



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245)
PvuII (239)
Bsu36I (291)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCAGTACCATTGGCATCATCGACCTCCCTCCAGCTCCTGGCTCTCG
1 M A S S T S L P A P G S R

BstAPI (639)
601 GCCTAAGAAGCCTCTAGGCAAGATGGCTGACTGGTTCAGGCAGACCCTGCTGAAGAAGCCAAAGAAGAGGCCAACTCCCCAGAAAGCACCTCCAGCGAT
13 P K K P L G K M A D W F R Q T L L K K P K K R P N S P E S T S S D
701 GCTTCACAGCCTACTCAGAGGACAGCCACTACCCCCAAGCCTCAGCTCAGTACAGTCTCCAGCCTGCCACCCACACATGCGAGTGACAGTGGCAGTA
47 A S Q P T S Q D S P L P P S L S S V T S P S L P P T H A S D S G S

BbsI (844)
Tth111I (865)
801 GTCGCTGGAGCAAAGACTATGACGTCTGCGTGTGCCACAGTGGGAAGACCTGGTGGCCGCCAGGACCTGGTCTCTACTTGGAAAGGCAGCACTGCCAG
80 S R W S K D Y D V C V C H S E E D L V A A Q D L V S Y L E G S T A S
901 CCTGCGCTGCTTCTGCAACTCCGGGATGCAACCCAGCGGCGCTATAGTGTCCGAGCTGTGCCAGGCACTGAGCAGTAGTCACTGCCGGGTGCTGCTC
113 L R C F L Q L R D A T P G G A I V S E L C Q A L S S S H C R V L L

PstI (1045)
1001 ATCAGCCGGGCTTCTTCAGGACCCCTGGTGAAGTACCAGATGCTGCAGGCCCTGACCAGGCTCCAGGGGCCAGGGCTGCACCATCCCCCTGCTGT
147 I T P G F L Q D P W C K Y Q M L Q A L T E A P G A E G C T I P L L

Bsp120I (1161)
1101 CGGCTCAGCAGAGCTGTTACCCACCTGAGCTCCGATTTCATGTACTACGTGCGATGGCAGGGCCCTGATGGTGGCTTTCGTAAGTCAAAGAAGCTGT
180 S G L S R A A Y P P E L R F M Y Y V D G R G P D G G F R Q V K E A V
1201 CATGCGTTGTAAGTACTACAGGAGGAGAAGGGGAACGGGATTCAGTACAGTATCTGATCTACTTTGACTTTTAGGAGACAGCCCTGTAGCCTAGTAG
213 M R C K L L Q E G E G E R D S A T V S D L L •

MseI (1324)
NheI (1318)
1301 TTCAAAGCGCAGCTTCTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAAGTGAATGCAGTAAAAAATGCTTTATTT

HpaI (1456)
MfeI (1467)
1401 GTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACCAAGTTAACCAACAACCAATTGCATTTTATGTTTCAGGTTTCAGGG

EcoRI (1552)
1501 GGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCT
1601 CTACTGAAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACCTTCTTTCATGGAGTT

SapI (1734)
SspI (1791)
1701 TAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGAAAAATTCAG

SwaI (1805)
1801 AAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTG
1901 GACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAAT
141 • N R T Y K L P I L E E I

BstXI (2095)
2001 GGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACC
128 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 C M G C P S V V
2101 CTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGG
94 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 V A S G I A I A

StuI (2230)
2201 CTTGACGACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTT
61 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 I A A G V H H K

BbsI (2376)
XmnI (2372)
2301 GTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCCTATAG
28 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 T K M

AseI (2438)
2401 TGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCT

2501 CTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTC **SpeI (2593)**

2601 AAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCAT

2701 CATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCA **SnaBI (2721)**

2801 TTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGAGTTTACCATAACTCCACCCATTGACGTCAATGGAAAG **NdeI (2826)**

2901 TCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGT

3001 AACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTTCCATAGGCTCCGCC **PacI (3012)**
PstI (3005)
SdaI (3004) **BspLU11I (3022)**

3101 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGT

3201 GCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGTATCTC

3301 AGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCA **ApaLI (3336)**

3401 ACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG

3501 GCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA

3601 CAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGT

3701 CTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC **EagI (3772)**
PacI (3752) **SwaI (3761)** **NotI (3771)** **AGCGGCCGAATAAAATATCTTTATTTTCA**

3801 TTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCA

3901 GTGCAAGTGCAGGTGCCAGAACATTTCTATCGAA