



PvuI (7)
SgfI (6)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCC

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCTCTAGGTAAGTTAAAGTCAAGTGCAGACC

NgoMIV (441)
401 GGGCCTTTGTCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560) **BstXI (560)** **SfiI (591)**
BstEII (555) **XcmI (587)**
AgeI (552) **Neol (587)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCCACCATGGTGTGCCCCAGGGGCTGCTCTCCATGGCCCTGCT

1 M V L A Q G L L S M A L L

BstAPI (651) **SdaI (692)**
601 GGCCTGTGCTGGGAGCGCAGCCTGGCAGGGGCGAGAAGAAACCATCCCCTGCAGACCCTGCGTGTACAACGACTACACCAGCCACATCACCTGCAGG

13> A L C W E R S L A G A E E T I P L Q T L R C Y N D Y T S H I T C R

701 TGGGAGACACCCAGGATGCCAGCGGCTCGTCAACGTGACCCCTATTCGCCGGGTGAATGAGGACCTCTGGAGCCAGTGTCTGTGACCTCAGTGTATG

47> W A D T Q D A Q R L V N V T L A I R R V N E D L L E P V S C D L S D

801 ACATGCCCTGGTCAAGCTGCCCATCCCGCTGCGTGCAGGATGTGTATTCCCTGCCAGAGTTTGTGCTCACTGACGTTGACTACTTCTCAT

80> D M P W S A C P H P R C V P R R C V I P C Q S F V V T D V D Y F S F

901 CCAACCAGACAGGCTCTGGGACCCCGGCTCACCGTCACTGTGACCCAGCATGTCCAGCTCCTGAGCCAGGGACCTGCAGATCAGCACCGACCGAGGAC

113> Q P D R P L G T R L T V T L T Q H V Q P P E P R D L Q I S T D Q D

1001 CACTTCTGCTGACCTGGAGTGTGGCCCTGGGAGTCCCAGAGCCACTGGTGTGCCAGGGGATCTGGAGTTTGGAGTGTCTACAAGCGGCTTCAGG

147> H F L L T W S V A L G S P Q S H W L S P G D L E F E V V Y K R L Q

BstAPI (1161)
1101 ACTCTGGGAGGACGCAGCCATCCTCCTCCTCAACACCTCCCAGGCCACCCTGGGGCCAGAGCACCTCATGCCAGCAGCACCTACGTGGCCCGAGTACG

180> D S W E D A A I L L S N T S Q A T L G P E H L M P S S T Y V A R V R

XcmI (525)
1201 GACCCGCTGGCCCCAGGTTCTCGGCTCTCAGGACGTCCAGCAAGTGGAGCCAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAG

