



PvuI (7)
 SgfI (6)

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA EcoNI (96)

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 NaeI (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560)
 BstEII (555)
 KasI (535) AgeI (552)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCCTACCTGAGATCACCGGTCCACCATGGAGCAGTGGGATCACTTTCACAATCAACAGGAGGA

601 CACTGATAGTGTCCGAATCTGTGAAATTTGATGCTCGCTCAATGACAGCTTTGCTTCTCCGAATCTAAAAACAGCCCTTCCCTTCAAGAGAACTG
 13> T D S C S E S V K F D A R S M T A L L P P N P K N S P S L Q E K L
 701 AAGTCTTCAAAGCTGCACTGATTGCCCTTTACCTCCTCGTGTTCGAGTTCATCCCTCTCATTGGAATAGTGGCAGCTCAACTCCTGAAGTGGGAAA
 47> K S F K A A L I A L Y L L V F A V L I P L I G I V A A Q L L K W E
 801 CGAAGAATTGCTCAGTTAGTTCAACTAATGATATAACTCAAAGTCTCACGGAAAAGGAAATGACAGCGAAGAGGAAATGAGATTTCAAAGAAT
 80> T K N C S V S S T N A N D I T Q S L T G K G N D S E E E M R F Q E V
 901 CTTATGGAACACATGAGCAACATGGAGAAGAGAAATCCAGCATATTTAGACATGGAAGCCAACCTCATGGACACAGAGCATTTCAAATTTTCAGCATG
 113> F M E H M S N M E K R I Q H I L D M E A N L M D T E H F Q N F S M

PstI (1030)

1001 ACAACTGATCAAAGATTTAATGACATTTCTGCGAGCTAAGTACCTTGTTCCTCAGTCCAGGGACATGGGAATGCAATAGATGAAATCTCCAAGTCTC
 147> T T D Q R F N D I L L Q L S T L F S S V Q G H G N A I D E I S K S
 1101 TAATAAGTTTGAATACCACATTGCTTGAATTTGAGCTCAACATAGAAAATCTGAATGGCAAAATCCAAGAGAATACCTTCAAACAACAAGAGGAAATCAG
 180> L I S L N T T L L D L Q L N I E N L N G K I Q E N T F K Q Q E E I S

ScaI (1296)

1201 TAAATAGAGGAGCGTGTTTACAATGTATCAGCAGAAATTATGGCTATGAAAGAAGAACAAGTGCATTTGGAACAGGAAATAAAAGGAGAAGTGAAGTA
 213> K L E E R V Y N V S A E I M A M K E E Q V H L E Q E I K G E V K V

XmaI (1392)
 SmaI (1392)

1301 CTGAATAACATCACTAATGATCTCAGACTGAAAGATTGGGAACATTCTCAGACCTTGAGAAAATACACTTTAATTCAAGGTCTCCTGACCCCGGGTG
 247> L N N I T N D L R L K D W E H S Q T L R N I T L I Q G P P G P P G
 1401 AAAAGGAGATCGAGTCCCACTGGAGAAAGTGGTCCACGAGGATTTCCAGGTCCAATAGGTCTCCGGTCTTAAAGGTGATCGGGAGCAATTGGCTT
 280> E K G D R G P T G E S G P R G F P G P I G P P G L K G D R G A I G F
 1501 TCCTGGAAGTTCGAGGACTCCAGGATATGCCGAAGGCCAGGAAATTTGACCAAAAGCCAGAAAGGGGAAAAGGGGAGTGGAAACACATTAACCTCA
 313> P G S R G L P G Y A G R P G N S G P K G Q K G E K G S G N T L T P

BsrBI (1626) PvuI (1689)

1601 TTTACGAAAGTTCGACTGGTGGTGGGAGCGGCCCTCACGAGGGGAGAGTGGAGATACTCCACAGCGGCCAGTGGGGTACAATTTGTGACGATCGCTGGG
 347> F T K V R L V G G S G P H E G R V E I L H S G Q W G T I C D D R W

ApaLI (1756)

1701 AAGTGGCGTTGGACAGGTCTGTGTAGGAGCTTGGGATACCCAGGTGTTCAAGCCGTGCACAAGGCAGCTCACTTTGGACAAGGTACTGGTCCAATATG
 380> E V R V G Q V V C R S L G Y P G V Q A V H K A A H F G Q G T G P I W
 1801 GCTGAATGAAGTGTGTTTGGTGGGAGAGAATCATCTATTGAAGAATGAAAATTCGGCAATGGGGACAAGAGCCTGTTACATTCTGAAGATGCTGGA
 413> L N E V F C F G R E S S I E E C K I R Q W G T R A C S H S E D A G

Ppu10I (1917) MscI (1960)
 NsiI (1917) NheI (1954)

1901 GTCACCTGCACTTTAATGCATCATATTGTCATTCACAACATATGAAATCGCTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAA
 447> V T C T L •

HpaI (2092)

2001 CCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAA

EcoRI (2188)

2101 CAACAATTGCATTCAATTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAATGTGGTATGGAATTTCAAAAT

2201 ACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCA

2301 TTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTTAAAGATAGTGTATTTTCCCAAGGTTTGAAGTGTGCTTCTTCTTTATGTTTTAAATGCAC

SspI (2427) SmaI (2441)

2401 TGACCTCCACATTCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCT

2501 CAAGGCCCTTCATAATATCCCCAGTTTAGTGTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTA

2601 GTTCTGGTGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAG
 140> N R T Y K L P 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

SacI (2702)
2701 ATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCT
106 I L E R C M G 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
StuI (2866)
Eco147I (2866)
2801 TCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCC
73 Q G N S V A 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
2901 AGTCTTGGTCTGATGGCCGCCGACATGGTGTCTTGTCCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGTGA
40 T K T R I A A 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
BspHI (3016) AseI (3074)
3001 GAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGG
6 S I N F T K M
SacI (3131)
3101 CGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGT
SpeI (3229)
3201 TACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCT
SnaBI (3357)
3300 ATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAGGTCAT
NdeI (3462)
3400 GTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTT
3500 TACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTGGTGG
PstI (3641) SdaI (3640) PacI (3648) BspLU11I (3658)
3600 GCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTA
3698 AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT
3798 ATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA
ApaLI (3972)
3898 AGCGTGGCGCTTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCG
3998 ACCGCTGCGCCTTATCCGTAACATATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC
4098 GAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT
4198 ACCTTCGGA AAAAGAGTTGGTAGCTCTTGATCCGCAAACAACACCCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAA
PacI (4388)
4298 AAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAAC
EagI (4408)
SwaI (4397) NotI (4407)
4398 ATTTAAATC AGCGGCCCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACA
4498 AAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA