



PvuI (7)
SgfI (6)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGTGCCTA
101 GAGAAGGTGGCGGGGTAAGTGGAAAGTGATGCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **BspHI (561)**
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCCATCATGATGCTGCCTCGCCCTGGCTGGGACTCTGATCC
1 M M S A S R L A G T L I

NcoI (603) **Ppu10I (679)** **NsiI (679)**
601 CAGCCATGGCCTTCTCTCTGCGTGAGACCCGAAAGCTGGGAGCCCTGCGTGGAGGTGGTTCCATAATTACTTATCAATGCATGGAGCTGAATTTCTA
13 P A M A F L S C V R P E S W E P C V E V V P N I T Y Q C M E L N F Y
701 CAAAAATCCCGACAACCTCCCTTCTCAACCAAGAACCTGGACCTGAGCTTTAATCCCTGAGGCATTTAGGCAGCTATAGCTTCTTCAAGTTTCCAGAA
46 K I P D N L P F S T K N L D L S F N P L R H L G S Y S F F S F P E
801 CTGAGGTGCTGGATTTATCCAGGTGTGAAATCCAGACAATTAAGATGGGCATATCAGAGCCTAAGCCACCTCTACCTTAATATTGACAGGAAACC
80 L Q V L D L S R C E I Q T I E D G A Y Q S L S H L S T L I L T G N
901 CCATCCAGAGTTAGCCCTGGGAGCCTTTCTGGACTATCAAGTTTACAGAAGCTGGTGGCTGTGGAGACAACTAGCATCTAGAGAAGTTCCCAT
113 P I Q S L A L G A F S G L S S L Q K L V A V E T N L A S L E N F P I
1001 TGGACATCTCAAACTTTGAAAGAACTTAATGTGGCTCACAATCTTATCCAATCTTTCAAATACCTGAGTATTTTCTAATCTGACCAATCTAGAGCAC
146 G H L K T L K E L N V A H N L I Q S F K L P E Y F S N L T N L E H
1101 TTGACCTTCCAGCAACAAGATTCAAAGTATTTATTGCACAGACTTCCGGGTTCTACATCAAATGCCCTACTCAATCTCTTTAGACCTGTCCCTGA
180 L D L S S N K I Q S I Y C T D L R V L H Q M P L L N L S L D L S L
1201 ACCATGAACTTTATCCAACAGGTGCATTTAAAGAAATTAGGCTTCATAAGCTGACTTAAGAAATAATTTGATAGTTAAATGTAATGAAAACCTG
213 N P M N F I Q P G A F K E I R L H K L T L R N N F D S L N V M K T C

BstXI (729) **Bsu36I (757)**
1301 TATTCAAGGTCTGGCTGGTTTAGAAGTCCATCGTTTGGTCTGGGAGAATTTAGAAATGAAGGAACTTGGAAAAATTTGACAAATCTGCTCTAGAGGGC
246 I Q G L A G L E V H R L V L G E F R N E G N L E K F D K S A L E G
1401 CTGTGCAATTTGACCATTGAAGAATTCGATTAGCATACTTAGACTACTACCTCGATGATATTATTGACTTATTTAATGTTTGACAAATGTTTCTTCAT
280 L C N L T I E E F R L A Y L D Y Y L D D I I D L F N C L T N V S S
1501 TTTCCCTGGTGAGTGTGACTATTGAAAGGTAAGAACTTTTCTTATAATTTTCGATGGCAACATTTAGAATTAAGTAACTGTAATTTGGACAGTTTCC
313 F S L V S V T I E R V K D F S Y N F G W Q H L E L V N C K F G Q F P
1601 CACATTGAACTCAAATCTCAAAAGGCTTACTTTCACTTCCAACAAAGGTGGGAATGCTTTTTCAGAAGTTGATCTACCAAGCCTTGAGTTTCTAGAT
346 T L K L K S L K R L T F T S N K G G N A F S E V D L P S L E F L D
1701 CTCAGTAGAAATGGCTTGGATTTCAAAGTTGCTGTTCTCAAAGTATTTTGGGACAACCAGCCTAAAGTATTTAGATCTGAGCTTCAATGGTGTATTATTA
380 L S R N G L S F K G C C S Q S D F G T T S L K Y L D L S F N G V I
1801 CCATGAGTTCAAATCTTTGGGCTTAGAACAAC TAGAACATCTGGATTTCCAGCATTCCAATTTGAAACAAATGAGTGAGTTTTCAGTATTCCTATCACT
413 T M S S N F L G L E Q L E H L D F Q H S N L K Q M S E F S V F L S L
1901 CAGAAACCTATTACCTTGACCTTTCTCATACTCACACAGAGTTGCTTTCAATGGCATCTTCAATGGCTTGTCCAGTTCGAAAGTCTGAAATGGCT
446 R N L I Y L D I S H T H T R V A F N G I F N G L S S L E V L K M A
2001 GGCAATCTTTCCAGGAAAACCTTCCAGATATCTTCAAGAGCTGAGAACTTGACCTTCTGGACCTCTCTCAGTGTCAACTGGAGCAGTTGTCTC
480 G N S F Q E N F L P D I F T E L R N L T F L D L S Q C Q L E Q L S
2101 CAACAGCATTTAACTCACTCTCCAGTCTCAGTACTAAATATGAGCCACAACAACTTCTTTTTCATTGGATAGCTTTCTTATAAGTGTCTGAACTCCCT
513 P T A F N S L S S L Q V L N M S H N N F F S L D T F P Y K C L N S L
2201 CCAGGTTCTTGATTACAGTCTCAATCACATAATGACTTCCAAAAACAGGAACACAGCATTTCCAAGTAGTCTAGCTTTCTTAAATCTTACTCAGAAT
546 Q V L D Y S L N H I M T S K K Q E L Q H F P S S L A F L N L T Q N
2301 GACTTGTGTTGACTTGTGAACACCAGAGTTTCTGCAATGGATCAAGGACCAGAGCCAGCTCTTGGTGAAGTTGAACGAATGGAATGTGCGACACCTT
580 D F A C T C E H Q S F L Q W I K D Q R Q L L V E V E R M E C A T P
2401 CAGATAAGCAGGGCATGCCTGTGCTGAGTTTGAATATCACCTGTGAGTGAATAAGACCATCATTGGTGTGCTGGTCCCTCAGTGTGCTTGTAGTATCTGT
613 S D K Q G M P V L S L N I T C Q M N K T I I G V S V L S V L V V S V
2501 TGTAGCAGTTCTGGTCTATAAGTTCTATTTTCACTGATGCTTCTGCTGGCTGCATAAAGTATGGTAGAGGTGAAAACATCTATGATGCCTTTGTTTATC
646 V A V L V Y K F Y F H L M L L A G C I K Y G R G E N I Y D A C F V I
2601 TACTCAAGCCAGGATGAGGACTGGGTAAGGAATGAGCTAGTAAAGAAATTTAGAAGAAGGGGTGCCTCCATTTTCAGCTCTGCTTCACTACAGAGACTTTA
680 Y S S Q D E D W V R N E L V K N L E E G V P P F Q L C L H Y R D F
2701 TTCCCGGTGGCCATTGCTGCCAATCATCCATGAAGGTTTCCATAAAAGCCGAAAGGTGATTGTTGTTGTTGCCAGCACTTTCATCCAGAGCCGCTG
713 I P G V A I A A N I I H E G F H K S R K V I V V V S Q H F I Q S R W

