PREOMICS

Quick Start Guide: ProteoVision™

Things to know before you start

Accepted input file formats

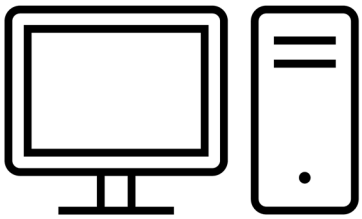
ProteoVision accepts the following file formats:

- *.tsv files (Spectronaut®, DIA-NN and Sage)
- *.parquet (ProteoScape®)
- *.txt (evidence and protein.txt; MaxQuant)

Spectronaut® report scheme

A custom Spectronaut report scheme **ReportProteoVision.rs** is available in the extracted .exe directory.

- Import scheme into Spectronaut®: go to “Report” → ”Import scheme“
- Export .tsv



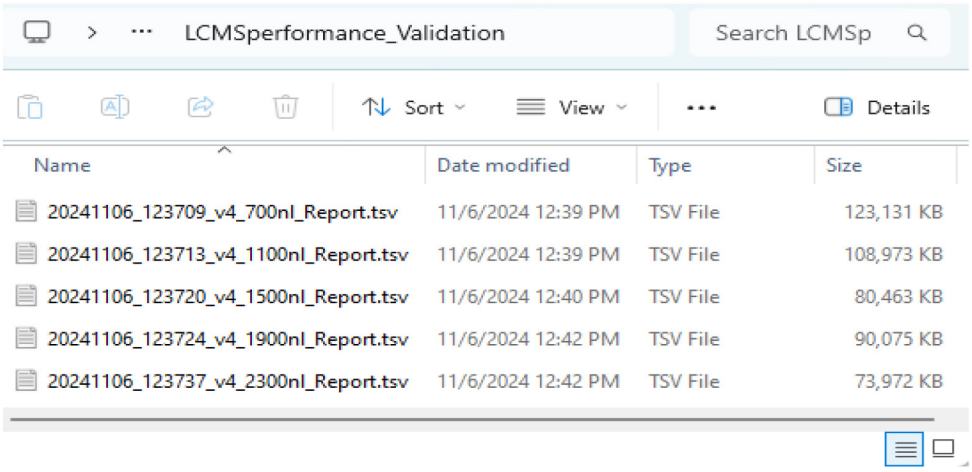
Organize input files

ProteoVision supports two scenarios for organizing your input files (search results).

Scenario 1: All input files in one folder

In this scenario, all search result files are in a single shared folder.

- Select the parent folder containing all input files.
- ProteoVision will automatically detect and include all compatible files.
- Subfolders within the parent folder will also be scanned.



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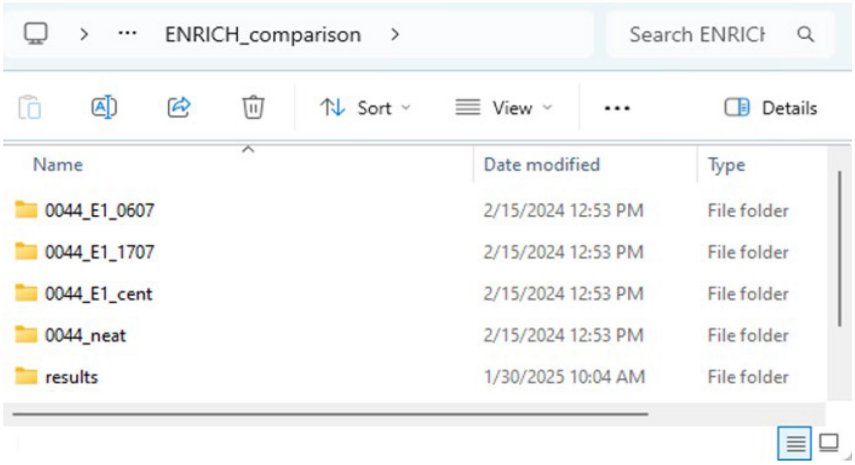
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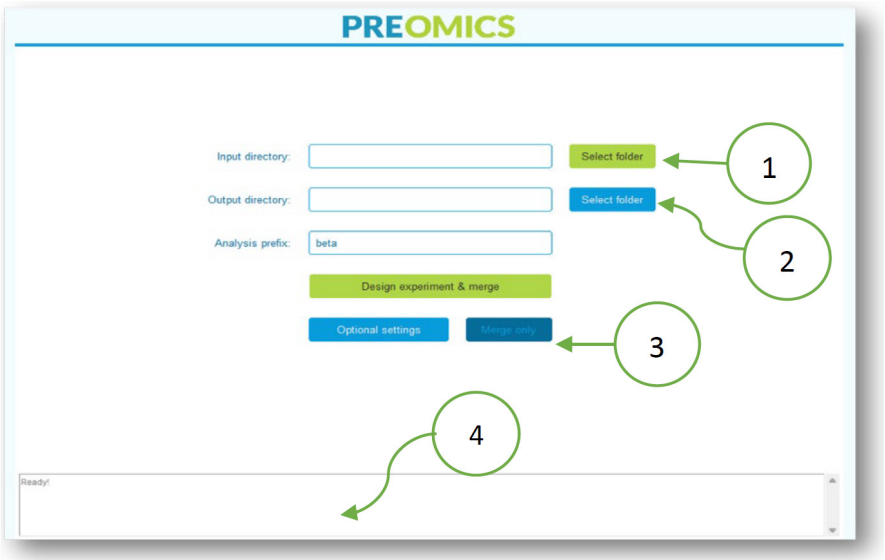
Scenario 2: Input files in individual folders

In this scenario, input files are organized into separate folders by condition or experiment.

- Each condition has its own subfolder.
- Select the parent folder containing all condition subfolders.
- ProteoVision will automatically organize files by folder structure.
- Condition names will be derived from folder names.

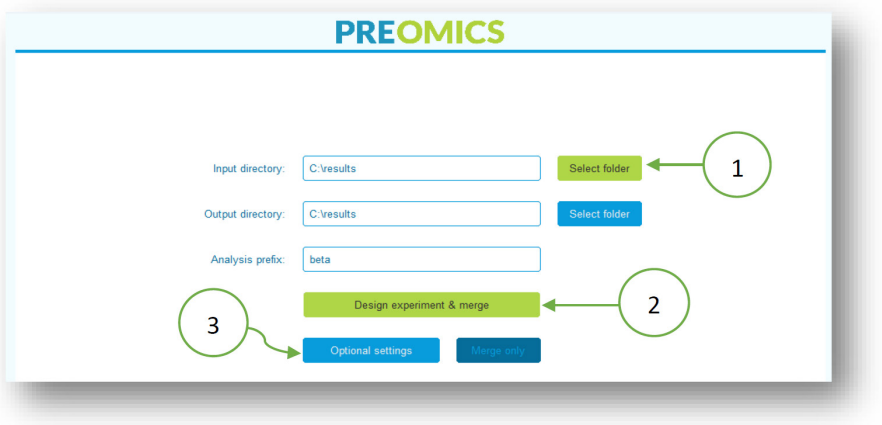


Graphical User Interface (GUI)



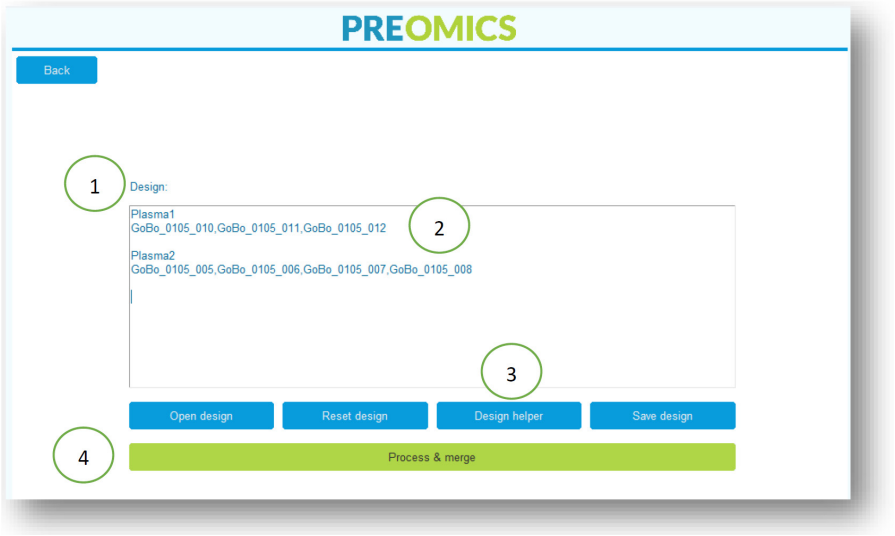
1. Green buttons - Necessary settings required to proceed with analysis.
2. Blue buttons - Optional settings for advanced customization.
3. Inactive buttons - Only activated when prerequisite requirements are fulfilled.
4. **Process log** - Tracks and reports progress updates in real-time.

