

Welcome to ModFinder, a simple tool for Modifications combiatorial analysis.

Setup config file:

The config.ini file in the config directory has a path variable in the Defaults section. Change that to a useful path.

INPUT:

The general workflow requires the input of a protein sequence in fasta format, either manually or from a fasta file, and the input of a molecular weight, again either manually or from a file. The mass file can be an excel or text file holding mass information in the first column.

ModFinder was designed to read output toplevel tables exported from ThermoFisher Scientific ProteinDeconvolution and BioPharma Finder. There can be problems with files that contain IFINITE VALLUES. Reading those excel tables breaks the import, so be sure to remove those columns if necessary.