

# Workflow for the processing of bottom-up label-free proteomic experiments

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## INTRODUCTION

One of the major challenges in the proteomic field nowadays is **effective bioinformatical processing of high-throughput quantitative and qualitative data**, integration of complex datasets and subsequent mapping onto biological processes.

We developed a **workflow for the processing of label-free bottom-up proteomic experiments** using the **KNIME software**, an open-source platform comprising a variety of tools for data-mining, reporting and visualization, allowing to use both built-in and own nodes and metanodes. Here the workflow was applied for the analysis of BioID data of Wnt/PCP proteins.

## MATERIAL & METHODS

The workflow was built under the KNIME platform version 3.7.0a (<https://hub.docker.com/r/cfprot/knime>) utilizing both built-in and in-house developed nodes and metanodes available at [https://github.com/OmicsWorkflows/KNIME\\_metanodes](https://github.com/OmicsWorkflows/KNIME_metanodes).

The input file for the workflow is the proteinGroups.txt table generated by MaxQuant software, but in general any data table in wide format can be applied.

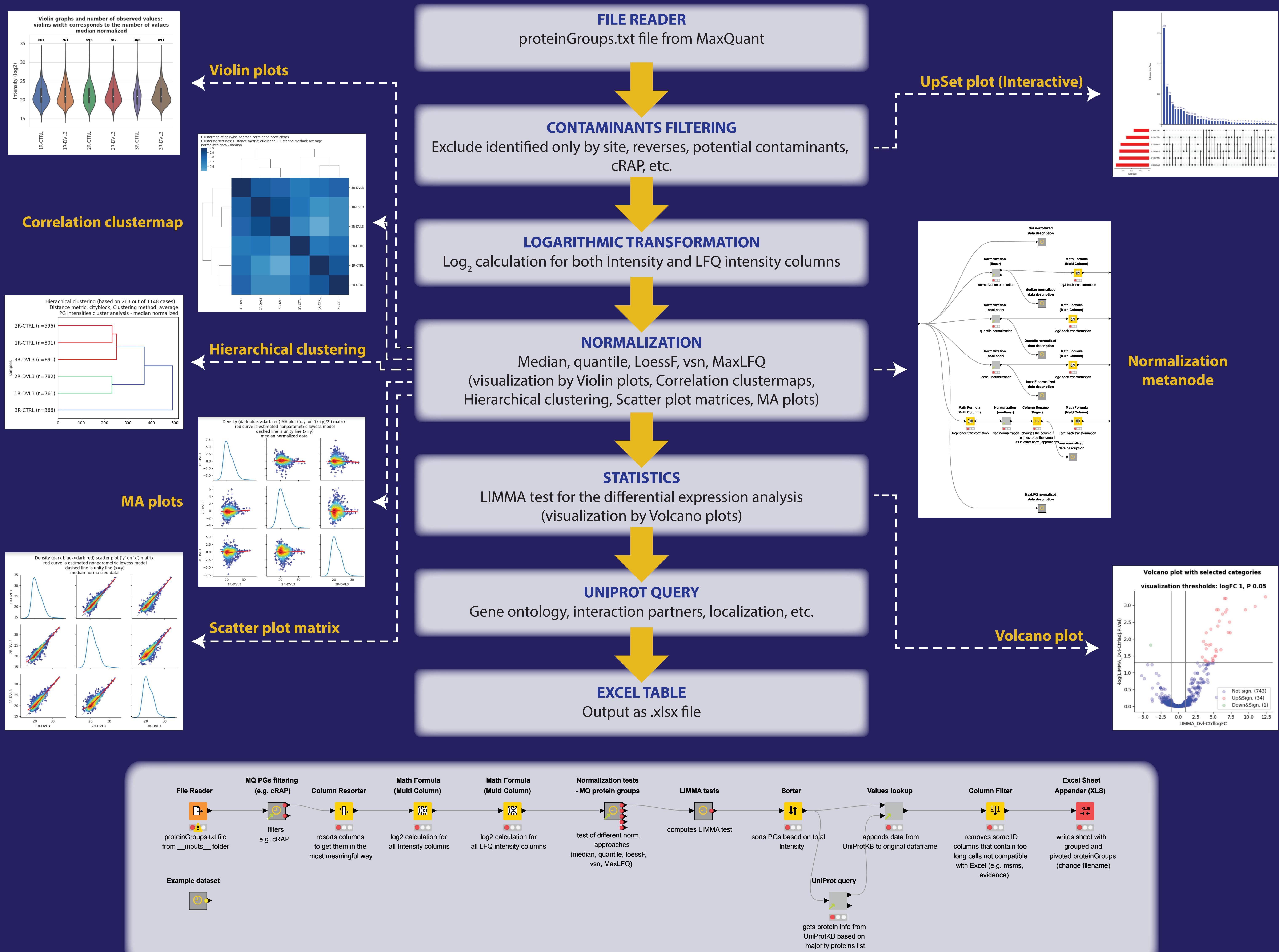


Image of the workflow as depicted in KNIME. Example dataset is also provided.

## CONCLUSIONS

- » We developed a KNIME workflow for the processing of bottom-up label-free mass spectrometry data
- » Wide variety of visualization and processing tools, customizability to particular user's requirements
- » Possibility to use additional nodes/metanodes and scripting (R/Python, JavaScript extensions are supported)
- » The workflow improves clarity of the concretely applied data processing pipeline and speeds up MS data processing coming from similar experimental design
- » **The workflow is available at [https://github.com/OmicsWorkflows/KNIME\\_workflows](https://github.com/OmicsWorkflows/KNIME_workflows)**