



150

PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCCGCCGCCCTACCTGAGGCC
PvuII (239)
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NgoMI (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTACCATTGGCGTGGCGGTGCCCCAGGATGGGCAGGGTCCCCTG
NcoI (560)
SmaI (590)
601 GGCCTGGTGTGGCGCTGTGCGGCTGGGCGTGCATGGCCCCAGGGGACGCGAGGCTGAAGAAAGTCCCTTCGTGGGCAACCCAGGGAATATCACAGGT
13> A W C L A L C G W A C M A P R G T Q A E E S P F V G N P G N I T G
XmaI (701)
701 GCCCGGGACTCACGGGACCCTTCGGTGTGAGCTCCAGGTTCCAGGGAGAGCCCCGAGGTACATTGGCTTCGGGATGGACAGATCCTGGAGCTCGCGG
47> A R G L T G T L R C Q L Q V Q G E P P E V H W L R D G Q I L E L A
801 ACAGCACCAGACCCAGGTGCCCTGGGTGAGGATGAACAGGATGACTGGATAGTGGTCCAGCAGCTCAGAATCACCTCCCTGCAGCTTTCCGACACGGG
80> D S T Q T Q V P L G E D E Q D D W I V V S Q L R I T S L Q L S D T G
901 ACAGTACCAGTGTGGTGTTCGGGACATCAGACCTTCGTGTCCAGCCTGGCTATGTTGGGCTGGAGGGCTTGCCTACTTCTGGAGGAGCCCGAA
113> Q Y Q C L V F L G H Q T F V S Q P G Y V G L E G L P Y F L E E P E

SmaI (1050)
1001 GACAGGACTGTGGCCGCAACACCCCTTCAACCTGAGCTGCCAAGCTCAGGGACCCAGAGCCCGTGGACCTACTCTGGCTCCAGGATGCTGTCCCC
147> D R T V A A N T P F N L S C Q A Q G P P E P V D L L W L Q D A V P
MseI (1100)
1101 TGGCCACGGCTCCAGGTCACGGCCCCAGCGCAGCCTGCATGTTCCAGGGCTGAACAAGACATCCTCTTCTCCTGCGAAGCCATAACGCCAAGGGGT
180> L A T A P G H G P Q R S L H V P G L N K T S S F S C E A H N A K G V
1201 CACCACATCCGACAGCCACCATCACAGTGTCCCCAGCAGCCCCGTAACCTCCACCTGGTCTCCCGCAACCCACGGAGCTGGAGGTGGCTTGGACT
213> T T S R T A T I T V L P Q Q P R N L H L V S R Q P T E L E V A W T

BsrBI (1308) 1301 CCAGGCTGAGCGGCATCTACCCCTGACCCACTGCACCTGCAGGCTGTGCTGTGACAGCATGGGATGGGCATCCAGGCGGGAGAACCAGACCCCCAG
247> P G L S G I Y P L T H C T L Q A V L S D D G M G I Q A G E P D P P
BsiBI (1365)
BsaBI (1365)
1401 AGGAGCCCTCACCTCGAAGCATCCGTGCCCCCATCAGCTTCGGTAGGCAGCCTCCATCCTCACACCCCTTATCACATCCGCGTGGCATGCGCACCAG
280> E E P L T S Q A S V P P H Q L R L G S L H P H T P Y H I R V A C T S
SphI (1489)
1501 CAGCCAGGCCCCCTCATCCTGGACCCACTGGCTTCTGTGGAGACGCCGGAGGAGTGCCTCCGCCCCCTGAGAACATTAGTGTACGCGGAATGGG
313> S Q G P S S W T H W L P V E T P E G V P L G P P E N I S A T R N G

XmaI (1628)
1601 AGCCAGGCTTCGTGCATTGGCAAGAGCCCCGGCGCCCTGCAGGGTACCCTGTTAGGGTACCGGCTGGCGTATCAAGGCCAGGACACCCAGAGGTGC
347> S Q A F V H W Q E P R A P L Q G T L L G Y R L A Y Q G Q D T P E V
1701 TAATGGACATAGGGCTAAGGCAAGAGGTGACCTGGAGCTGCAGGGGACGGGTCTGTGTCCAATCTGACAGTGTGTGGCAGCCTACACTGCTGCTGG
380> L M D I G L R Q E V T L E L Q G D G S V S N L T V C V A A Y T A A G

PvuII (1867)
1801 GGATGGACCTGGAGCCTCCAGTACCCCTGGAGGCTGGCGCCAGGGCAAGCACAGCCAGTCCACCAGCTGGTGAAGGAACCTTCAACTCCTGCCTTC
413> D G P W S L P V P L E A W R P G Q A Q P V H Q L V K E P S T P A F
SgrAI (1978)
1901 TCGTGGCCCTGGTGTATGACTGCTAGGAGCAGTCTGGCCGCTGCCTGTGCTCCTATCTTGGCTCTTCTTCTGTCACCGGCGAAAGAAGGAGACCC
447> S W P W W Y V L L G A V V A A A C V L I L A L F L V H R R K K E T

FspI (2060)
2001 GTTATGGAGAAGTGTGTAACCAACAGTGGAAAGAGGTGAACTGGTAGTCAGGTACCCTGCGCAAGTCTACAGTCTGCGGACCACTGAAGCTACCTT
480> R Y G E V F E P T V E R G E L V V R Y R V R K S Y S R R T T E A T L

DraIII (2161)
2101 GAACAGCTGGGCATCAGTGAAGAGCTGAAGGAGAAGCTGCGGGATGTGATGGTGGACCGGCACAAGGTGGCCCTGGGAAGACTCTGGGAGAGGGAGAG
513> N S L G I S E E L K E K L R D V M V D R H K V A L G K T L G E G E

XcmI (2240) 2201 TTTGAGCTGTGATGGAAGGCCAGCTCAACCAGGACGACTCCATCCTCAAGGTGGCTGTGAAGACGATGAAGATTGCCATCTGCACGAGGTGAGAGCTGG
547> F G A V M E G Q L N Q D D S I L K V A V K T M K I A I C T R S E L
2301 AGGATTTCTGAGTGAAGCGGTGTCATGAAGGAATTTGACCATCCCAACGTCAAGGCTCATCGGTGTCTGTTTCCAGGGTCTGAACGAGAGAGCTT
580> E D F L S E A V C M K E F D H P N V M R L I G V C F Q G S E R E A G S F
2401 CCCAGCACCTGTGGTCTTACCTTTTCAATGAAACATGGAGACCTACACAGCTTCTCCTCTATTCCCGGCTCGGGGACCCAGCCAGTGTACTGCCCACT
613> P A P V V I L P F M K H G D L H S F L L Y S R L G D Q P V Y L P T

BsiBI (2271)
BsaBI (2271)

2501 CAGATGCTAGTGAAGTTCATGGCAGACATCGCCAGTGGCATGGAGTATCTGAGTACCAAGAGATTTCATACACCGGGACCTGGCGGCCAGGAACTGCATGC
647▶ Q M L V K F M A D I A S G M E Y L S T K R F I H R D L A A R N C M SphI (2594)

BspLU11I (2609) BglII (2648)
2601 TGAATGAGAACATGTCCGTGTGTGGCGGACTTCGGGCTCTCCAAGAAGATCTACAATGGGGACTACTACCGCCAGGGACGTATCGCCAAGATGCCAGT
680▶ L N E N M S V C V A D F G L S K K I Y N G D Y Y R Q G R I A K M P V

Tth111I (2728)
2701 CAAGTGGATTGCCATTGAGAGTCTAGCTGACCGTGTCTACACAGCAAGAGCGATGTGTGGTCTTCGGGGTACAATGTGGGAGATTGCCACAAGAGGC
713▶ K W I A I E S L A D R V Y T S K S D V W S F G V T M W E I A T R G

2801 CAAACCCATATCCGGCGTGGAGAACAGCGAGATTTATGACTATCTGCGCCAGGAAATCGCCTGAAGCAGCCTGCGGACTGTCTGGATGGACTGTATG
747▶ Q T P Y P G V E N S E I Y D Y L R Q G N R L K Q P A A D C L D G L Y

2901 CCTTGATGTCGGGTGCTGGGAGCTAAATCCCCAGGACCGCCAAGTTTACAGAGTGCGGGAAGATTTGGAGAACACACTGAAGGCCTTGCCTCTGC
780▶ A L M S R W E L N P Q D R P S F T E L R E D L E N T L K A L P P A

3001 CCAGGAGCCTGACGAAATCCTCTATGTCAACATGGATGAGGGTGGAGTTATCTGAACCCCTGGAGCTGCAGGAGGAGCTGACCCCCAACCCAGCCA
813▶ Q E P D E I L Y V N M D E G G G Y P E P P G A A G G A D P P T Q P

Bsu36I (3103) BsrBI (3188)
3101 GACCCTAAGGATTCTGTAGCTGCCTCACTGCGGCTGAGGTCCATCCTGCTGGACGCTATGCTCTGCCTTCCACAACCCCTAGCCCCGCTCAGCCTG
847▶ D P K D S C S C L T A A E V H P A G R Y V L C P S T T P S P A Q P

MscI (3277) NheI (3271)
3201 CTGATAGGGGCTCCCCAGCAGCCCCAGGGCAGGAGGATGGTGCCTGAGACAACCCCTCCACCTGGTACTCCCCTAGCTGGCCAGACATGATAAGATACAT
880▶ A D R G S P A A P G Q E D G A •

3301 TGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGC

HpaI (3409) MfeI (3420)
3401 AATAACAAGTTAAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAAACCTCTACAATGTG

EcoRI (3505)
3501 GTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGG
3601 GCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGTTTGAAGTAGCTCTTCAATTTCT

SspI (3744) SmaI (3758)
3701 TTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTA
3801 GGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAA
3901 GCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGT
4001 CAGGAGCATAGTCAGAGATGAGCTCTGACAGTCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCAGAGTAGGGGTGCTGACAGCCAC
4101 AATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACA
4201 GCAGAGATGATCTCCCCAGTCTGGTCCGATGGCCGCCCCGACATGGTGCTTGTGCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCA
4301 GCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCCTATAGTGAGTTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGT
4401 CAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGGC

XmnI (4325) VspI (4391) AseI (4391)
4500 TCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATC

SpeI (4546)
4599 CCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGG

SnaBI (4674) Eco105I (4674)
4699 AAAGTCCCATAAGGTCATGTAAGTGGCATAATGCCAGCGGGCCATTTACCGTATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTATGT
4799 ACTGCCAAGTGGGCGATTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCA

NdeI (4779)
4899 ATGGGCGGGGCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTG C A G G T T A A T T A A G A A C A T G T G A G C A A A A G G C C A G C
4997 AAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTG
5097 GCGAAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCC

PaeI (4965) BspLU11I (4975)
5197 GCCTTTCTCCCTTCCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCAGC
5297 AACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGG

5397 TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGC
5497 GCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGC
5597 AGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGT

EagI (5725)

PacI (5705) SwaI (5714) **NotI (5724)**

5697 CATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACAT
5797 ACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCGAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA