



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC Bsu36I (291)

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMIV (441) 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
AgeI (552) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCCATGGGCAGGACTGGCTGCTGCCAGGCTCCTCCTTTCC
1 M G R Y W L L P G L L L S
601 CCTGCCTCTGGTAACTGGGTGGAGCACTTCCAAGTGCCTGGTACCGAAGGCTCCCGACTGCCCTGGTCTCCCGCTATTTACATTCTGCCGCCATTCC
13 L P L V T G W S T S N C L V T E G S R L P L V S R Y F T F C R H S

SphI (718) 701 AAGCTATCCTTTCTGTGCATGCCTTCCGTGAGCAACCTGACACAGACCTTGAAGTTGTACCTCGGACTGTGGAGGGGCTGCTGCCTCGGTGGTACTG
47 K L S F L A A C L S V S N L T Q T L E V V P R T V E G L C L G G T
801 TGTCTACTCTGCTCCAGATGCTTTCTGCTTTTCTGGTCTCAAGTCTGGCACTGAGTCTGCACCTTACCAACTTCTGCCAGGAGCTCTCCGGGG
80 V S T L L P D A F S A F P G L K V L A L S L H L T Q L L P G A L R G

BglII (946) 901 TCTGGACAGTTGCAGAGCCTCTTTTTTTGACTCTCCTCTTAGGAGATCTCTTTTCTACCTCCTGATGCCTTCAGTGACCTGATTTCCCTCCAGAGA
113 L G Q L Q S L S F F D S P L R R S L F L P P D A F S D L I S L Q R
1001 CTCCATATCTGCGCCCTTGCTGGATAAGAAGGCAGGATCCGCCTGCCTCCCGGTCTGCAATGGCTGGGTGTACAGCTCAGTTGCATTGAGGACGTTG
147 L H I S G P C L D K K A G I R L P P G L Q W L G V T L S C I Q D V

BglII (1122) 1101 GAGAGCTGGCTGGTATGTTCCAGACTGCTGGTGAAGTTCTCCTCCAGGTTTCTGGGACCCTGCAGAAGTTGGATCTGTATCCAACCGGAAGCTGAA
180 G E L A G M F P D L V Q G S S S R V S W T L Q K L D L S S N R K L K

SandI (1213) 1201 GATGGCTAGTCTGGTCCCTCCAGGCTCCAGTGGAGATTCTGGACCTGACAAGAACCAGCTGGATGCTGTGTGGCTGAAGGGCCTGGGACTTCAG
213 M A S P G S L Q G L Q V E I L D L T R T P L D A V W L K G L G L Q

BstAPI (1318) 1301 AAAGCTGATGCTTGTATGCACAGACTGCCACGCGGAGCTGGCTGCTGAGGCTGTTGCCACTTTGAGCTGCAGGGCTGATTGTGAAAGAAAGCAAGA
247 K L D V L Y A Q T A T A E L A A E A V A H F E L Q G L I V K E S K

BsaBI (1403) 1401 TAGGATCTATATCTCAGGAGGCTCTGGCTTCTGCCACAGCCTGAAGACCTTGGGTCTTTCAAGCACTGGCCTAACCAAGCTTCCACCAGGCTTCTGAC
280 I G S I S Q E A L A S C H S L K T L G L S S T G L T K L P P G F L T

AvrII (1507) **BspEI (1531)** 1501 TGCCATGCTAGGCTTCAGCGACTGGAGCTGTCCGAAACCAACTGCAGAGCGCGTGTGTGCATGAATGAGACGGGAGATGTGTCAGGACTCACAACT
313 A M P R L Q R L E L S G N Q L Q S A V L C M N E T G D V S G L T T

FspI (1622) 1601 CTGGATCTGTCAGGCAACAGGTTGGCGATCCTGCTCCAGCCGCTTCTCTGCTTACCCACTTGCAGAGCTGCTGCTTCGTTACAACCAGCTGCTTT
347 L D L S G N R L R I L P P A A F S C L P H L R E L L R Y N Q L L
1701 CCCTGGAGGATACCTATTCCAGAGCTCCAGCAACTAGAGACTTGAAGCTGGATGGAAACCCCTGCTTACCTGGTAAGAACTGTTGGCGGCTCT
380 S L E G Y L F Q E L Q Q L E T L K L D G N P L L H L G K N W L A A L
1801 GCCTGCATTGACCACCCTTAGCTTGTAGATACCAAATACGGATGAGCCAGAGCCTGGCTTCTGGGAGCAAAGAATCTGCATACCTGAGCCTGAAG
413 P A L T T L S L L D T Q I R M S P E P G F W G A K N L H T L S L K

BsrBI (1904) **Bsu36I (1970)** **Tth111I (1992)** 1901 CTTCCCGCTCCTCCTGCTCCGGCAGTATTGTTCTGCCCATGTATCTGACCAGCTTAGAGCTTATATAGCCTCAGGCACGAGCACTGGACGCTGT
447 L P A L P A P A V L F L P M Y L T S L E L H I A S G T T E H W T L

SandI (2065) 2001 CCCAGCGATCTTTCCTTCTTGGAGACCTTGAATAAGCGCGGGGACTGAAGCTGAAGCTGGGGTCCCAGAATGCTTCTGGGGTCTTCCCTGCTCT
480 S P A I F P S L E T L T I S G G L K L G S Q N A S G V F P A L

Acc65I (2149) 2101 CCAGAAGCTCCTCCTGCTCAAGAACAGCTTGGATGCCTTCTGCTCCAGGGTACCTCCAACCTCTTCTCTGGCAGCTCCCCAACTTCACTCCTTGAGG
513 Q K L S L L K N S L D A F C S Q G T S N L F L W Q L P K L Q S L R
2201 GTATGGGGTGTGGAAACAGCTCCAGACCTGCTTATCACTGGGCTGCCAGCTACGGGAGCTGAAGCTGGCGTGCCTTCACTCCATAACCCAGCCC
547 V W G A G N S R P C L I T G L P S L R E L K L A S L Q S I T Q P
2301 GTTCGGTGCAGCTGGAGGAGCTGGTGGGTGACCTTCCACAGCTCCAGGCTTAGTGCTATCCAGCACAGGCTCAAGTCACTGTGCGCGCTGCTTTCCA
580 R S V Q L E E L V G D L P Q L Q A L V L S S T G L K S L S A A A F Q
2401 GCGCTGCACAGTCTCCAGGCTTAGTGCTAGAATACGAGAAGGACTTGTGCTGAGGACAGCTGAGGGAGTACAGCCCTCAGATGCCCACTATATA
613 R L H S L Q V L V L E Y E K D L M L Q D S L R E Y S P Q M P H Y I

NcoI (2551) 2501 TACATTCTGGAGTCAAACCTGGCCTGCCACTGTGCCAATGCGTGGATGGAGCCATGGGTTAAGCGGTCCACTAAAACGTACATATACATAAGAGACAATC
647 Y I L E S N L A C H C A N A W M E P W V K R S T K T Y I Y I R D N
2601 GCTTATGTCCAGGACAAGACAGGCTCTCTGCTAGGGGTTCCCTTCCCTCTTCTCTGGGACCACTGCCCCAGACGTTGGAGCTGAAACTCTTTTGGC
680 R L C P G Q D R L S A R G S L P S F L W D H C P Q T L E L K L F L A

SdaI (2772)
2701 TAGTTCCTGCCTTGGTGTTCATGCTAATTGCCTTGCCTCTCCTCCAAGAAGCCAGGAACCTTTGGATCCCCTACCTGCAGGCCTTGTTCAGGGTTGGCTC
713▶ S S A L V F M L I A L P L L Q E A R N S W I P Y L Q A L F R V W L
BamHI (2762)
2801 CAGGGTCTGAGGGTAAGGGAGACAAGGGGAAGAGGTTCCTTTTGATGTATTCGTGTCCCCTGCAGGCAAGACCAGGGCTGGGTGATAGAGAACTTC
747▶ Q G L R G K G D K G K R F L F D V F V S H C R Q D Q G W V I E E L
XmnI (2829)
2901 TGCTGCTCTGGAGGGCTTCCTCCAGCTGGCCTGGCCTCTGTCTCCCGAGCGTGACTTTGAGCCTGGTAAGGATGTAGTTGATAATGTGGT
780▶ L P A L E G F L P A G L G L R L C L P E R D F E P G K D V V D N V V
MscI (3086)
3001 AGATAGCATGTTGAGCAGCCGTACCACACTCTGCGTGTGAGTGGCAGGCCCTGTGTAACCCCGATGCCGCTGGAGCTCCGCTTGCCACCTCTCTC
813▶ D S M L S S R T T L C V L S G Q A L C N P R C R L E L R L A T S L
BstBI (3197)
Bsp119I
3101 CTCCTGGCTGCCCGTCCCCCAGTGTGCTGCTAGTCTTCTTGAACCCATTTCTCGGCACCAGCTTCCGGTTACCACAGACTGGCTCGGCTGCTTC
847▶ L L A A P S P P V L L L V F L E P I S R H Q L P G Y H R L A R L L
PshAI (3208)
3201 GAAGAGGAGACTACTGTCTGTGGCCCGAGGAAGAGGAGAGAAAGAGTGGGTTCTGGACTTGGCTGAGGAGCAGGCTAGGGTAGCCATAGCCAGCACTGGT
880▶ R R G D Y C L W P E E E E R K S G F W T W L R S R L G •
MscI (3340)
NheI (3334)
3301 GTGGGGTGGTGCATGTGAATTTTGGGGTGGGGTGTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGA
HpaI (3472) MfeI (3483)
3401 AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAACATTCATTCTTTA
EcoRI (3568)
3501 TGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAA
3601 CCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCAC
SapI (3750)
3701 CTTCTTTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGTTTGAAC TAGCTTTCATTCTTTATGTTTTAAATGCACTGACCTCCCACATCCCTTT
SspI (3807) SmaI (3821)
3801 TTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCC
3901 CCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGG
4001 GGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCC
133▶ 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
4101 ACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCA
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
4201 GACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCG
66▶ 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 A
XmnI (4388)
4301 CCCGACATGGTCTTGTGTCCTCATAGAGCATGGTGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCAT
33▶ 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 (4454)
4401 GGTGGCCCTCTATAGTGAAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTTGCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACG
4501 GTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCC
SpeI (4609)
4601 CGTTGATTTACTAGTCAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGTATCCACGCCATTGATGACT
SnaBI (4737)
4701 GCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGC
NdeI (4842)
4801 GGGCATTACCCTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACCTTGTACTGCTCAAGTGGGCGAGTTACCCTAAATACTCCACCCAT
4901 TGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTTGGGCGGTGAGCCAGGCGGGCCAT
SdaI (5020) PacI (5028) BspLU11I (5038)
5001 TTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCGTTT
5101 TTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC
5201 CTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTC
ApaLI (5352)
5301 ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCAGAAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAAAC
5401 TATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAG

5501 AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG
5601 CTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTG
5701 ATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAA
5801 AATATCTTTATTTTCATTACATCTGTGTGGTTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCA
5901 AAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTATCGAA