



150

PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC **HindIII (245)**

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGCGGGCGTCGCGACCCCTGCGCAACGGGTGCGG **NcoI (560)**
BstEII (555) 1▶ M A G V A T P C A N G C G **NruI (572)**

601 GCCTGGCGCACCCCTCCGAAGCCGAGGTGCTGCACCTCTGCCGACGCTCGAGGTGGGACCGTATGACTTTGTTCTACTCCAAGAAGTCGACGCGGCCA **XhoI (646)**

701 GAACGGAAGACCTTCCAGGTCAAGTTGGAGACGCGCCAGATCACATGGAGCCGCGCGGACAAAATCGAGGGTCCATTGATATCCGAGAAATCAAGG **SacII (750)** **EcoRV (781)**

801 AGATCCGTCAGGGAAGACTTCTCGGACTTTGACCGCTACCAAGAAGACCTGCCTTCCGCCAGATCAATCACACTGCTTTGTCTATGGAAT **47▶ E R K T F Q V K L E T R Q I T W S R G A D K I E G S I D I R E I K**

901 GGAATCCGCTTGAAGACCTGAGCCTGCAAGCCACATCTGAGGATGAAGTGAACATGTGGATCAAGGGCTTAACTTGGCTAATGGAGATACACTGCAG **80▶ E I R P G K T S R D F D R Y Q E D P A F R P D Q S H C F V I L Y G M**

1001 GCAGCCACCCCTGCAATTTGAGAGGTGGCTCCGGAAGCAGTTCTACTCAGTGGATCGTAACCGAGAGGATCGTATATCAGCCAAGGACTTGAAGAACA **113▶ E F R L K T L S L Q A T S E D E V N M W I K G L T W L M E D T L Q**

147▶ A A T P L Q I E R W L R K Q F Y S V D R N R E D R I S A K D L K N **BsrBI (1147)**

1101 TGCTGTCTCAGGTCAACTACCGAGTCCCAATATGCGCTTCTCCGAGAGCGGCTGACGGACCTTGAACAGCGCAGCGGGGACATCACCTACGGGCAGTT **180▶ M L S Q V N Y R V P N M R F L R E R L T D L E Q R S G D I T Y G Q F**

1201 TGCTCAGCTGTACCGCAGCCTCATGTACAGCGCCAGAAGACGATGGACCTTCCCTTCTTGGAAACCAACGCTTTGAGGACTGGAGAGCGTCCGGAGCAT **BsrGI (1223)**

213▶ A Q L Y R S L M Y S A Q K T M D L P F L E T N A L R T G E R P E H **SalI (1363)**

1301 TGCCAGGTGTCCTTTCTGAGTTCAGCAGTTCCTCCTTGAATACCAGGGGAGCTGTGGCTGTCGACCGGCTCCAGGTGCAGGAATTCATGCTCAGCT **247▶ C Q V S L S E F Q Q F L L E Y Q G E L W A V D R L Q V Q E F M L S**

1401 TCCTTCGAGACCCCTTGCAGAGATTGAGGAGCCATACTTCTTCTTGGATGAGCTTGCACCTTCTGTTCTCCAAAGAGAACAGCGTGTGGAAGTACA **280▶ F L R D P L R E I E E P Y F F L D E L V T F L F S K E N S V W N S Q**

1501 GCTGGATGCTGTGTGCCCGACACCATGAACAACCCTCTCTACTATTGGATCTCCTCCTCACATAATACGTACCTGACTGGGACCAGTTCTCCAGT **SnaBI (1569)**

313▶ L D A V C P D T M N N P L S H Y W I S S S H N T Y L T G D Q F S S **NcoI (169)**

1601 GAGTCCTCCTGGAAGCCTATGCTCGCTGCCTGAGGATGGGCTGTCGCTGCATTGAGTTGACTGCTGGGATGGGCCAGATGGGATGCCAGTCATTTACC **347▶ E S S L E A Y A R C L R M G C R C I E L D C W D G P D G M P V I Y**

1701 ATGGGCACACTCTCACCACCAAGATCAAGTTCTCTGACGTCTGCACACCATCAAGGAGCATGCTTTTCGTAGCCTCAGAGTACCCAGTCATCCTGTCCAT **SphI (1758)**

380▶ H G H T L T T K I K F S D V L H T I K E H A F V A S E Y P V I L S I **BstXI (1877)**

1801 CGAGGACCACTGCAGCATTGCCAGCAGAGAAACATGGCTCAGCACTTCCAGAAAGGTGCTTGGCGACACACTCCTTACCAAGCTGTGGACATTGCTGCT **413▶ E D H C S I A Q Q R N M A Q H F R K V L G D T L L T K C P V D I A A**

1901 GATGGCCTTCTTCTCCCAACCAGCTCAGGAGGAAGATCCTTATTAAGCACAAGAAGTGGCTGAGGGCAGTGCCTATGAGGAGGTGCCTACCTCTGTGA **447▶ D G L P S P N Q L R R K I L I K H K K L A E G S A Y E E V P T S V**

2001 TGTACTCCGAGAATGACATCAGTAACTCCATCAAGAATGGTATCCTTACTTGGAGGACCCCGTGAATCATGAGTGGTATCCCACTACTTCTGTTCTGAC **480▶ M Y S E N D I S N S I K N G I L Y L E D P V N H E W Y P H Y F V L T**

2101 TAGCAGCAAGATCTACTACTCTGAGGAGACCAGCAGTACCAGGGCAATGAGGATGAAGAGGAGCCGAAGGAGGCCAGCAGCAGCACAGAGCTGCACTCG **BglIII (2108)** **XhoI (2196)**

513▶ S S K I Y Y S E E T S S D Q G N E D E E E P K E A S S S T E L H S **ScaI (2273)**

2201 AGTGAGAAGTGGTTCCACGGGAAGCTCGGGGCTGGACGTGACGGGCGGCACATTGCTGAGCGCTGCTCACTGAGTACTGCATAGAGACTGGGGCTCCTG **547▶ S E K W F H G K L G A G R D G R H I A E R L L T E Y C I E T G A P**

2301 ATGGCTCCTTCTAGTGCAGAAAGTGAACCTTCTGGGTGACTACACGCTGCTTTTCTGGCGAATGGGAAAGTCCAGCACTGCCGATCCACTCCCG **580▶ D G S F L V R E S E T F V G D Y T L S F W R N G K V Q H C R I H S R**

2401 GCAGGATGCTGGGACTCCTAAGTTCTTCTGACAGATAACCTTGTCTTGGACTCTCTATGACCTCATCACATTATCAGCAAGTACCCTGCGCTGC **613▶ Q D A G T P K F F L T D N L V F D S L Y D L I T H Y Q Q V P L R C**

2501 AATGAGTTTGAATGCGCCTTTTACAGCCCTGTTCCACAGACGAATGCCATGAGAGCAAGAGTGGTACCACGCAAGCCTGACTAGAGCTCAGGCTGAAC **647▶ N E F E M R L S E P V P Q T N A H E S K E W Y H A S L T R A Q A E**

2601 ATATGCTGATGCGAGTGCCTCCGGGATGGGGCTTCTGGTGGGAAACGAATGAGCCTAACTCATATGCCATCTCTTCCGGGCTGAGGGAAAGATCAA **XmaI (2618)**

680▶ H M L M R V P R D G A F L V R K R N E P N S Y A I S F R A E G K I K

2701 GCACTGCCGAGTACAGCAGGAAGGCCAGACAGTGTGCTGGGAACTCTGAGTTTGACAGCCTGGTTGACCTCATCAGCTACTATGAGAAGCACCCCCTG
713▶ H C R V Q Q E G Q T V M L L G N S E F D S L V D L I S Y Y E K H P L
2801 TACCGCAAATGAAGCTACGCTACCCATCAACCGVAGGAGGACTGGAGAAGATCGGGACAGCTGAACCCGATTATGGGGCACTATACGAGGGCCGCAACC
747▶ Y R K M K L R Y P I N E E A L E K I G T A E P D Y G A L Y E G R N
2901 CTGGTTTCTATGTGGAGGCAAACCTATGCCAATTTCAAGTGTGCGAGTAAAAGCCCTCTTCTGACTACAAGGCCAGAGAGAGGATGAGCTGACCTTAC
780▶ P G F Y V E A N P M P T F K C A V K A L F D Y K A Q R E D E L T F T
3001 CAAGAGTGCCATCATCCAGAATGTGGAAAAGCAAGATGGTGGCTGGTGGCGAGGGGACTATGGTGGGAAGAAGCAGCTGTGGTCCCTCAAACCTATGTG
813▶ K S A I I Q N V E K Q D G G W W R G D Y G G K K Q L W F P S N Y V
3101 GAAGAGATGATCAATCCAGCAGCTCTAGAGCCTGAGAGGGAGCACCTGGATGAGAACAGCCCACTGGGGGACTTGTCTGCGAGGGGCTTTAGATGTGCCAG
847▶ E E M I N P A V L E P E R E H L D E N S P L G D L L R G V L D V P

BsaBI (3207)

SphI (3260)

3201 CTTGTGAGATCGCCATCCGCTCTGAGGGCAAAAACAACCGGCTCTTCTGCTTCTCCATCAGCATGCCATCAGTGGCTCAGTGGTCCCTGGATGTTGCAGC
880▶ A C Q I A I R P E G K N N R L F V F S I S M P S V A Q W S L D V A A
3301 TGACTCACAGGAGGAGTTACAGGACTGGGTGAAAAAGATCCGTGAAGTTGCCAGACTGCAGATGCCAGGCTCACTGAGGGAAAAGATGATGGAGAGGAGG
913▶ D S Q E E L Q D W V K K I R E V A Q T A D A R L T E G K M M E R R

NgoMIV (3440)

3401 AAGAAGATCGCCTTGGAGCTCTCCGAGCTTGTGGTCTACTGCCGGCCGTTCCCTTTGATGAAGAGAAGATTGGCACAGAACGTGCTTGTACCGGGACA
947▶ K K I A L E L S E L V V Y C R P V P F D E E K I G T E R A C Y R D
3501 TGTCTCCTTTCCGAAACCAAGGCTGAGAAGTGTGAACAAGGCCAAAGGAAAGTTCCCTCAGTACAACCGGCTGCAGCTCTCGCGCATCTACCC
980▶ M S S F P E T K A E K Y V N K A K G K K F L Q Y N R L Q L S R I Y P
3601 TAAGGGCCAGAGGCTAGACTCCTCAATTATGACCCTCTGCCATGTGGATCTGCGGTAGCCAGCTTGTAGCACTCAATTTCCAGACCCAGACAAGCCT
1013▶ K G Q R L D S S N Y D P L P M W I C G S Q L V A L N F Q T P D K P
3701 ATGCAGATGAACAGGCCCTCTTCAATGGCTGGTGGCATTGTGGCTATGTGCTGCAGCAAGCACCATGAGAGAGCAAGCCTTTGACCCCTTTGATAAGA
1047▶ M Q M N Q A L F M A G G H C G Y V L Q T P S T M R D E A F D P F D K
3801 GCAGTCTCCGAGGCTGGAACCTGTGTCAATTTGATTGAGGTGCTGGGGCCAGGCATCTGCCGAAGAATGGCCGGGTATTGTGTCTCTTTGTGGA
1080▶ S S L R G L E P C V I C I E V L G A R H L P K N G R G I V C P F V E
3901 GATTGAGTGGCTGGGGCTGAGTACGACAGCACCAAGCAAAAGACGGAGTTGTAGTGGACAACGGACTGAACCTGTGTGGCCTGCTAAGCCCTTCCAC
1113▶ I E V A G A E Y D S T K Q K T E F V V D N G L N P V W P A K P F H
4001 TTCCAGATCAGTAACCCAGAGTTTCTGCTTCTGCGCTTTGTGGTGTATGAGGAAGACATGTTTAGTGACCAGAATTCTTGGCTCAGGCTACTTTCCAG
1147▶ F Q I S N P E F A F L R F V V Y E E D M F S D Q N F L A Q A T F P

StuI (4104)

4101 TAAAAGGCTGAAGACAGGATATAGAGCAGTGCCTTTGAAGAACAACCTACAGTGAAGACCTGGAGTTGGCTCCCTGCTCATCAAGATTGACATTTTCCC
1180▶ V K G L K T G Y R A V P L K N N Y S E D L E L A S L L I K I D I F P

PshAI (4216)

XmaI (4292)

BstEII (4213)

Bsp120I (4289)

4201 TGCTAAGGAGAACGGTGACCTCAGTCCCTTTCAGTGGCATATCCCTAAGGGAACGGGCTCAGATGCCTCCAGCCAGCTGTTCCATGTCGGGGCCCGGGAA
1213▶ A K E N G D L S P F S G I S L R E R A S D A S S Q L F H V R A R E

Scal (4390)

4301 GGGTCTTTGAAGCCAGATACCAGCAGCATTGAAGATTTCCGCATCTCGCAGGAGCATCTAGCAGACCATTTGACAGTCCGGGAACGAAGTACTTCAG
1247▶ G S F E A R Y Q Q P F E D F R I S Q E H L A D H F D S R E R S T S

BamHI (4431)

NheI (4496)

4401 ATGGTCTTCTCAGCCACTAACCTTATTGAGGATCCCTTACATGACAAGCTGTGGAAGTGTCTCTTTAAATACCCAGTGGCTAAGAAGATGCTGGCTA
1280▶ D G P S S A T N L I E D P L H D K L W K C S L •

MscI (4502)

4501 CCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGC

HpaI (4634) **MfeI (4645)**

4601 TTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAACAACAACAATTGCATTCTTTATGTTTCAGTTTCAGGGGAGGTGTTGGAGGTTTTTTAA

4701 AGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCACTTGAATCCTTTCTGAGG

4801 GATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTATTTTCCCA

SspI (4969)

Swal (4983)

4901 AGGTTTGAAGTACTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTGAGAAATAATTTAAATACATCATTG

5001 CAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCT

5101 TTAATAGAAATTTGACAGCAAGAAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCA
1414 • N R T Y K L P I L E E I T T K V L K G

BstXI (5273)

5201 TTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCAT

1204 N M E I L V F C D P A Y D S I L E R C M G C P S V V R I S R D V E D

5301 CAGAGTAGGGGCTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTACGACAGACAGTGACCCT

874 S Y P H R V A V I T D F D K Q G N S V A S G I A I A E A C V T V R

StuI (5408)

5401 GCCATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTG

544 G I Y A E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T

5501 ATCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCAATGATGGCCCTCTATAGTGAGTCGATTATACATATGCCG

204 I K E T A V E V L E L D Q Q S I N F T K M

AseI (5616)

5601 ATATACTATGCCGATGATTAATTGTCAAACAGCGTGATGGCGTCTCCAGCTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCA

SpeI (5771)

5700 CGTACAGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTACTAGTCAAAAACAACCTCCATTGACG

5799 TCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTA
SnaBI (5899)
5899 ATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGT
5999 ACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATG
6099 GGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAAT
SdaI (6182)PacI (6190)
6197 AAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA
6297 AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGAC
6397 CCTGCCGTTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTT
6497 CGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACT
ApaLI (6514)
6597 TATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACAC
6697 TAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGC
6797 GGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACG
6897 AAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGT
PacI (6930) SmaI (6939) EagI (6950) NotI (6949)
6997 TTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAGGTGCCA
7097 GAACATTTCTCTATCGAA