2801 GTGTATCTTTGAATATGAGATTGCTCAGACCTGGCAGTTTCTGAGCAGTCGTGCTGGTATCATCTTCATTGCTCCTGCAGAAGGTGGAGAAGACCTGCTC
746▶ C I F E Y E I A Q T W Q F L S S R A G I I F I V L Q K V E K T L L
Tth111I (2957)

2901 AGGCAGCAGGTGGAGCTGTACCCGCTTCTCAGCAGGAACACTTACCTGGAGTGGGAGGACAGTGTCTGGGGCGGCACATCTTCTGGAGACGACTCAGAA
780▶ 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 R
MscI (3089)
NheI (3083)

3001 AAGCCTGCTGGATGGTAAATCATGGAATCCAGAAGGAACAGTGGGTACAGGATGCAATTGGCAGGAAGCAACATCTATCTGAGCTAGCTGGCCAGACAT
813▶ K A L L D G K S W N P E G T V G T G C N W Q E A T S I •
3101 GATAAGATACATTGATGAGTTTGGACAAACCACAACACTAGAATGCAGTGAACAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACC

HpaI (3221)

3201 ATTATAAGCTGCAATAAAACAAGTTAAACAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACC

EcoRI (3317)

3301 TCTACAAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCA
3401 TAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTAG

SwaI (3570)

3501 CTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAA

EcoO109I (3631)

3601 TGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGAACCTTTAATAGAAATTG
3701 GACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGA
141▶ • N R T Y K L P I L E E I T T K V L K G N M E I L
SacI (3831) BstXI (3860)

3801 GCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTG
116▶ 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 S Y P H
StuI (3995)

3901 CCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCC
83▶ 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 G I Y A
4001 TCAATGTGGACAGCAGAGATGATCTCCCAAGTCTGGTCTGATGGCCGCCGACATGGTGTCTTGTCTCCTATAGAGCATGGTATCTTCTCAGTGG
49▶ 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 I K E T A
BspHI (4145)

4101 CGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCG
16▶ V E V L E L D Q Q S I N F T K M
AseI (4203) SacI (4260)

4201 ATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTAC

SpeI (4358)

4300 CGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAA
SnaBI (4486)

4399 GACTTGAAAATCCCCTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA
NdeI (4591)

4499 CTGCCAAGTAGGAAAAGTCCATAAGGTCATGTAAGTGGGATAATGCCAGGCGGGCCATTTACCCTGATTGACGTCAATAGGGGGCGTACTTGGCATATGA
4599 TACACTTGATGTAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCA
SdaI (4769) PacI (4777) BspLU11I (4787)

4699 TTATTGACGTCAATGGGGCGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAG
4797 CAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGCGCTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTC
4897 AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCTTTCCCCCTGGAAGTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACC
4997 GGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCCAAGCTGG
ApaLI (5101)

5097 GCTGTGTGCACGAACCCCCGTTGACGCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCCGGTAAGACACGACTTATCGCCACTGGC
5197 AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA
5297 TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGGTTGGTAGCTCTTGTATCCGGCAACAAACACCCTGGTAGCGGTGGTTTTTTTG
5397 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTA
EagI (5537)
PacI (5517) SwaI (5526) NotI (5536)

5497 AGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAAT
5597 CGTAACTAACATACGCTCTCCATCAAAAACAAACGAAACAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCAGGTGCCAGAACATTTCTCTA
5697 TCGAA