



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
 101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC **Bsu36I (291)**
 301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

AgeI (552) **BspLU11I (560)** **SacII (588)**
 501 TCTGTTTGTCCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTGCGTGGGGGCTCGGCGGTGGCCGCGGCGCTG **1** M C V G A R R L G R G P C
 601 TCGGGCTCTGCTCCTCTGGGCCTGGGGCTGAGCACCGTGCAGGGGCTCCACTGTGTCGGGGACACCTACCCAGCAACGACCGGTGCTGCCACGAGTGC **AgeI (680)**
13▶ A A L L L L G L G L S T V T G L H C V G D T Y P S N D R C C H E C

BsrBI (732) **DraIII (744)** **Tth111I (781)**
 701 AGGCCAGGCAACGGGATGGTGGAGCCGCTGCAGCCGCTCCAGAACACGGTGTGCCGTCGCGGGCCGGGCTTCTACAACGACGTGGTCAGCTCCAAGC **47**▶ R P G N G M V S R C S R S Q N T V C R P C G P G F Y N D V V S S K

BstAPI (803) **DraIII (813)** **BsrBI (841)** **PvuII (850)** **Tth111I (871)**
 801 CGTGCAAGCCCTGCACGTGGTGTAACTCAGAAGTGGGAGTGAAGCGGAAGCAGCTGTGCACGGCCACACAGGACACAGTCTGCCGCTGCCGGGCGGGCAC **80**▶ P C K P C T W C N L R S G S E R K Q L C T A T Q D T V C R C R A G T

BbrPI (813) **ApaLI (855)** **StuI (977)**
 901 CCAGCCCTGGACAGCTACAAGCCTGGAGTTGACTGTGCCCCCTGCCCTCCAGGGCACTTCTCCCGAGCGACAACAGCCGCTGCAAGCCTGGACCAAC **113**▶ Q P L D S Y K P G V D C A P C P P G H F S P G D N Q A C K P W T N

BstAPI (1017) **NgoMIV (1029)** **SmaI (1067)**
 1001 TGCACCTTGGCTGGGAAGCACACCTGCAGCCGCGCCAGCAATAGCTCGGACGCAATCTGTGAGGACAGGGACCCCGAGCCACGCAGCCCGAGGAAACCC **147**▶ C T L A G K H T L Q P A S N S S D A I C E D R D P P A T Q P Q E T

Bsp120I (1101) **SmaI (1161)** **XmaI (1189)**
 1101 AGGGCCCCCGGCCAGGCCATCACTGTCCAGCCCACTGAAGCCTGGCCAGAACCTCACAGGACCTCCACCCGGCCCGTGGAGGTCCCGGGGGCCG **180**▶ Q G P P A R P I T V Q P T E A W P R T S Q G P S T R P V E V P G G R

Bsp120I (1245) **BstXI (1256)** **BspEI (1280)**
 1201 TGGGTTGCCGCATCCTGGCCTGGCCCTGGTGTGGGGCTGCTGGGCCCTGCTGGCCCTGTACCTGCTCCGGAGGACAGAGGCTG **213**▶ A V A A I L G L G L V L G L L G P L A I L L A L Y L L R R D Q R L

BspEI (1337) **BglIII (1388)**
 1301 CCCCCGATGCCACAAGCCCCCTGGGGAGGAGTTTCCGGACCCCATCCAAGAGGAGCAGGCCGACGCCACTCCACCCTGGCCAAAGATCTGACGCT **247**▶ P P D A H K P P G G S F R T P I Q E E Q A D A H S T L A K I •
 1401 AGCTGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTG

HpaI (1535) **MfeI (1546)**
 1501 CTTTATTTGTAACCATTATAAGCTGCAATAAACCAAGTTAAACAACAATTGCATTATTTATGTTTCAGGTTCAAGGGGAGGTGTGGAGGTTTTTTA

EcoRI (1631)
 1601 AAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAG
 1701 GGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCC

SapI (1813) **SspI (1870)** **SwaI (1884)**
 1801 AAGGTTTGAAGTACTCTTCATTCTTTATGTTTTAAATGCACTGACCTCCCACATCCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATT
 1901 GCAATGAAATAAATGTTTTTATTAGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACC
 2001 TTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGTTGCC

SacI (2145) **BstXI (2174)**
 2101 ATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCCCTGATGGATCTGTCCACCTCA **121**▶ N M E I L 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
 2201 TCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGCTTGTCTCAGCAGACCCAAATGGCAATGGCTTACAGCACAGACGTGACCC **87**▶ D S Y P H 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

StuI (2309)
 2301 TGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCACTTGGTCTGATGGCCGCCGACATGGTCTTGTGTCTCATAGAGCATGGT **54**▶ G I Y A 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

BbsI (2455) **XmnI (2451)**
 2401 GATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCTTGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCC **21**▶ I K E T A V E V L E L D Q Q S I N F T K M

2501 **AseI (2517)** **SacI (2574)**
GATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCCAC

2601 **SpeI (2672)**
CGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGT

2701
CAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAA

SnaBI (2800)
2801 TACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTA

NdeI (2905)
2901 CTTGGCATATGATACACTTGATGTACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGG

PacI (3091)
SdaI (3083)
3001 GAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAG

BspLU11I (3101)
3101 AACATGTGAGCAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAA

3201 ATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCT

3301 GCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCG

ApaLI (3415)
3401 TCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCCTGCGCCTTATCCGGTAACACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTAT

3501 CGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG

3601 AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGT

3701 GGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAA

EagI (3851)
PacI (3831) **SwaI (3840)** **NotI (3850)**
3801 ACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTT

3901 TTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGAA

4001 CATTTCTCTATCGAA