Getting started: Select input



1. **Select folder**: Input folder path containing SN, MQ, DIANN result files. Selecting parent folders also works.
2. **Design experiment & merge:** Reads in available results and opens design window after brief loading.
3. Please see Optional settings.

Design experiment and start

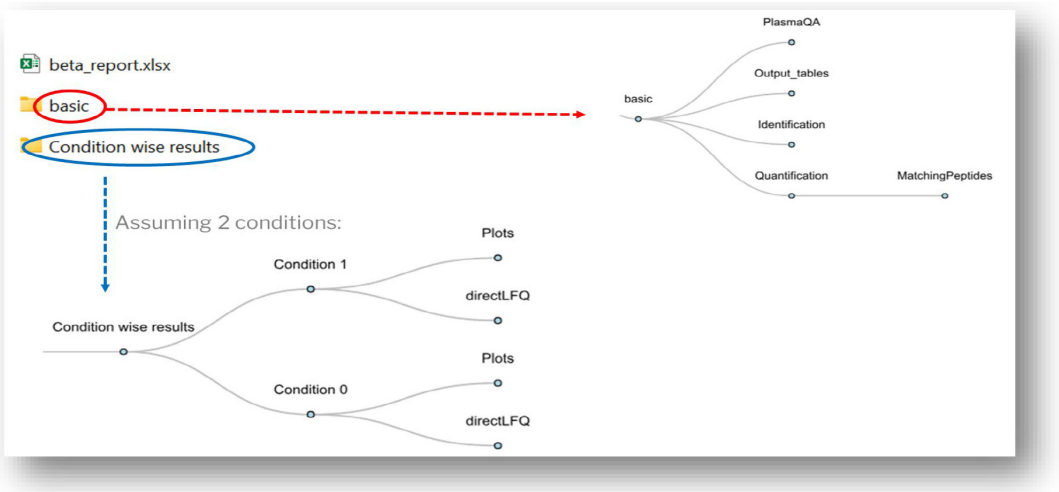


1. **Design experiment.**
   Proceed with the design derived from input / Open a previously saved design / Adjust the design in the textbox (or) Use the design helper.
2. The condition name(s) will be derived from the input file name (scenario 1) or the parent folder name (scenario 2). See page 4 for details. Condition names can also be edited directly.
   NOTE: Spaces between conditions are required!
3. See Design helper.
4. Click **“Process and merge”.**

Result and output

Result folder structure

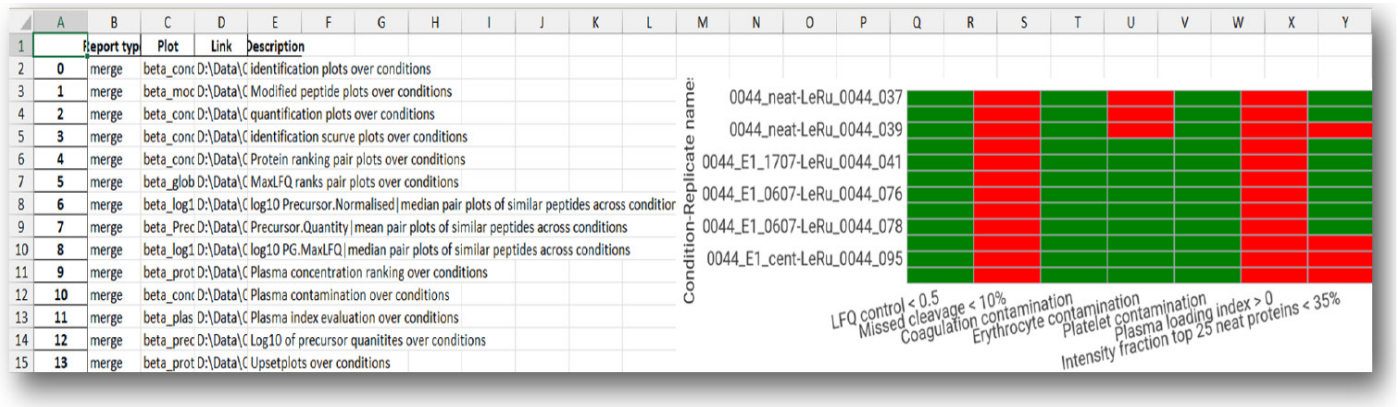
After processing completes, ProteoVision generates a comprehensive results folder at the specified output path, which includes the presentation of the results in an MS-PowerPoint (.pptx) file.



Overview report

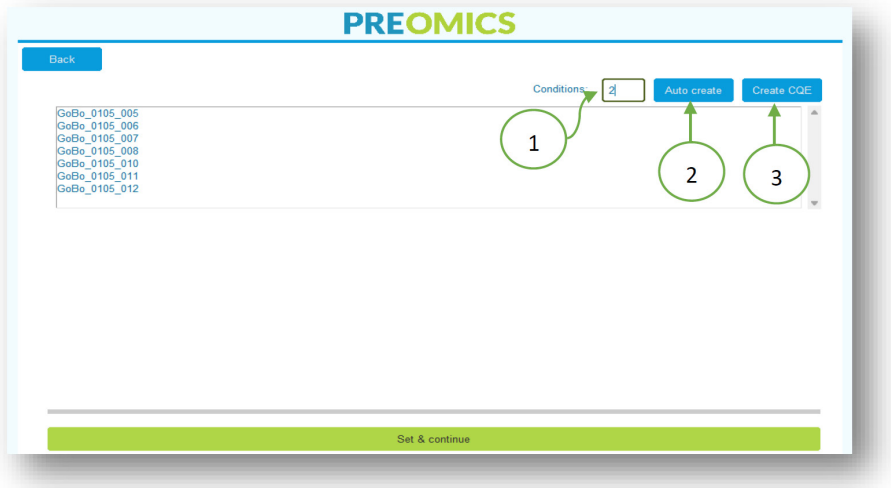
The overview report, located in the “results” folder, provides a summary of all selected and generated basic and optional plots. It serves as the initial entry point for analysis, offering a quick assessment of results. LC-MS runs that do not meet the criteria are highlighted in red.

Exemplary report:

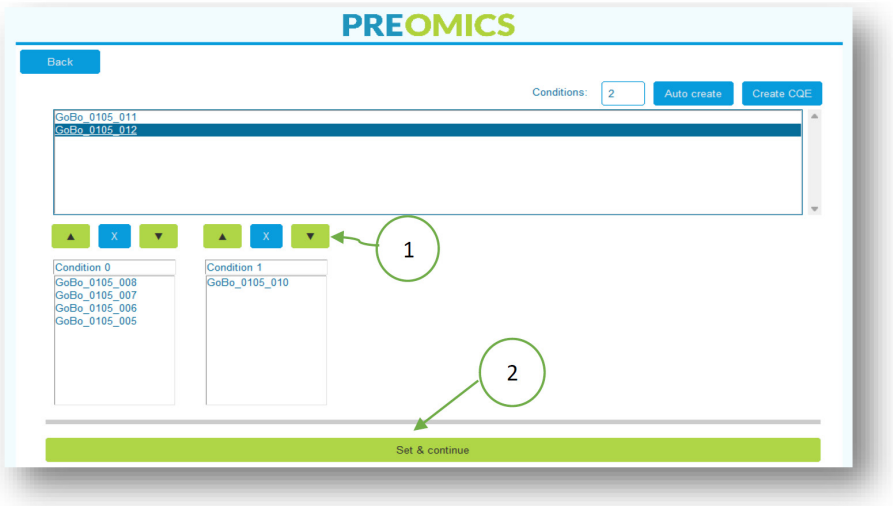


	Report typ	Plot	Link	Description
0	merge	beta_conc	D:\Data\C	identification plots over conditions
1	merge	beta_moc	D:\Data\C	Modified peptide plots over conditions
2	merge	beta_conc	D:\Data\C	quantification plots over conditions
3	merge	beta_conc	D:\Data\C	identification scurve plots over conditions
4	merge	beta_conc	D:\Data\C	Protein ranking pair plots over conditions
5	merge	beta_glob	D:\Data\C	MaxLFQ ranks pair plots over conditions
6	merge	beta_log1	D:\Data\C	log10 Precursor.Normalised|median pair plots of similar peptides across conditior
7	merge	beta_Prec	D:\Data\C	Precursor.Quantity|mean pair plots of similar peptides across conditions
8	merge	beta_log1	D:\Data\C	log10 PG.MaxLFQ|median pair plots of similar peptides across conditions
9	merge	beta_prot	D:\Data\C	Plasma concentration ranking over conditions
10	merge	beta_conc	D:\Data\C	Plasma contamination over conditions
11	merge	beta_plas	D:\Data\C	Plasma index evaluation over conditions
12	merge	beta_prec	D:\Data\C	Log10 of precursor quanitites over conditions
13	merge	beta_prot	D:\Data\C	Upsetplots over conditions

Design helper (optional)



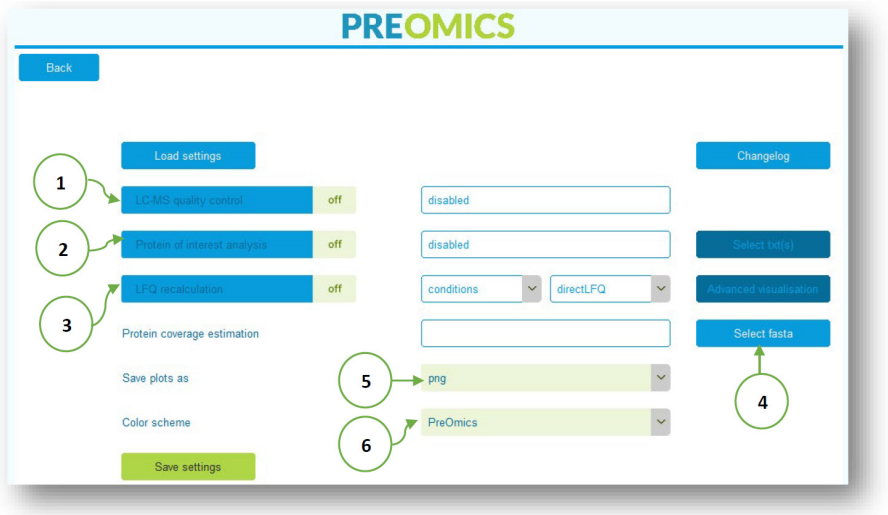
1. **Enter** desired number of experimental conditions.
2. Click **“Auto create”** to activate condition settings.
3. **Create CQE**: For analyzing CQE data, please refer to FAQ Question 8 for details.



1. Name and arrange each condition with relevant LC-MS runs.
   Each Condition box offers three key functions:
   i. Select LC-MS runs in the condition box and move them up (click arrow up).
   ii. Delete the condition and bring existing LC-MS runs back to the main list.
   iii. Move selected LC-MS runs in the main list to the Condition box (select the runs and click arrow down).
2. Click **“Set & continue”** to confirm the desired experimental design and proceed.

   NOTE: In any list box, multiple LC-MS runs can be selected using click & drag.

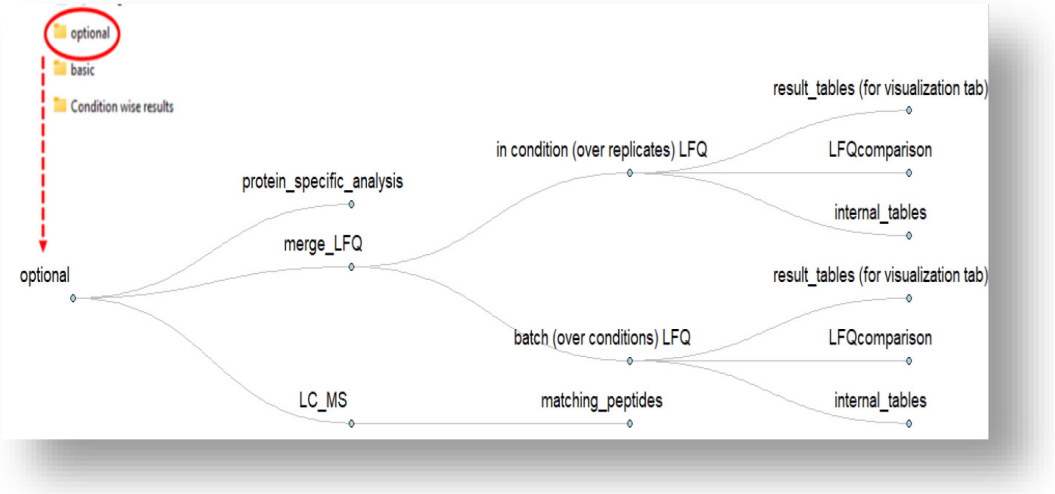
Optional settings:



1. Activate LC-MS performance analysis and set the cycle time.
2. Activate protein of interest (POI) analysis and select *.txt files with target proteins.
3. Activate LFQ recalculation (of Precursor.Quantity) and select whether it should be performed across “replicates” or “conditions” using “directLFQ” or “MaxLFQ”.
4. Upload a FASTA file for optional protein coverage plots.
5. Choose the file format for saving plots.
6. Select the color scheme for plots.

Optional output:

Based on your optional settings selections, ProteoVision generates additional output files in the results folder.



Generated optional output:

Based on your settings, additional files are generated:

- Protein_specific_analysis
- Merge_LFQ
- LC_MS

Questions & contact

For further information, please visit our FAQs and website via the links below.

- **FAQs:** Consult the ProteoVision™ FAQs
- **Website:** www.preomics.com/products/proteovision