



PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTGCCTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTCGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

KasI (535)
PstI (575)

501 TCTGTTCTGCGCGCTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTAGAGGGCCAACATGTGGCTGCAGAATTTACTTTTCTGGGCA

1► M W L Q N L L F L G

601 TTGTGGTCTACAGCCTCTCAGCACCCACCGCTCACCCACTCAGTGCACCCGGCCTTGAAGCATGTAGAGGCCATCAAAGAAGCCCTGAACCTCCTGGA

701 TGACATGCCTGTCACGTTGAATGAAGAGGTAGAAGTCGTCTTAACGAGTTCTCCTTCAAGAAGTAACATGTGTGCAGACCCGCTGAAGATATTTCGAG

801 CAGGGTCTACGGGCAATTTACCAAACCTAAGGGCGCCTTGAACATGACAGCCAGCTACTACCAGACATACTGCCCCCAACTCCGGAACGGACTGTG

901 AAACACAAGTTACCACCTATGCGGATTTTATAGACAGCCTTAAACCTTTCTGACTGATATCCCTTTTGAATGCAAAAAACCAGGCCAAAAATGAGGAAG

101 CCCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTGTGAT

BsrBI (628)
BspLU11I (567)

1101 GCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACCAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGG

KasI (833)
XmnI (787)

1201 TTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTT

1301 TTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGA

SapI (1420)
BspEI (883)

1401 TTTTCCAAGTTTGAAGTCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGAAAATATTCAGAAAATATTTAAATA

NheI (1004)
EcoRV (956)

1501 CATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAA

1601 AGGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTCTCGGTGACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCA

1701 GCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCGCACATGCCACAGGGGCTGACCCCTGATGGATCTGTC

1801 CACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCCTGCTCAGCAGACCCAATGGCAATGGCTTACGACAGACA

1901 GTGACCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGTCCTCATAGA

2001 GCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGCATGATTATA

2101 CTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGAC

2201 CTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACCTCCCA

2301 TTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGA

2401 TGACTAATACGTAGATGTAAGTCCCAAGTAGGAAAGTCCATAAGTGCATGTAAGTGGGCATAATGCCAGGCGGGCATTACCGTCAATGACGTCAATAGG

NdeI (2512)
 2501 GGGCGTACTTGGCATATGATACACTTGATGTA CTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTT

PacI (2698)
PstI (2691)
SdaI (2690)
 2601 ACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGGTCTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTT

BspLU11I (2708)
 2701 AATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCAT

 2801 CACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTC

 2901 CGACCTGCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGTGTAGGT

ApaLI (3022)
 3001 CGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTT CAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC

 3101 GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT

 3201 AACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGG

 3301 TAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGG

EagI (3458)
PacI (3438) SwaI (3447) **NotI (3457)**
 3401 AACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGT

 3501 TGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGT
 3601 GCCAGAACATTTCTCTATCGAA