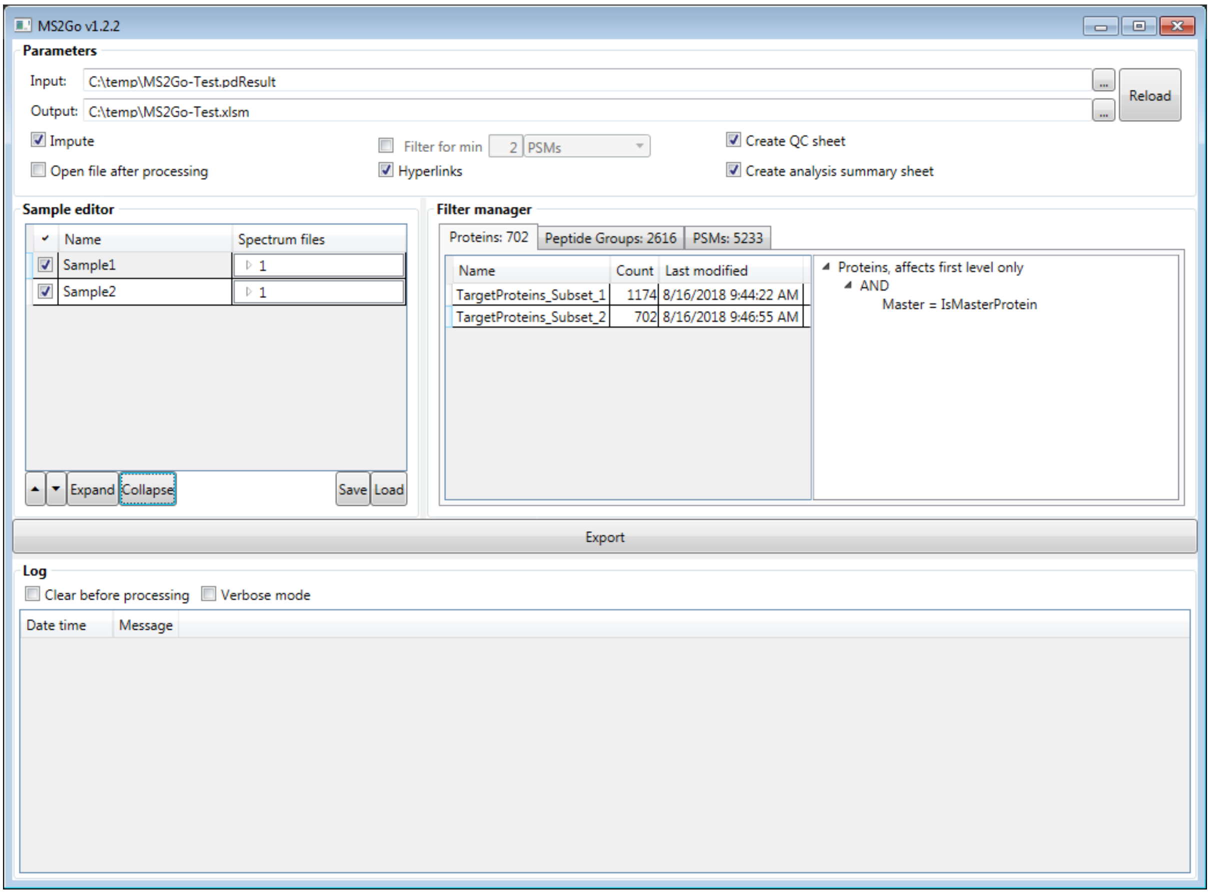
MS2Go User manual

Overview

The basic user interface of MS2Go is divided into various segments looks like this:



Input: C:\temp\MS2Go-Test.pdResult

Output: C:\temp\MS2Go-Test.xlsm

☑ Impute
☐ Open file after processing
☐ Filter for min 2 PSMs
☑ Hyperlinks
☑ Create QC sheet
☑ Create analysis summary sheet

✓	Name	Spectrum files
☑	Sample1	1
☑	Sample2	1

Name	Count	Last modified
TargetProteins_Subset_1	1174	8/16/2018 9:44:22 AM
TargetProteins_Subset_2	702	8/16/2018 9:46:55 AM

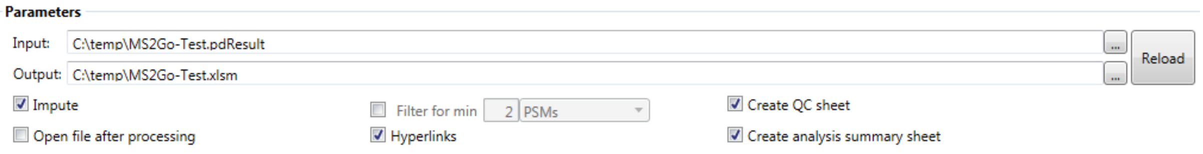
Proteins, affects first level only
  AND
    Master = IsMasterProtein

☐ Clear before processing
☐ Verbose mode

Date time	Message

Parameters section

This section administrates the basic parameters required for exporting.



Parameters

Input: C:\temp\MS2Go-Test.pdResult

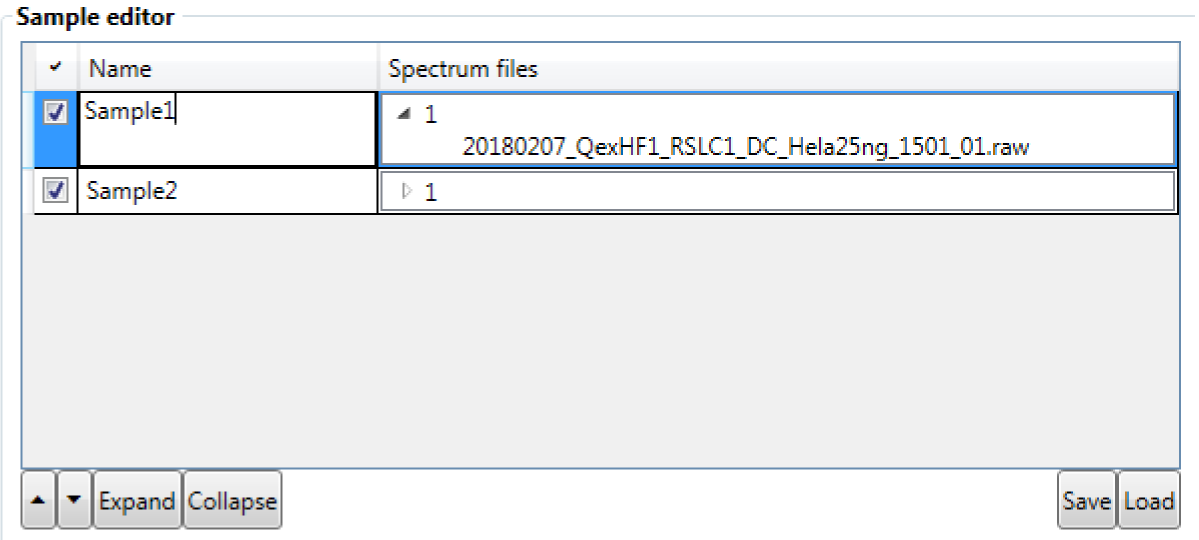
Output: C:\temp\MS2Go-Test.xlsm

☑ Impute
☐ Open file after processing
☐ Filter for min 2 PSMs
☑ Hyperlinks
☑ Create QC sheet
☑ Create analysis summary sheet

The following parameters can be set:

Name	Description
Input	The path to the *.pdResult file. Can be also set via the corresponding '...'-button, in this case the output file path is set with the same file name, but different extension. **IMPORTANT:** A *.pdResultView file with the same name has to be in the same folder.
Output	The path to the *.xlsm file. Can be also set via the corresponding '...'-button
Impute	Turns area value imputation on/off. Requires *NormalisationPlus* in the PD workflow, otherwise this option has no effect.
Open file after processing	Opens the exported file in Excel after processing is finished.
Filter for min ...	Filters the proteins based on a minimum number of PSMs/peptides/unique peptides.
Hyperlinks	Turns hyperlinking between sheets on/off. (Huge result files tend to exceed Excel's maximum number of hyperlinks per sheet.)
Create QC sheet	Determines whether sheet *Quality control* is created, or not.
Create Analysis summary sheet	Determines whether sheet *Analysis summary* is created, or not.

Sample editor



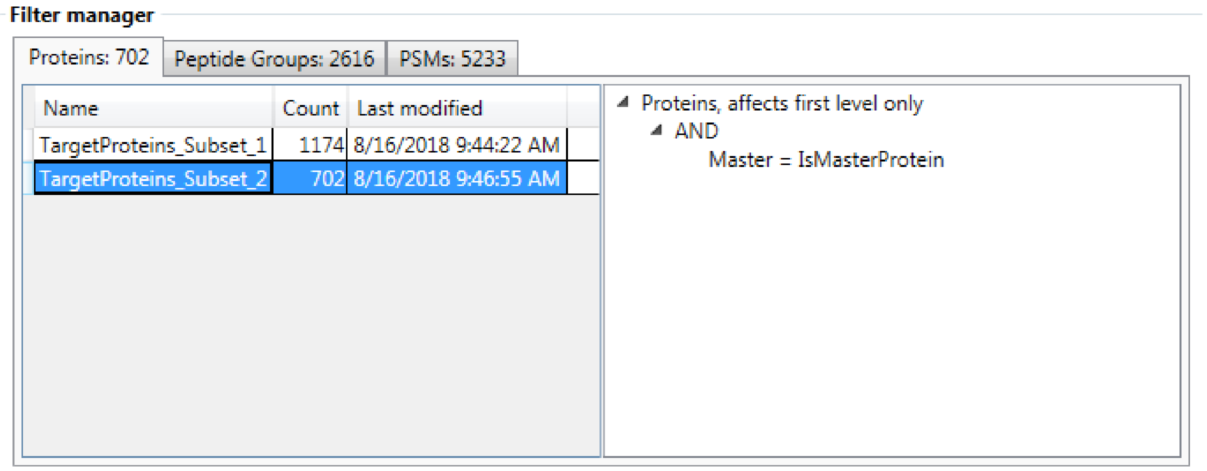
✓	Name	Spectrum files
☑	Sample1	◢ 1 20180207_QexHF1_RSLC1_DC_Hela25ng_1501_01.raw
☑	Sample2	▷ 1

Here the samples can be manipulated in multiple ways:

- Rename
- Move position
- Exclude

The changes made can be saved/load by file. To reset the sample settings, simply press the 'Reload' button in 'Parameters' section.

Filter manager



Name	Count	Last modified
TargetProteins_Subset_1	1174	8/16/2018 9:44:22 AM
TargetProteins_Subset_2	702	8/16/2018 9:46:55 AM

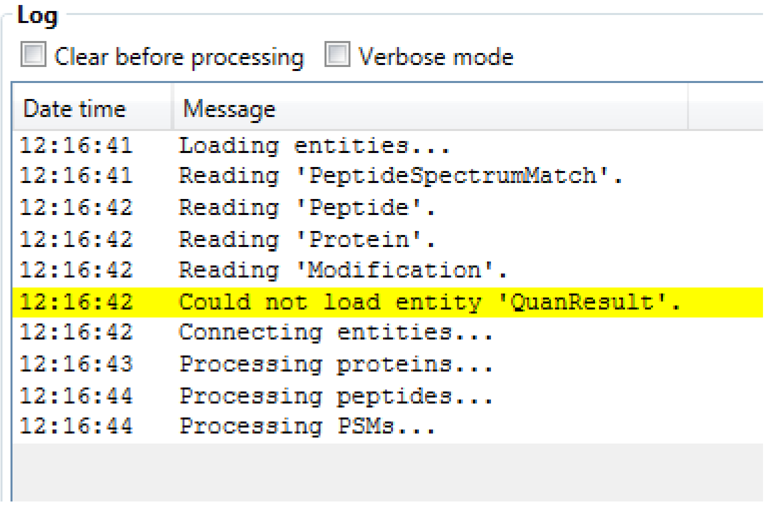
◢ Proteins, affects first level only
  ◢ AND
    Master = IsMasterProtein

In this section the filter applied to the result can be chosen (per default the latest filters are selected).
The left segments groups the filters by item type, including the item count.
The right segment displays the filter properties in a tree view.

Log panel

The Log panel tracks all messages which occur during processing (for a more detailed logging, enable the option **Verbose mode**).

Note: The messages are also logged to file (see Folder *logs* in the MS2Go application directory).



```
12:16:41   Loading entities...
12:16:41   Reading 'PeptideSpectrumMatch'.
12:16:42   Reading 'Peptide'.
12:16:42   Reading 'Protein'.
12:16:42   Reading 'Modification'.
12:16:42   Could not load entity 'QuanResult'.
12:16:42   Connecting entities...
12:16:43   Processing proteins...
12:16:44   Processing peptides...
12:16:44   Processing PSMs...
```