CJunction User Guide

2021/06/24



In the second step above, the input file needs to satisfy the following format, with the contents of each line separated by commas: name of the MS raw file, scan number of the MS2 spectrum, peptide identified by de novo sequencing, monoisotopic mass of the precursor ion, and charge, respectively.

39 20,0.02&0.05.csv × "20150708_QE3_UPLC8_DBJ_QC_HELA 39frac Trypsin 1.raw",10003,VVVLALVPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10003,VVVLAVLPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10003,VVVLAVLPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10003,VVVLGLLPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10003,VVVLGLLPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10003,VVVLLAVPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10003,VVVLLGLPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10003,VVVLVALPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10003,VVVLVALPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10003,VVVLVLAPR,483.33044,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10026,FPLFGVAR,453.76578,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10026,FPLFGVAR,453.76578,2 20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10026,FPLFRAR,453.76578,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10026,FPLFVGAR,453.76578,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10026,FPLFVGAR,453.76578,2 "20150708_QE3_UPLC8_DBJ_QC_HELA_39frac_Trypsin_1.raw",10026,FPLGVFAR,453.76578,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10026,LMLFGVAR,453.76578,2 "20150708 QE3 UPLC8 DBJ QC HELA 39frac Trypsin 1.raw",10026,LMLFGVAR,453.76578,2 "20150708_QE3_UPLC8_DBJ_QC_HELA_39frac_Trypsin_1.raw",10026,MLLFGVAR,453.76578,2 "20150708 QE3_UPLC8 DBJ_QC_HELA 39frac Trypsin 1.raw",10026,MLLFGVAR,453.76578,2

- 1. When the program is finished running, two files are available: Result.txt and JunctionPeptide.fasta.
- 2. In the Result.txt, all of the possible junction peptides corresponding to the MS2 spectrum are shown after the colon in each row.
- 3. JunctionPeptide.fasta provides all possible non-redundant junction peptides enumerated from the MS dataset.

