



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA **EcoNI (96)**

101 GAGAAGGTGGCGGGGTAAGTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 **PvuII (239)** **Bsu36I (291)**
EcoNI (287) GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 **NgoMIV (441)** GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

501 **KasI (535)** **AgeI (552)** TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCATCATGATTCTCGCATCCGCTGGCTGTGGCCACGATCCC
1 M I P R I R L A V A T I P

NcoI (602) **SmaI (638)** **NsiI (678)** 601 AGCCATGGCCTTCTCCTGCCTGAGATCTGAGAGCTGGGACCTTGCCTGACAGGTGGTTCCTAACATTAGTTACCAATGCATGGAGCTGAATTTCTAC
13> A M A F L S C L R S E S W D P C V Q V V P N I S Y Q C M E L N F Y
701 AAAATCCCTGACAACATCCACATCAGTCAAGATACTGGACCTGAGCTTTAACTACCTGAGTCATTTAGACAGCAATAGCTTCTCCAGCTTTCCAGAAC
47> K I P D N I P T S V K I L D L S F N Y L S H L D S N S F S S F P E

NsiI (848) **BsaBI (847)** 801 TGCAGGTGCTGGATTATCCAGATGTGAAATTCAGACAATTGACGATGATGCATATGACAGGCTAAATACCTTTCCACCTTGATACTGACGGAAATCC
80> L Q V L D L S R C E I Q T I D D D A Y Q G L N Y L S T L I L T G N P
901 TATCCAGAGTTTAGCCCTGGGAGCCTTTCTGGACTACCAAGTTTACAGAAGCTGGTTCGCGTTGAGACAACTAGCGTCTCTAGAGGACTTCCCATT
113> I Q S L A L G A F S G L P S L Q K L V A V E T N L A S L E D F P I
1001 GGACATCTAAAACCTTGAAGGAGCTTAATGTGGCTCAACATCATATCATTCTTTCAAGTTACCTGAATATTTTCTAACCTGCCAACCTGGAGCATT
147> G H L K T L K E L N V A H N H I H S F K L P E Y F S N L P N L E H
1101 TGGATCTTTCTAAGAACAAAATCGAAAATATTTATCATGAACACTTGCAGGTTCTACATCAAGTGCCCTACTCAATCTCTTTTAGACTTGTCCCTGAA
180> L D L S K N K I E N I Y H E H L Q V L H Q V P L L N L S L D L S L N
1201 CCCTTTAACTTTATTGAACCAGGTGCCTTTAAACAAAATTAGGCTCAATGGATTGACTTTGCGAAGTAATTTTAAATAGTTGCGATGTAATGAAAACCTGT
213> P L N F I E P G A F N K I R L N G L L R S N F N S D V M K T C
1301 ATTCAGGTCTGGCTGGTTCAAAAATCAATCAGTTGGTTTTGGGAGAATTTAAAAATGAAAGAACTTGGAAAAGTTTTGACAAAATCTGTCTGGAGGAAAC
247> I Q G L A G S K I N Q L V L G E F K N E R N L E S F D K S V L E E

BspEI (1424) **EcoRI (1444)** 1401 TGTGCAATTTGACCCTTGAACAGTTCCGGATAGCACACTTTGGTGAATTTCCAGATGATGTTTCTGACTTATTTAATTGTTGGCAAATGCCTCTGTGAT
280> L C N L T L E Q F R I A H F G E F P D D V S D L F N C L A N A S V I

XmnI (1531) **HpaI (1573)** 1501 TTCTCTGTTGAGTCTGAATTTGCGTGGTCTAGAAGCCCTTCTAATGATTTCCAGTGGCAACACTTAGAAGTGGTAACTGTAACCTTCAACAATTTCT
313> S L L S L N L R G L E A L P N D F R W Q H L E V V N C K L Q Q F P

NdeI (1648) 1601 GCATTGAAGTTCAACTCTCTCAAAAAGTTGTTTTCAAAGACAATAAACATATGCACACTTTTACTGAAATTAACCTGCCAAACCTTTCAGTTTCTAGATC
347> A L K F N S L K K F V F K D N K H M H T F T E I N L P N L Q F L D
1701 TCAGTGAAATCACTTGAGCTTTAAAGGTTGCTGTTCTACAATGAATTTGGGACAACCAAAGTGAAGCATTAGATCTGAGCTTCAATGAAATCATTAC
380> L S G N H L S F K G C C S H N E F G T T K L K H L D L S F N E I I T
1801 CATGAAGTCAAACTTATGAGCACTAGAGCAACTAGAACTCCAGTATCCAGCTTCCAGTGGTGAACAGGCTAATGACTTTTCCATTTCTATCCTC
413> M K S N F M G L E Q L E Y L D F Q H S S L K Q A N D F S I A F L S L
1901 AGAAACCTCCATTACCTTGATATTTCTTATACTAACATCCAGTGTGCTTCCGTGGCATTGTTGCTGGCTTGGTCAGCCTCCAAACCTTGAATAAGGCTG
447> R N L H Y L D I S Y T N I H V V F R G I F A G L V S L Q T L K M A
2001 GCAATTTCTTTCAGAACAACTTGTCTCCTGATGCTTACAGATCTGACTAATTAATCCTCCTGGACCTCTCAAGTGTCAACTGGAACAGGTATCCCA
480> G N S F Q N N L L P D V F T D L T N L I L L D L S K C Q L E Q V S Q

AvrII (2119) **Bsu36I (2196)** 2101 GAGGGCATTTCATCCCTCCCTAGGCTTCAGGTGCTAAATATGAGTCACAACAGACTCTTGTCTTGGATACGCTTCTTATAAACCACTCCACTCCCTC
513> R A F H S L P R L Q V L N M S H N R L L F L D T L P Y K P L H S L
2201 AGGATTCTGGATTGCAGTTACAATCTTATCGTGGCCTCCAAGGAACAAGAACTACAGCATCTGCCAAGGAGCCTAGCTTTTTTAAATCTCACTAAGAATG
547> R I L D C S Y N L I V A S K E Q E L Q H L P R S L A F L N L T K N

BsrGI (2386) 2301 ACTTTTCTGTGCGTGTGAACACCAGACTTTCTTGCAGTGGGTCAGGACCAGAAGCAGCTCCTTGTGGGAGCTGAGCAAATGGTGTGACACAACTTT
580> D F S C A C E H Q T F L Q W V K D Q K Q L L V G A E Q M V C T Q P L
2401 AGAAATCGAGGACTGCCTGTGCTGAGTTTCAGGAACGCCACCTGTGAGTAAAGCAGGCGCTCATTAGTGCCTGAGTCTCACCTTCTCTCTGGTATCT
613> E M Q D L P V L S F R N A T C Q I S E A V I S A S V L T F L L V S
2501 GTGGCAGGAATCTGGTCTATAAGTTCTATTTCCACTTGTGCTTTTTGTGGGCTGCAAAAAATATGGCAGAGGTGAAAGCACCTATGACGCCTTTGTTA
647> V A G I L V Y K F Y F H L L L F V G C K K Y G R G E S T Y D A F V
2601 TCTACTCCAGCCAGGACGAAGACTGGGTGAGGAATGAAGTGGTAAAGAACTTGGAGGAGGGGGTGCCTTTTTCATCTCTGCCTTCACTACAGAGACTT
680> I Y S S Q D E D W V R N E L V K N L E E G V P P F H L C L H Y R D F
2701 CATTCCCGGTGTGGCCATCGCTGCTAACATCATCCAGGAAGGTTTCCACAAAAGCTCGGAAGGTTATTGTCGTGGTGTCCAGCATTCATACAGAGCCGA
713> I P G V A I A A N I I Q E G F H K S R K V I V V V S Q H F I Q S R

NgoMIV (2854) 2801 TGGTGATCTTTGAGTATGAGATTGCCAGACCTGGCAGTTTCTGAGGAGTATGCCGGCATCATCTTCATCGTCTGAGAAAGTTGGAGAAGTCCCTGC
747> W C I F E Y E I A Q T W Q F L R S H A G I I F I V L Q K L E K S L

Tth111I (2959)

2901 TGC GGCAGCAGGTGGAGCTGTATCGCCTTCTCAGCAGGAATACCTACCTGGAGTGGGAGGACAGCGTCCTGGGGCGGCACATCTTCTGGAGACGACTCAA
780▶ L R Q Q V E L Y R L L S R N T Y L E W E D S V L G R H I F W R R L K

NcoI (3022)

3001 GAAAGCCTTGCTGGATGGTAAACCATGGAGTCCAGAAGGAACAGAGGATTGAGAAAGCAACCAGCATGATACAACAGCCTTCACTTAAGGAGGGAAAAC
813▶ K A L L D G K P W S P E G T E D S E S N Q H D T T A F T •

NheI (3119)

3101 CCCAACGTGTCCCTTGGTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATT

HpaI (3257)

3201 TGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAATTGCATTCAATTTATGTTTCAGGTTTCAGG

EcoRI (3353)

3301 GGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTTAACCTCCAATCAAGCC
3401 TCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGT
3501 TTAAGATATAGTGTATTTTCCCAAGTTTGAAC TAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTCA

SwaI (3606)

3601 GAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTT
3701 GGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGAGGGGATGAGTTCCTCAA
141▶ • N R T Y K L P I L E E I

SacI (3867) **BstXI (3896)**

3801 TGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCAC
128▶ 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 P S V V
3901 CCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATG
95▶ 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 G I A I

StuI (4031)

4001 GCTTCAGCACAGACAGTGCACCTGCCAATGTAGGCCTCAATGGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCT
61▶ 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 V H H K

XmnI (4173)

4101 TGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCTCCTATA
28▶ 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 (4239) **SacI (4296)**

4201 GTGAGTCGTATTATACTATGCGGATATACTATGCGGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGC

SpeI (4394)

4301 TCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAG
4400 TCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA CTGCCAAAACCGCATC

SnaBI (4522)

4500 ATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTA CTGGCATAATGCCAGGCGGGCCATTTACCGT

NdeI (4627)

4600 CATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCTCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAA
4700 AGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTGTTGGCGGTGACCCAGGCGGGCCATTTACCGTAAAGTTAT

SdaI (4805) **PacI (4813)** **BspLU11I (4823)**

4800 GTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGAAAAGGCCAGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTC
4898 CGCCCCCTGACGAGCATCAAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCC
4998 TCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTA

ApaLI (5137)

5098 TCTCAGTTCGGTGTAGGTCGTTCTGCTCCAAGCTGGGCTGTGTGACGAAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAG
5198 TCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGT
5298 GGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGG
5398 CAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACG

EagI (5573)

5498 GGGTCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGATTTGGTTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATT
5598 TTCATTACATCTGTGTGTTGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCT
5698 CCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA