



3201 CGGTCTGCGCTGCGGGACGCGGAATTGAATTATGGCCACACACAGTGGCGCGGCGACTTCCAGTTCAACATCAGCCGCTACAGTCAACAGCAACTGATG
968▶ nGlyLeuArgCysGlyThrArgGluLeuAsnTyrGlyProHisGlnTrpArgGlyAspPheGlnPheAsnIleSerArgTyrSerGlnGlnGlnLeuMet

NdeI (3365)

3301 GAAACCAGCCATCGCCATCTGCTGCACGCGGAAGAAGGCACATGGCTGAATATCGACGGTTTCCATATGGGGATTGGTGGCAGCAGCTCTGGAGCCCGT
1002▶ GluThrSerHisArgHisLeuLeuHisAlaGluGluGlyThrTrpLeuAsnIleAspGlyPheHisMetGlyIleGlyGlyAspAspSerTrpSerProS
NheI (3487)

EcoRI (3481)

3401 CAGTATCGCGGAATTACAGCTGAGCGCGGTCGCTACCATTACCAGTTGGTCTGGTGTCAAAAATAATAATCTAGTCGAGAATTCGCTAGCTCGACATG
1035▶ erValSerAlaGluLeuGlnLeuSerAlaGlyArgTyrHisTyrGlnLeuValTrpCysGlnLys•••

3501 ATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTGAAAT

MfeI (3661)

3601 TTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAACAAACAATTGCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTG

DraI (3749)
Swal (3752)

3701 TGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTAGATCCATTAAATGTTAATTAAGTCCATGACCAAATCCCTAACGTGAGTTTTTC
DraI (3710)

3801 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCACAAAAAACACCGG

3901 CTACCAGCGGTGGTTTGTGGCCGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAACTACTGTTCTTCTAG

4001 TGTAGCCGTAGTTAGGCCACCACCTCAAGAACTCTGTAGCACCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA

4101 GTCGTGTCTTACCGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTGGGCTGAACGGGGGTTCTGTGCACACAGCCAGCTTGGAGCGA

4201 ACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGGCCACGCTTCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGG

4301 TCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT

BspLU11I (4490)

4401 GTGATGCTCGTCAGGGGGCGGAGCCTATGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGTGGCCTTTTGTCCACATGTTCTTA

AseI (4528) SfiI (4579) **MscI (4590)**

4501 ATTAATTTTTCAAAGTAGTTGACAATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACTCACTATAGGAGGGCCATCATGGCCAAGTTGAC
1▶MetAlaLysLeuTh

4601 CAGTGTGTCCAGTGTCTCACAGCCAGGATGTGGCTGGAGCTGTTGAGTTCTGGACTGACAGGTTGGGTTCTCCAGAGATTTGTGGAGGATGACTTT
5▶rSerAlaValProValLeuThrAlaArgAspValAlaGlyAlaValGluPheTrpThrAspArgLeuGlyPheSerArgAspPheValGluAspAspPhe

4701 GCAGGTGTGGTCCAGAGATGATGTACCCTGTTTCATCTCAGCAGTCCAGGACCAGTGGTGCCTGACAACACCTGGCTTGGTGTGGTGGAGGACTGG
39▶AlaGlyValValArgAspAspValThrLeuPheIleSerAlaValGlnAspGlnValValProAspAsnThrLeuAlaTrpValTrpValArgGlyLeuA

4801 ATGAGCTGTATGCTGAGTGGAGTGGTGGTCTCCACCACTTCAGGGATGCCAGTGGCCCTGCCATGACAGAGATTGGAGAGCAGCCCTGGGGAGAGA
72▶spGluLeuTyrAlaGluTrpSerGluValValSerThrAsnPheArgAspAlaSerGlyProAlaMetThrGluIleGlyGlyGluProTrpGlyArgGly

DraIII (4940) SfiI (4988)

4901 GTTTCGCCCTGAGAGACCCAGCAGGCAACTGTGTGCACTTTGTGGCAGAGGAGCAGGACTGAGGATAAGAATTGAGTTTCAGAAAAGGGGCGCTGAGTGCC
105▶uPheAlaLeuArgAspProAlaGlyAsnCysValHisPheValAlaGluGluGluAsp•••

5001 CCCTTTTTCAACTTAATTA