213> T R L A P G S R L S G R P S K W S P E V C W D S Q P G D E A Q P Q

1301 AACCTGGAGTGTCTTTGACGGGGCCCGCTGCTCAGCTGCTCCTGGGAGGTGAGGAAGGAGGTGGCCAGCTCGGTCTCCTTTGGCCTATTCTACAAGC

247> N L E C F F D G A A V L S C S W E V R K E V A S S V S F G L F Y K

1401 CCAGCCAGATGCAGGGGAGGAGTGTCCCCAGTGTGAGGGAGGGCTCGGAGCCCTCCACAGCCAGGACCCAGATTCCCGTGGCCGACCC

280> P S P D A G E E E C S P V L R E G L G S L H T R H H C Q I P V P D P

1501 CGGACCCACGGCAATACATCGTCTCTGTTCAAGGAGGGCAGAGAAACACATAAAGAGCTCAGTGAACATCCAGATGGCCCTCCATCCCTCAAC

313> A T H G Q Y I V S V Q P R R A E K H I K S S V N I Q M A P P S L N

1601 GTGACCAAGGATGGAGACAGCTACAGCCTGCGTGGGAAACAATGAAAATGCGATACGAACACATAGACCACACATTTGAGATCCAGTACAGGAAAGACA

347> V T K D T G D S Y S L R W E T M K M R Y E H I D H T F E I Q Y R K D

BbrPI (1704)
1701 CGGCCACGTGGAAGGACAGCAAGACCGAGACCCTCCAGAACGCCACAGCATGGCCCTGCCAGCCTCCAGCCCTCCACCAGGTACTGGCCAGGGTGAG

380> T A T W K D S K T E T L Q N A H S M A L P A L E P S T R Y W A R V R

BssHII (1852)
1801 GGTCAAGACCTCCCGCACCGGCTACAACGGGATCTGGAGTGTGAGTGGAGTGGAGCGGCTCCTGGGACACCCAGTCCGGTGTGCCTATGTGGGTGCTGGCC

413> V R T S R T G Y N G I W S E W S E A R S W D T E S V L P M W V L A

FspI (1970)
1901 CTCATCGTGTCTTCTCACCATCGTGTGCTCCTGGCCCTCCGCTTCTGTGGCATCTACGGGTACAGGCTGCGCAGAAAAGTGGGAGGAGAAGATCCCCA

447> L I V I F L T I A V L L A L R F C G I Y G Y R L R R K W E E K I P

2001 ACCCCAGCAAGAGCCACCTGTTCCAGAACGGGAGCGCAGAGCTTTGGCCCCAGGCGAGCATGTCCGGCTTCACTAGCGGGAGTCCCCACACCAGGGGCC

480> N P S K S H L F Q N G S A E L W P P G S M S A F T S G S P P H Q G P

2101 GTGGGGACGCCGCTCCCTGAGCTGGAGGGGGTGTCCCTGTAGGATTCGGGGACAGCGAGGTGTACCTCTACCATAGAGGACCCCAAGCATGTCTGT

513> W G S R F P E L E G V F P V G F G D S E V S P L T I E D P K H V C

BglII (2238)
2201 GATCCACCATCTGGGCTGACACGACTCCAGCTGCCTCAGATCTACCCACAGAGCAGCCCCCAGCCCCAGCCAGGCCCCGCTGCCGCTCCACACAC

547> D P P S G P D T T P A A S D L P T E Q P P S P Q P G P P A A S H T

Bsp120I (2332) **BsrBI (2358)**
2301 CTGAGAAACAGGCTTCCAGCTTTGACTTCAATGGGCCCTACCTGGGGCCGCCACAGCCGCTCCCTACCTGACATCCTGGGCCAGCCGAGCCCCACA

580> P E K Q A S S F D F N G P Y L G P P H S R S L P D I L G Q P E P P Q

SmaI (2431)
2401 GGAGGGTGGGAGCCAGAAGTCCCCACCTCCAGGGTCCCTGGAGTACCTGTGTCTGCTGCTGGGGGGCAGGTGCAACTGGTCCCTCTGGCCCAGGCGATG

613> E G G S Q K S P P G S L E Y L C L P A G G Q V Q L V P L A Q A M

2501 GGACCGGACAGGCGTGAAGTGGAGAGAAGGCCGAGCCAGGGGCTGACGGAGTCCCTCCCTGGAGTCCGGGGAGGCCCTGCCCTCCTGCTCTTG

647> G P G Q A V E V E R R P S Q G A A G S P S L E S G G G P A P P A L

2601 GGCAAGGGTGGGAGGACAGGACAAAAGGACAGCCCTGTGGCTATACCCATGAGCTCTGGGACACTGAGGACCTGGAGTGGCCTCTGTTATGTCTC

680> G P R V G G Q D Q K D S P V A I P M S S G D T E D P G V A S G Y V S

2701 CTCTGCAGACCTGGTATTCACCCAAACTCAGGGGCTCGTGTCTCCCTAGTTCCTCTCTGGGCTCCCTCAGACCAGACCCCAAGCTTATGTCTC

713> S A D L V F T P N S G A S S V S L V P S L G L P S D Q T P S L C P

5601 ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACACAGTTAAGGGATTTTGGTCATGG

EagI (5724)

PacI (5704) SwaI (5713) **NotI (5723)**

5701 CTAGTTAATTAACATTTAAATC **AGCGGCCG**CAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCT

5801 CTCCATCAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA