

Example

>reference sequence

atgggctgcacgctgagcgccgaggacaaggcggcggtggagcggagtaagatgatcgaccgcaacctccgtgaggacggcgagaaggcggcgcgcgaggtcaagctgctgctgctcggtgctggtgaatctggtaaaagtacaattgtgaag

cagatgaaaattatccatgaagctggttattcagaagaggagtgtaaacaatacaaagcagtggtctacagtaacaccatccagtcaattattgctatcattagggctatggggaggttgaagatagactttggtgactcagcccgggcggatgatgcac

gccaactctttgtgctagctggagctgctgaagaaggctttatgactgcagaacttgctggagttataaagagattgtggaaagatagtggtgtacaagcctgtttcaacagatcccgagagtaccagcttaatgattctgcagcatactatttgaatgactt

ggacagaatagctcaaccaaattacatcccgactcaacaagatgttctcagaactagagtgaaaactacaggaattgttgaaacccattttactttcaaagatcttcattttaaaatgtttgatgtgggaggtcagagatctgagcggaagaagtggattcatt

gcttcgaaggagtgacggcgatcatcttctgtgtagcactgagtgactacgacctggttctagctgaagatgaagaaatgaaccgaatgcatgaaagcatgaaattgtttgacagcatatgtaacaacaagtggtttacagatacatccattatactttttcta

aacaagaaggatctctttgaagaaaaaatcaaaaagagccctctcactatatgctatccagaatatgcaggatcaaacacatatgaagaggcagctgcatatattcaatgtcagtttgaagacctcaataaaagaaaggacacaaaggaaatatacaccca

cttcacatgtgccacagatactaagaatgtgcagtttgtttttgatgctgtaacagatgtcatcataaaaaataatctaaaagattgtggtctcttttaa

> sequencing results (please activate reverse complement option, as it was sequenced from the 3’ end of the gene)

aaCGAAGGcTCAGTCGangacTGGGCCTTTCGCCCGGGCTAATTAGGGGGTGTCGCCCTTAGGTACGAACTCGATTGACGCGTCTCAGGGGCAAAAAACCCCTCAAGACCCGTTTAGAGGCCCCAAGGGGTTATGCTAGGGGGTTAAAAGAGACCACAATCTTTTAGATTATTTTTTATGATGACATCTGTTACAGCATCAAAAACAAACTGCACATTCTTAGTATCTGTGGCACATGTGAAGTGGGTGTATATTTCCTTTGTGTCCTTTCTTTTATTGAGGTCTTCCGCCTGACATTGAATATATGCAGCTGCCTCTTCATATGTGTTTGATCCTGCATATTCTGGATAGCATATAGTGAGAGGGCTCTTTTTGATTTTTTCTTCAAAGAGATCCTTCTTGTTTAGAAAAAGTATAATGGATGTATCTGTAAACCACTTGTTGTTACATATGCTGTCAAACAATTTCATGCTTTCATGCATTCGGTTCATTTCTTCATCTTCAGCTAGAACCAGGTCGTAGTCACTCAGTGCTACACAGAAGATGATCGCCGTCACTCCTTCGAAGCAATGAATCCACTTCTTCCGCTCAGATCTCTGACCTCCCACATCAAACATTTTAAAATGAAGATCTTTGAAAGTAAAATGGGTTTCAACAATTCCTGTAGTTTTCACTCTAGTTCTGAGAACATCTTGTTGAGTCgnnntGTAATTTGGTTGAGCTATTCTGTCCAaGTCATTC

click "check" button.

Alternatively, Use File/Open to open a fasta file with sequencing resutls, or several files at once.

Empty files will crash the program.

Use Report Mut From/ To fields to limit the range in which the program reports identified mutations. In this example 300-355 would be appropriate choice.