Q H T L
SrfI (3091)
2998 GTTGCAGGAAGAGCTGCGGCGCTGCCAGCGGCTCGGGGAAGAGCGGGCAACTGAAGCTGGCAGCCTGGAGGCCAGGCTCCGAGAGAGCGAGCAAGCCCGG
812▶ L Q E E L R R C Q R L G E E R A T E A G S L E A R L R E S E Q A R
NgoMIV (3128)
3098 GCCCTGCTGGAGCGGGAGGCTGAAGAGATCCGCGCGCAGCTTGCAGCCTTGGGCCAAAACGAGCCACTCCCGGCAGAAGCGCCCTGGGCTCGCAGGCCTC
846▶ A L L E R E A E E I R R Q L A A L G Q N E P L P A E A P W A R R P
3198 TGGACCCACGGCGCCGACGCTTCCAGCGGGCGACGCTTATACTTGAGCTTCAATCCCCCCAGCCAGTCGAGGCCATGACCGCCTGGATTGCGCTGT
879▶ L D P R R S L P A G D A L Y L S F N P P Q P S R G H D R L D L P V
3298 GACTGTTTCGTTCCCTCCACCGACCTTTGATGACCGAGAGGCGCAAGAAGCTTGGTAGCCCGAGGATCGACTACAGGACAGCAGTGACCTGATACTGGT
912▶ T V R S L H R P F D D R E A Q E L G S P E D R L Q D S S D P D T G
XhoI (3440)
3398 AGTGAGGAGGAAGTCAGTAGCCGCTGTCTCCACCTCACAGTCTCGAGACTTACCCGAATGCAGGACATTCTGAAGAGACAGAAAGCCGAGATGGGG
946▶ S E E E V 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
NheI (3532)
3498 AGCCACAGCTTTCAGAGAGCTAAGGGGACACTTCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACAGTAATGCAGTG
979▶ E P T A S E S •
HpaI (3670) MfeI (3681)
3598 AAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAATTGCATTCATTTT
EcoRI (3766)
3698 ATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATCTCAAAATACAGCATAGCAAACTTTA
3798 ACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCA
3898 CCTTCTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTT
SspI (4005) SwaI (4019)
3998 TTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATC
4098 CCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGG
141▶ • N R T Y K L
SacI (4280)
4198 GGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGC
133▶ 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 M G
BstXI (4309)
4298 CACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGC
100▶ 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 V A
4398 AGACCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCC
67▶ 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 A
BbsI (4590)
XmnI (4586)
4498 GCCCCGACATGGTGTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACTCCACCAGTCCAGATCTGCTGAGAGATGTTGAAGTCTTCA
33▶ 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 K M
AseI (4652)
4598 TGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGAC
0▶
SacI (4709)
4698 GGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTC
SpeI (4807)
4798 CCGTTGATTTACTAGTCAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAC
SnaBI (4935)
4898 TGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGACTGGCATAATGCCAGG
NdeI (5040)
4998 CGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGTACTGCAAGTGGGCAGTTCACCGTAAATACTCCACCCA
5098 TTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTGTTGGCGGTTCAGCCAGGCGGGCCA
PacI (5226)
5198 TTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTT
5298 TTTCCATAGGCTCCGCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGCGTTTCCC
5398 CCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACTGTCCGCCTTCTCCCTTCCGGAAGCGTGGCGCTTCTCATAGCT

ApaI (5550)

5498 CACGCTGTAGGTATCTCAGTTCGGGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCACCGCTGCGCCTTATCCGGTAA
5598 CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACA
5698 GAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGATTGGTA
5798 GCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTT

EagI (5986)

PacI (5966) SwaI (5975) NotI (5985)

5898 GATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAAT
5997 AAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAG
6097 CAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA