



SacI (2807)

2801 GAGAGCTCAGCCATTCTTGGTCCAATTTGAGCAAAAACAGCACCAGCTTCAACAGACTCAGGTGTTGTCCAAACTGCAACAGCAGCTCCATCATCTGCAA
98 S L E A M R P G I E A F V A G A E V S E P T T W V A V A A G D D A V
2901 CCCAAACTTTTCCAATGTCAGTCCCCTCTGGTGAGGAAGAGTTCTTGAGTCTGTCCACCTCTCAATGTGCCTGTCAGGGTCAACTGTGTGCCTTGT
65 W V K G I D L G V R T L F L E Q L E T V R E I H R D P D V T H R T
3001 TGCAGGGTAGTCTGCAAAAGCAGCAGCCAGTGTCTCACAGCTCTTGGAAACATCATCTCTGGTTGCCAGCCTCACTGTGGGTTTGTACTCAGTCATGGTG
32 A P Y D A F A A A L T R V A R P V D D R T A L R V T P K Y E T M

AseI (3152)

3101 GCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAACTACTGTTTGTAGGCGCCGGTCACAGCTTGATCTGTGA
3201 ACGGCGCAGAACAGAAAACGAAACAAAGACGTAGAGTTGAGCAAGCAGGGTCAGGCAAAGCGTGGAGAGCCGGCTGAGTCTAGGTAGGCTCCAAGGGAGC
3301 GCCGGACAAAAGGCCCGTCTCGACCTGAGCTTTAAACTTACCTAGACGGCGGACGCAGTTCAGGAGGCCACCACAGGCGGGAGGCGGCAGAACGCGACTCA

HindIII (3465)

3401 ACCGGCGTGGATGGCGGCCTCAGGTAGGGCGGCGGCGCTGAAGGAGAGATGCGAGCCCTCGAAGCTTCAGCTGTGTTCTGGCGGCAAACCCGTTGCG

Psp1406I (3508)

3501 AAAAAGAACGTTACGGCGACTACTGCCTTATATACGGTTCTCCCCACCCTCGGGAAAAGGCGGAGCCAGTACACGACATCACTTTCCAGTTTACC

AgeI (3621)

SpeI (3690)

3601 CCGCGCCACCTTCTTAGGCACCGGTTCAATTGCCACCCCTCCCCCAACTTCTCGGGACTGTGGCGATGTGCGCTCTGCCACTGACTAGTGGGCC
3701 CTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCT
3801 GACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCCT
3901 CTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTC
4001 GGTGTAGGTCGTTCCGCTCAAGCTGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCG
4101 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTA
4201 ACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAC
4301 CACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGAC

NotI (4468)

4401 GCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACA
4501 TCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCA
4601 AGTGCAGGTGCCAGAACATTTCTCTATCGAA