



PvuI (7)
SgfI (6)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGGGGTAAGTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGGCC
301 GCCATCCACGCGGTTGAGTGCCTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560) **BstEII (555)**
KasI (535) **AgeI (552)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCACCATGGGGTTTTGGATCTTAGCAATTCTCACAAATCTCAT
601 GTATTCACAGCAGCAAAGTTTAGTAAACAATCATGGGCGCTGGAAAATGAGGCTTTAATTGTAAGATGTCTAGACAAGGAAAACCTAGTTACACCGTG
13> Y S T A A K F S K Q S W G L E N E A L I V R C P R Q G K P S Y T V
1> M G F W I L A I L T I L M

Bsu36I (761) **PvuII (788)**
701 GATTGGTATTACTCACAAACAAAACAAAAGTATTCCCACTCAGGAAAGAAATCGTGTGTTTGCCTCAGGCCAACTCTGAAGTTTCTACAGCTGCAGTTG
47> D W Y Y S Q T N K S I P T Q E R N R V F A S G Q L L K F L P A A V
801 CTGATTCTGGTATTATACCTGTATTGTCAGAAGTCCCACATTC AATAGGACTGGATATGCGAATGTCACCATATATAAAAAACAATCAGATTGCAATGT
80> A D S G I Y T C I V R S P T F N R T G Y A N V T I Y K K Q S D C N V
901 TCCAGATTATTTGATGATTCAACAGTATCTGGATCAGAAAAAATTC AAAAAATTTATTGCTCACCATTGACCTCTACAACCTGGACAGCACCTCTT GAG
113> P D Y L M Y S T V S G S E K N S K I Y C P T I D L Y N W T A P L E
1001 TGGTTAAGAATTGTCAGGCTCTCAAGGATCAAGGTACAGGGCCACAGCTATTTTTGGTATTGATAATGTGATGACTGAGGACGCGAGGTGATTACA
147> W F K N C Q A L Q G S R Y R A H K S F L V I D N V M T E D A G D Y

Tth11I (1149)
1101 CCTGTAAATTTATACACAATGAAAATGGAGCCAATTATAGTGTGACGGCAGCCAGTCTTACGGTCAAGGATGAGCAAGGCTTTTCTCTGTTTCCAGT
180> T C K F I H N E N G A N Y S V T A T R S F T V K D E Q G F S L F P V
1201 AATCGGAGCCCCTGCACAAAATGAAAATAAGGAAGTGGAAAATGGAAAAACGCAAACTAATTGCTCTGCTTGTGTTTGGAAAAAGGCACTCAGTTCTTG
213> I G A P A Q N E I K E V E I G K N A N L T C S A C F G K G T Q F L
1301 GCTGCCGTCTGTGGCAGCTTAATGGAACAAAAATTACAGACTTTGGTGAACCAAGAAATTC AACAAGGAGGAAAGGCAAAATCAAAGTTTCAGCAATGGGC
247> A A V L W Q L N G T K I T D F G E P R I Q Q E E G Q N Q S F S N G

XbaI (1407)
1401 TGGCTGTCTAGACATGGTTTTAAGAATAGCTGACGTGAAGGAAGAGGATTTATTGCTGCAGTACGACTGTCTGGCCCTGAATTTGCATGGCTTGAGAAG
280> L A C L D M V L R I A D V K E E D L L L Q Y D C L A L N L H G L R R
1501 GCACACCGTAAGACTAAGTAGGAAAAATCCAATTGATCATCATAGCATCTACTGCATAATTGCAGTATGTAGTGTATTTTAAATGCTAATCAATGTCCTG
313> H T V R L S R K N P I D H H S I Y C I A A V C S V F L M L I N V L
1601 GTTATCATCCTAAAAATGTTCTGGATTGAGGCCACTCTGCTCGGAGAGACATAGCTAAACCTTACAAGACTAGGAATGATGAAAGCTCATGATGCTT
347> V I I L K M F W I E A T L L W R D I A K P Y K T R N D G K L Y D A
1701 ATGTTGTCTACCCACGGAACACAAATCCAGTACAGATGGGGCCAGCTGTGTAGAGCACTTTGTTCCAGATTTCTGCCTGATGTTCTTAAAAATAAATG
380> Y V V Y P R N Y K S S T D G A S R V E H F V H Q I L P D V L E N K C

