



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCTCTAGGTAAGTTAAAGTCAAGTGCAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTGTTTCGTTT

NcoI (560) **BstEII (555)** **XcmI (571)**
AgeI (552) **BstXI (571)** **SandI (598)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGCACGGCCACATCCCTGGTGGCTGTGCGTTCTGGG
601 GACCTGGTGGGGCTCTCAGTACTCCAGCCCCAAGAGCTGCCAGAGAGGCACTACTGGGCTCAGGAAAGCTGTGCTGCCAGATGTGTGAGCCAGGA
13▶ T L V G L S A T P A P K S C P E R H Y W A Q G K L C C Q M C E P G
701 ACATTCCTCGTGAAGACTGTGACCAGCATAGAAAGGCTGCTCAGTGTGATCCTTGATACCGGGGCTCCTTCTCTCTGACCACACCCGCCCC
47▶ T F L V K D C D Q H R K A A Q C D P C I P G V S F S P D H H T R P

801 ACTGTGAGAGCTGTCCGCACTGTAAGTCTTCTCGTTCGCAACTGCACCATCACTGCCAATGCTGAGTGTGCTGTGCAATGGCTGGCAGTGCAG
80▶ H C E S C R H C N S G L L V R N C T I T A N A E C A C R N G W Q C R

DraIII (912) **BsrBI (947)**
ApaLI (909)
901 GGACAAGGAGTGCACCGAGTGTGATCCTTCCAAACCTTCGCTGACCGCTCGGTGCTCTCAGGCCCTGAGCCACACCCCTCAGCCACCCACTTACCT
113▶ D K E C T E C D P L P N P S L T A R S S Q A L S P H P Q P T H L P

1001 TATGTCAGTGAGATGCTGGAGGCCAGGACAGCTGGGCACATGCAGACTCTGGCTGACTTCAGGCAGCTGCCTGCCCGACTCTCTACCCACTGGCCAC
147▶ Y V S E M L E A R T A G H M Q T L A D F R Q L P A R T L S T H W P

1101 CCCAAAGATCCCTGTGCAGCTCCGATTTTATTCGATCCTTGTGATCTTCTGGAATGTTCTTGTTCCTGTTTTCACCTGGCCGGCCCTGTTCCCTCATCA
180▶ P Q R S L C S S D F I R I L V I F S G M F L V F T L A G A L F L H Q

1201 ACGAAGGAAATATAGATCAAACAAAGGAGAAAGTCTGTGGAGCCTGCAGAGCCTTGTGTTACAGCTGCCCCAGGGAGGAGGGGAGCACCATCCCC
213▶ R R K Y R S N K G E S P V E P A E P C R Y S C P R E E E G S T I P

MscI (1093) **Bsp120I (1181)**
1301 ATCCAGGAGGATTACCGAAAACCGAGCCTGCCTGCTCCCCCTGAGCCAGCACCTGCGGGAGCTGCACTACAGCTAGCTGGCCAGACATGATAAGATACA
247▶ I Q E D Y R K P E P A C S P •

1401 TTGATGAGTTTGGACAAACCACAAGTGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTG

HpaI (1510) **MfeI (1521)**
1501 CAATAAACAAGTTAAACAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGT

EcoRI (1606)
1601 GGTATGGAATTCTAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGG

1701 GGCTGTTGCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGTTTGAAGTACTGCTTTCATTTCC

SspI (1845) **SwaI (1859)**
1801 TTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATT

1901 AGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACGCAAGAA

2001 AGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAG
141▶ 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

SacI (2120) **BstXI (2149)**
2101 TCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCA
112▶ 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 D S Y P H R V A V

2201 CAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGGCCCTCAATGTGGAC
79▶ 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 G I Y A E I H V

2301 AGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACC
46▶ 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 I K E T A V E V

BbsI (2430) **XmnI (2426)** **AseI (2492)**
2401 AGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTG
12▶ L E L D Q Q S I N F T K M

2501 TCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACGCCCATTTGCG
SacI (2549)

2601 TCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAATCC
SpeI (2647)

2701 CCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGA
SnaBI (2775)

2801 AAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTA
NdeI (2880)

2901 CTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAA

3001 TGGGCGGGGTCGTTGGGCGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAA
PacI (3066)
PstI (3059)
SdaI (3058) BspLU11I (3076)

3101 AGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCG
3201 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCC

3301 TTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTGCTCCAAGCTGGGCTGTGTGCACGAAC
ApaLI (3390)

3401 CCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTGAAGTCCAAACCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA

3501 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCT

3601 CTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGA

3701 TTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACACGTTAAGGGATTTTGGTCAT

3801 GGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACG
PacI (3806) SmaI (3815) EagI (3826)
NotI (3825)

3901 CTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA