

Getting started with MaxQuant

Welcome to the MaxQuant computational proteomics workflow. We hope that you will enjoy your time you will be spending with processing your data and that MaxQuant delivers some helpful results. Currently we support the following instrument types:

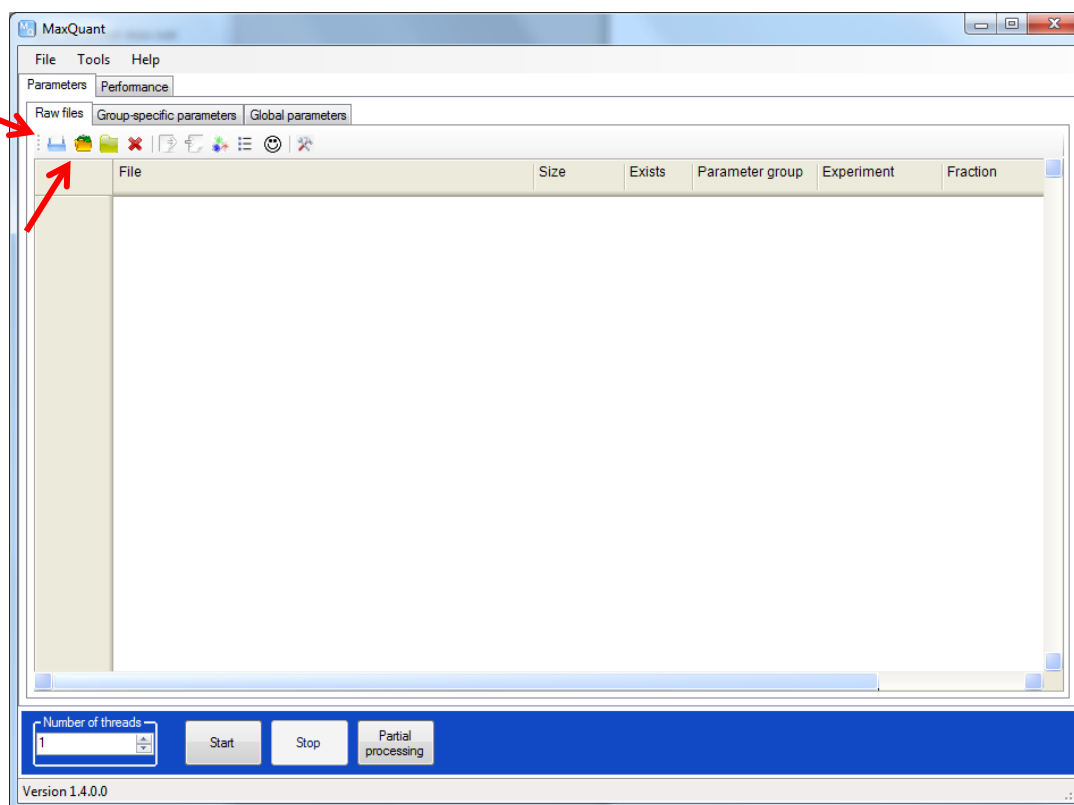
1. Thermo Velos
2. Thermo Orbitrap
3. Thermo FT
4. Thermo Exactive
5. Thermo Q Exactive
6. Thermo Orbitrap Elite

Many labeling technologies are supported. In fact, MS-level quantification labels can be freely configured. Supported sample labeling quantification techniques include:

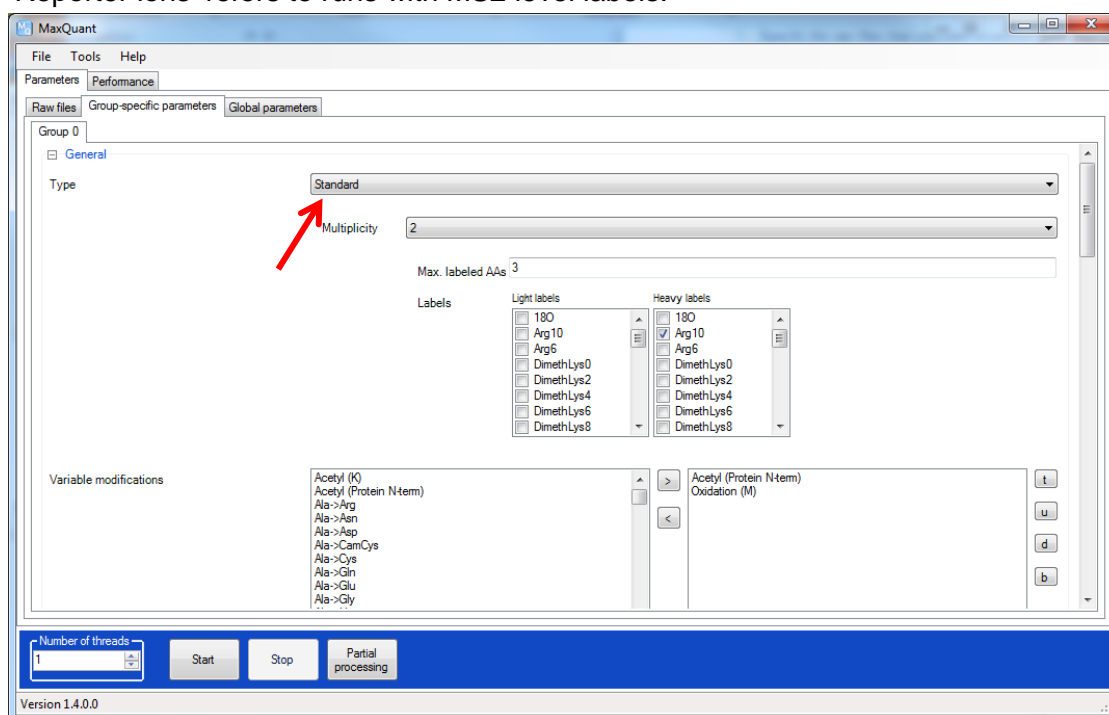
1. SILAC
2. Label-free quantification
3. Di-methyl
4. ICAT
5. ICPL
6. mTRAQ
7. iTRAQ
8. TMT

In case you are a first time user you might be worried by the many options and parameters that one can set in the user interface. In that case we have good news for you. In almost all use cases the standard values of most parameters are fine and you only need to adjust a small number of factors. Typically there is only little information that you need to provide. Every parameter in the interface has context help which you obtain by moving the mouse pointer to the beginning of the text string for this parameter and clicking on the question mark that will appear. Here are eight steps that you typically have to go through before MaxQuant can process your data:

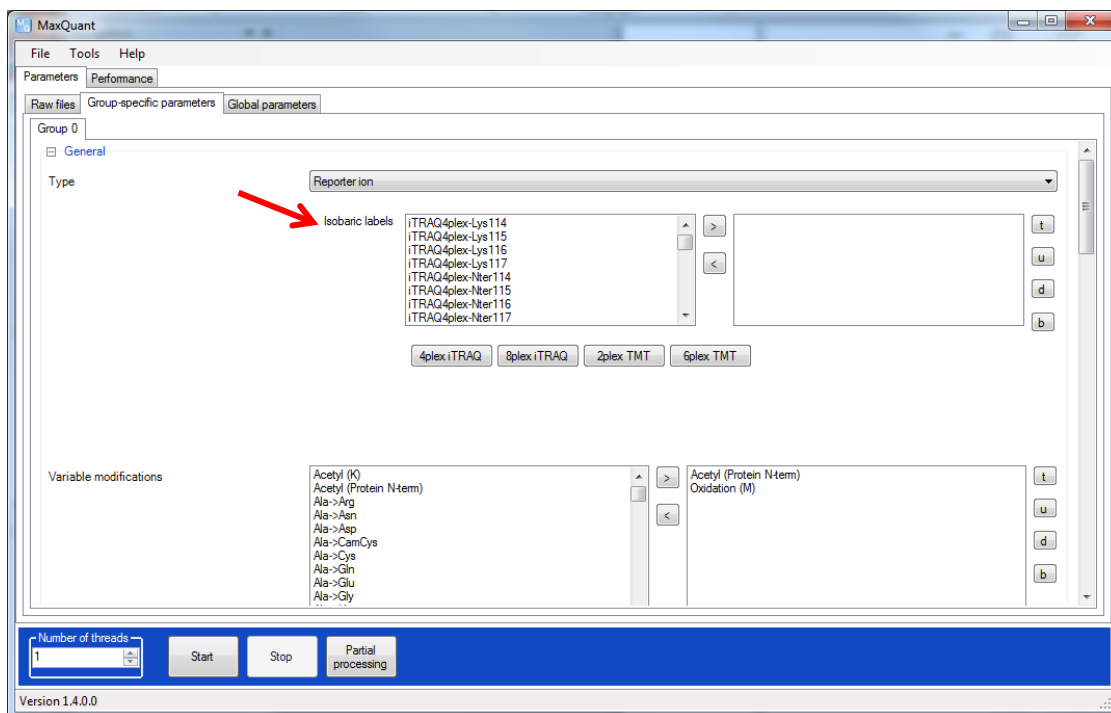
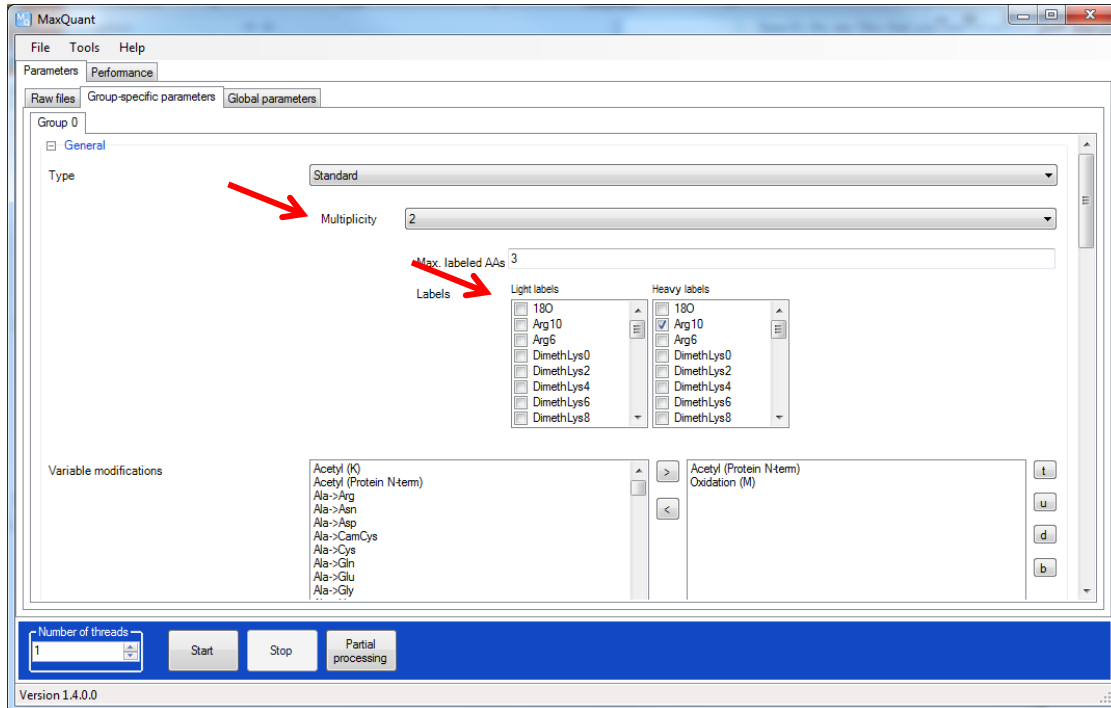
1. Specify the raw files that you want to process with MaxQuant.