Ppu10I (1812) **NsiI (1812)**
1801 TGGCTATACCTTATGCATTTATGGGAGAGATATGCTACCTGGAGAAGATGTAGTCACTGCAGTGGAAACCAACATACGAAAGAGCAGGCGGCACATTTTC
413> G Y T L C I Y G R D M L P G E D V V T A V E T N I R K S R R H I F
1901 ATCCTGACCCCTCAGATCACTCACAATAAGGAGTTTGCCTACGAGCAGGAGGTTGCCCTGCAGTGTGCCTCATCCAGAACGACGCCAAGGTGATACTTA
447> I L T P P I T H N K E F A Y G E Q E V A L H C A L I Q N D A K V I L
2001 TTGAGATGGAGGCTCTGAGCGAGCTGGACATGCTGCAGGCTGAGGCGCTTCAGGACTCCCTCCAGCATTTATGAAAGTACAGGGGACCATCAAGTGGAG
480> I E M E A L S E L D M L Q A E A L Q D S L Q H L M K V Q G T I K W R

Asp718I (2156) **Acc65I (2156)**
BbrPI (2149) **StuI (2192)**
2101 GGAGGACCACATTGCCAATAAAAAGTCCCTGAATTCTAAATCTGGAAGCACGTGAGGTACCAAAATGCCTGTGCCAAGCAAAATCCCAGAAAAGGCTCT
513> E D H I A N K R S L N S K F W K H V R Y Q M P V P S K I P R K A S

MscI (2240) **NheI (2234)**
2201 AGTTTGACTCCCTGGCTGCCGAGAAGCAATAGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGA
547> S L T P L A A Q K Q •

HpaI (2372)
2301 AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAACAACAACAATTGCATTATTTTA
2401 TGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAA
2501 CCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCAC
2601 CTTCTTTTCATGGAGTTTAAAGATATAGTATTTTCCCAAGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGACTGACCTCCACATTTCCCTTT

2701 **SspI (2707)** **SwaI (2721)**
TTAGTAAAATATTCCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCC

2801 CCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCGTGTACTTGAGGG
141 • N R T Y K L P
SacI (2982)

2901 GGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCC
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

BstXI (3011)

3001 ACAGGGGTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCA
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

StuI (3146)

3101 GACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCG
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
BspHI (3296)

3201 CCCCACATGGTCTTGTGTCTCATAGAGCATGGTGTCTTCTCAGTGGGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCAT
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
XmnI (3288)

AseI (3354)

3301 GATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGAC
SacI (3411)

3400 GGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTC

SpeI (3509)

3500 CCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA

SnaBI (3637)

3599 CTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTGATGACTGGGCATAATGCCAG

NdeI (3742)

3699 GCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCC

3799 ATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACCCAGGCGGGCC

SdaI (3920) **PacI (3928)** **BspLU11I (3938)**

3899 ATTTACCGTAAGTTATGTAACGCC T G 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 A A A A G G C C A G G A A C C G T A A A A A G G C C G T T G C T G G C
3997 G T T T T C C A T A G G C T C G C C C C C T G A C G A G C A T C A C A A A A T C G A C G C T C A A G T C A G A G G T G G C G A A C C C G A C A G G A C T A T A A A G A T A C C A G G C G T T T
4097 C C C C T G G A A G C T C C C T C G T G C G C T C T C T G T T C C G A C C T G C C G T T A C C G G A T A C T G T C C G C T T T C T C C T T C G G G A A G C G T G G C G T T T C T C A T A

ApaLI (4252)

4197 GCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCCTGCGCCTTATCCGG
4297 TAACTATCGTCTTGAGTCAAACCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCT
4397 ACAGAGTTCCTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG
4497 GTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCC

EagI (4688) **PacI (4668)** **SwaI (4677)** **NotI (4687)**

4597 TTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCA
4697 ATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAACGAAACAAACAAACT
4797 AGCAAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA