

# **msqrob2TMT: robust linear mixed models for inferring differential abundant proteins in labelled experiments with arbitrarily complex design - Highlights**

Stijn Vandebulcke      Christophe Vanderaa      Oliver Crook  
Lennart Martens      Lieven Clement

## **1 Highlights**

- Statistical workflows for differential abundance analysis in labelled proteomics.
- Enhanced sensitivity and specificity.
- Flexible modelling for experiments with both simple and complex designs.
- Benchmarked against DEqMS, MSstatsTMT, and msTrawler using two spike-in datasets.
- Transparent and modular workflows through open-source Bioconductor package msqrob2.