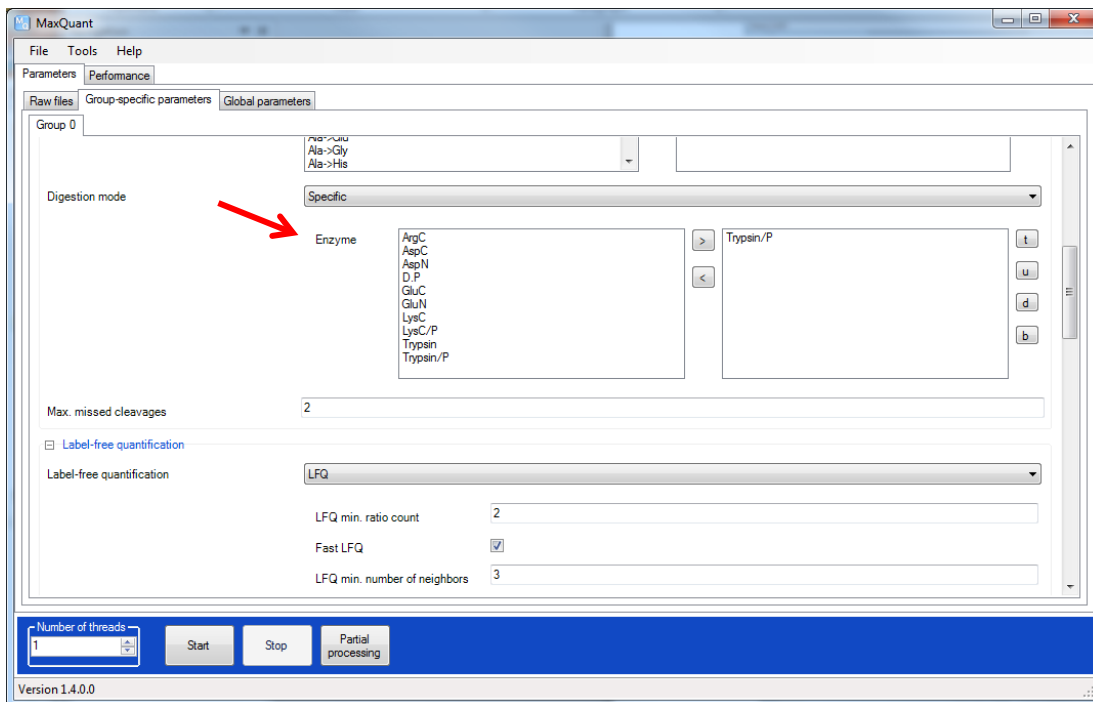
2. Specify the type of your LC-MS runs. 'Standard' means label free or MS1 labels. 'Reporter ions' refers to runs with MS2 level labels.



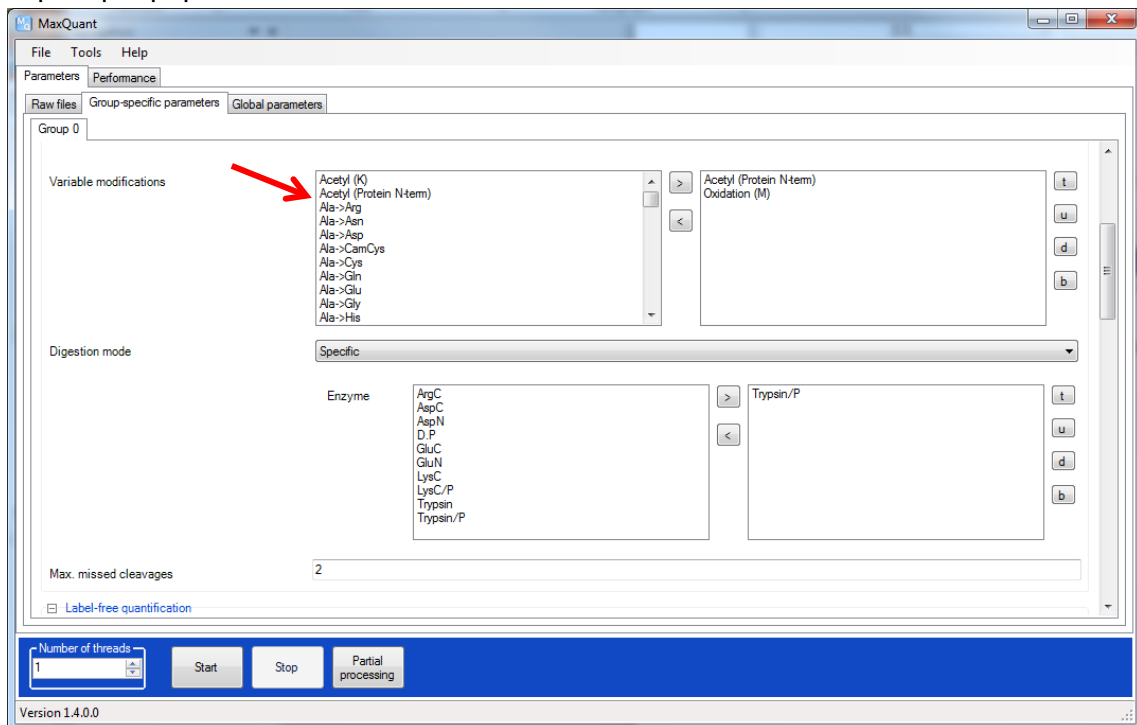
3. In case of 'Standard' LC_MS runs specify the multiplicity. Multiplicity = 1 stands for label free. Then, in case of MS1 level labeling specify the labels that were used in each channel. If the Type is 'Reporter ion', please specify the isobaric labels accordingly. There are pre-select buttons for four common isobaric label configurations.



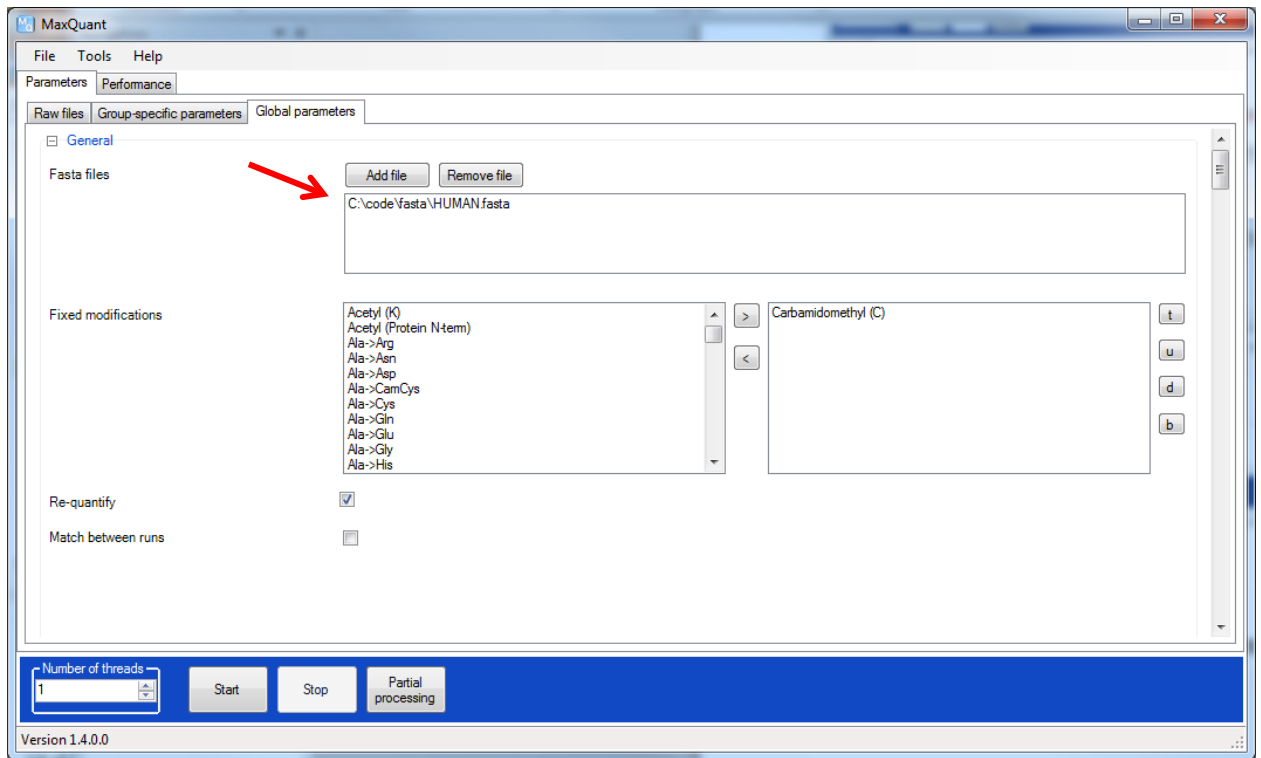
4. Specify the enzyme that was used for digestion of proteins to peptides. Trypsin is pre-selected.



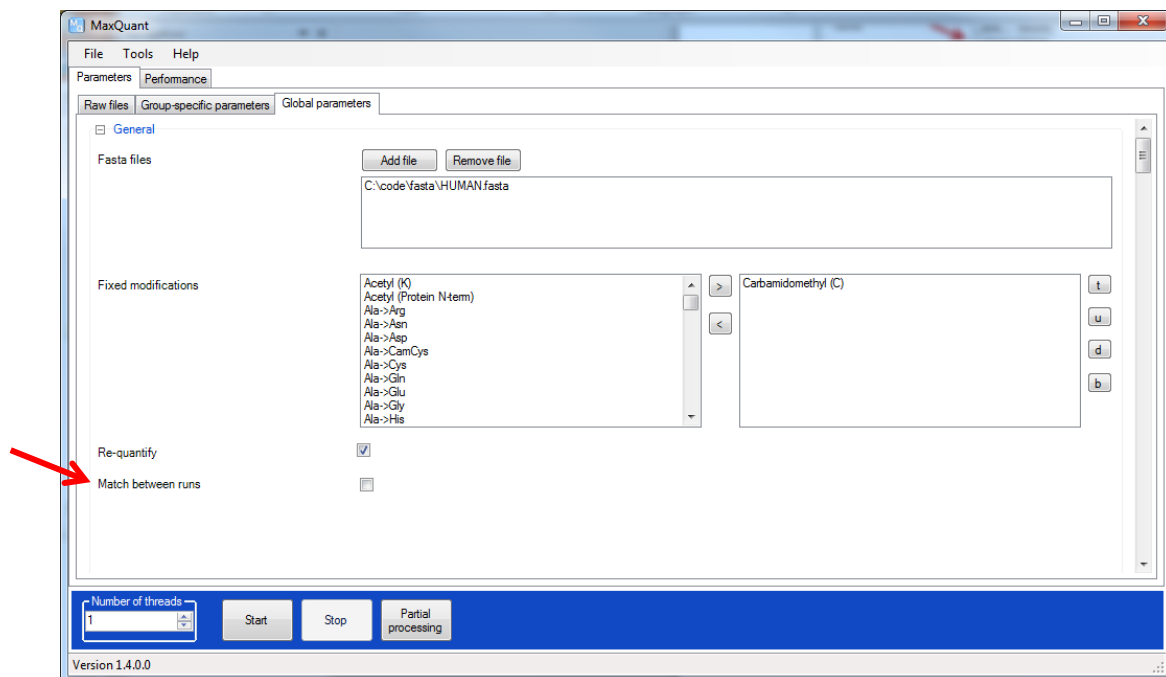
5. Optionally, add suitable variable modifications, e.g. phospho(STY) for samples enriched in phosphopeptides

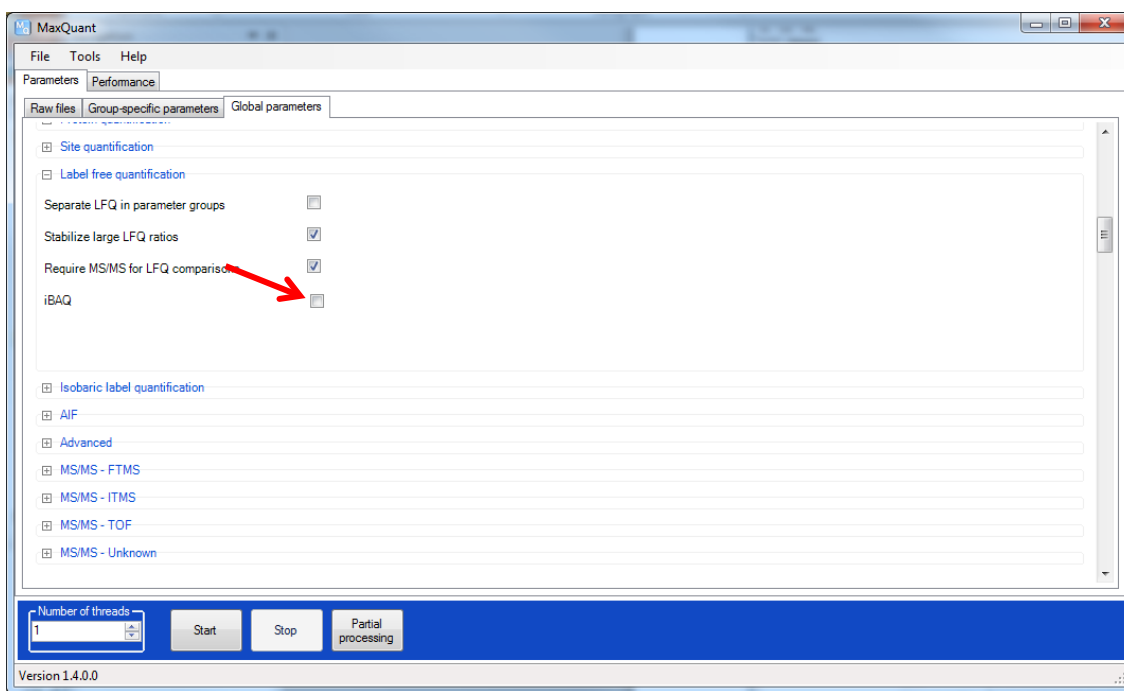
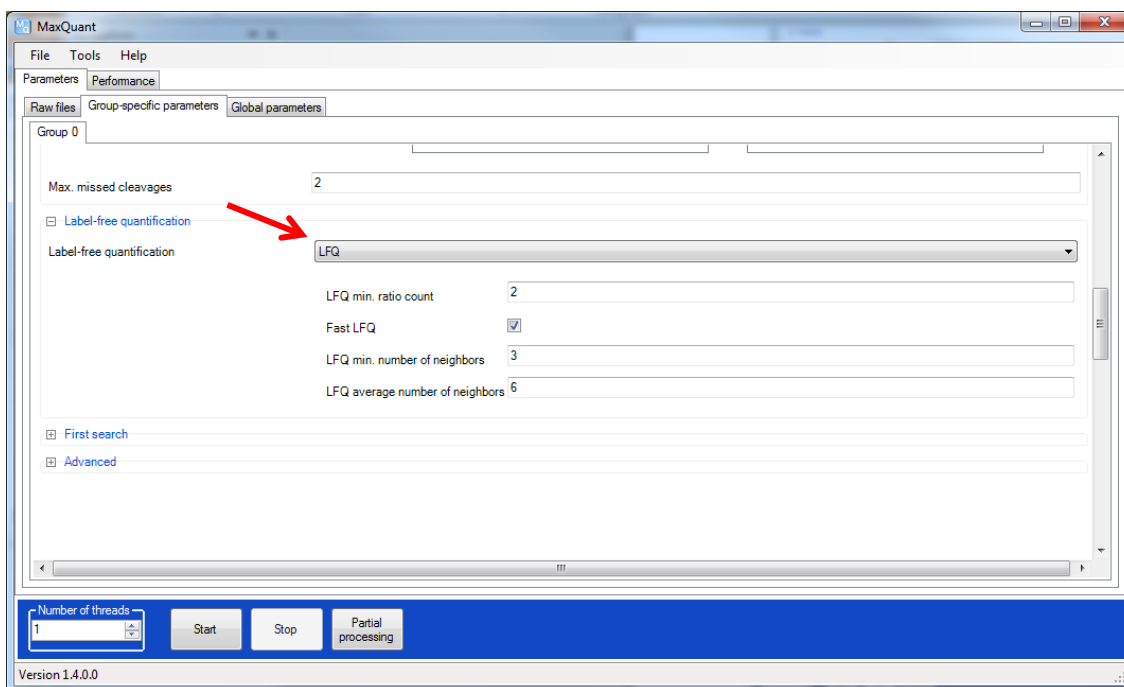


6. Specify the fasta file(s) with the protein sequences for the Andromeda search



7. Optionally use 'Match between runs', 'Label-free quantification' or 'iBAQ'.





8. Press start. You can monitor the progress on the 'Performance' page. A popup window saying 'Done' will appear when MaxQuant is finished. All result files will appear in the folder '..\combined\txt' as tab-delimited text files. The results can also be browsed with the program 'Viewer.exe'. All columns have interactive descriptions in the Viewer program. Just move the mouse over the beginning of the column title and click on the question mark that will appear. A pdf document with a description of all columns in all tables will be written to '..\combined\txt\tables.pdf'.