



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

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGCTCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGTCTTTGTTTCGTTT

BspHI (560)
AgeI (552)
501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTCATGAACCGAAGCATTCCCGTGGAGGTTGATGAATCAGA
601 ACCATTCCCGAGTCAATTGCTGAAACCGATCCCAAGAACTCTCCAGAAGAGGAATTGGAACCACTGCCCAATACAAGAACATGGCACCCAGCAGC
13> P F P S Q L L K P I P E Y S P E E E L E P P A P N T R N M A P S S
BstEII (759)
701 TTGTCTGTCTCCAGTGCCTCCCTGAAACTGGCAAACCACAGCCTGTGTCAACAACAGGTACCTGCGAGCTAAAGTCTGGAGGAAGTGAAG
47> L S V L Q C P P L K L A N H Q P V S Q Q V T C L R A K V L E E G E
801 CCAGTTTCTTTAGAAGGCACCTGAACTGGCAAAGATATTTCTCATGTTCTCTGGAGCCAGCGAGCTGAGTCTGAGCTCGGAGCCCTCCCTCCAGA
80> A S F F R R H P E L G K D I S S C S S G A S E P E S E L G A L P P E
901 GCATCGGTTACACTTACGAAAAACGAATAGATGGCTGGGATCTCAGCTTTACAGCTTCTCCTGACACTGGCCATGAATCAGACAAATCAGACCCA
113> H R F T L T E K R N R W L G S Q L S A A S P D T G H E S D K S D P

Bsp120I (1072)
1001 AGTTTACCTAATGCTTTGGCAGACTCCTCAGTGGTGGCAAGAGATGATGCCCGGGCCCGGCCCGGCTGGGCCACAGGCACAGGGCAGCCCCAG
147> S L P N A L A D S F S G G Q E M M P R P R P R P G P H R H R A A P

SdaI (1197)
1101 ATGTGCCACGATAGACACTGGCTATGATTTCCAGCCCCAAGATGTCTGGGCATCAGGCAGTTGGAGAGGCCATTGCCCTCACCTCCTCGTGTACCT
180> D V P T I D T G Y D S Q P Q D V L G I R Q L E R P L P L T S S C Y L
1201 GCAGGACCTCCCTGGGCCTGTAGGTCACAGGAATTGCCACCTCAGTTTGAAGTGTAGAGGTATCCAATGAACGCCAGCTGCTGCCGCCCATCCTTCC
213> Q D L P G P L R S R E L P P Q F E L E R Y P M N A Q L L P P H P S

Scal (1322) **Bsp120I (1339)** **DraIII (1351)**
1301 CCACAGGCCCCATGGAAGTGTGACTACTGCCCCGAGGGCCCTACCACCACAGGTGCCACACGGCCATGGCTACCTCCAGCAGCAGCCTACCAGC
247> P Q A P W N C Q Y Y C P G G P Y H H Q V P H G H G Y P P A A A Y Q

Scal (1401)
1401 AAGTACTCCAGCCTGCTCTGCTGCGCAGTGCCTTCTGCGGCAAGGGCAAGAGGCCACGCCCTGTGAGAAGTGCATCCTGAATGACTCCAGCCCCA
280> Q V L Q P A L P G Q V L P G A R A R G P R P V Q K V I L N D S S P Q

Bsu36I (1594)
1501 AGACCAAGAAGAGAGACCTGCACAGAGAGACTTCTTTCCCGAGGCTCCCGAGGGACCAGCTCTACCGCCACCATCTAATGGAGTGGAAAGCCCTGAG
313> D Q E E R P A Q R D F S F P R L P R D Q L Y R P P S N G V E A P E
1601 GAGTCCTTGGACCTTCTGCAGAGCTGAGACCACATGGTCCCAAGGCTCCATCCCTAGCTGCCGTGCTAGACCCCTAGCAACCCCTTAGCCCGAGGAA
347> E S L D L P A E L R P H G P Q A P S L A A V P R P P S N P L A R G

BstXI (1766)
1701 CTCTAAGAACCAGCAATTTGCCAGAAGAATTACGAAAGTCTTTATCACTTATTCTATGGACACAGCCATGGAGGTGGTGAATTTGTGAACCTTTCTGTT
380> T L R T S N L P E E L R K V F I T Y S M D T A M E V V K F V N F L L

XmnI (1803) **EcoRV (1855)** **Eco47III (1874)** **BsaBI**
1801 GGTGAACGGCTTCCAAACTGCGATTGACATATTTGAGGATAGAATCCGGGGTATTGATATCATAAATGGATGGAGCGCTATCTTCGAGATAAGACAGTG
413> V N G F Q T A I D I F E D R I R G I D I I K W M E R Y L R D K T V
1901 ATGATAATCGTAGCAATCAGCCCCAAATACAAACAGGATGTGGAAGGCGCTGAGTCGCAGCTGGACGAGGACGAGCATGGCTTACATACTAAGTACATTC
447> M I I V A I S P K Y K Q D V E G A E S Q L D E D E H G L H T K Y I

SapI (2061)
2001 ATCGGATGATGCAGATTGAGTTCATAAGTCAGGAAGCATGAAGTTCAGATTCATCCCTGTGCTTCCCAAATGCCAAGAAGGAGCATGTGCCGACCTG
480> H R M M Q I E F I S Q G S M N F R F I P V L F P N A K K E H V P T W
2101 GCTTCAGAACACTCATGTTTACAGCTGGCCCAAGAATAAGAAAAACATCCTGTGCGGCTGCTCAGGGAGGAAGATGTGGCTCCTCCCGAGGCCCT
513> L Q N T H V Y S W P K N K N I L L R L L R E E E Y V A P P R G P

Acc65I (2217) **NheI (2242)**
2201 CTGCCACCTTTCAGGTGGTACCCTTGTGACGATGGCCACTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAA
547> L P T L Q V V P L •

HpaI (2380)
2301 TGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCAT

EcoRI (2476)
2401 TCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAA
2501 AACTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGC

SapI (2658)
2601 AGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGTCTTTCATTTCTTTATGTTTTAAATGACTGACCTCCACA

2701 **SspI (2715)** **SwaI (2729)**
TTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCA

2801 TAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCAGCTTCTAGCTTTAGTTCTGGTGTGA
141 • N R T Y

2901 CTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTG
136 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 I L E R

3001 **BstXI (3019)**
CACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGC
102 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 Q G N S

3101 **StuI (3154)**
TCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCT
69 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 T K T R

3201 **XmnI (3296)**
GATGGCCGCCGACATGGTGGTGTGCTTCATAGAGCATGGTGTCTTCTAGTGGCAGCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAG
36 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 S I N F

3301 **BbsI (3300)** **AseI (3362)**
GTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTT
2 T K M

3401 ATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTTG

3501 **SpeI (3517)**
GAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATT

3601 **SnaBI (3645)**
GATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAA

3701 **NdeI (3750)**
TGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGCCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACT

3801 CCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCCAGCCAGG

3901 **SdaI (3928)** **PaeI (3936)** **BspLU11I (3946)**
CGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGC

4001 TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGC

4101 GTTTCCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCT

4201 **ApaLI (4260)**
CATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTAT

4301 CCGGTAACATATCGTCTTGTAGTCCAAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGG

4401 TGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGA

4501 GTTGGTAGCTCTTGATCCGGCAAACAACACCCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAG

4601 **EagI (4696)** **NotI (4695)**
ATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGC

4701 CGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACA

4801 AACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA