

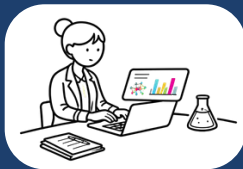
Tools, Databases and Support for Reproducible Proteomics

Proteomics is powerful – but complex

- ⚡ Large-scale LC-MS datasets
- ⚡ Complex multi-step analysis workflows
- ⚡ Quantification & normalization challenges
- ⚡ Biological interpretation is the bottleneck

💡 de.NBI helps you turn complex proteomics data into reliable biological insight.

For researchers like you



New to proteomics?

→ Guided workflows & training

Limited time?

→ Ready-to-use tools

Complex data?

→ Expert support

Explore our 30+ proteomics tools and databases:



de.NBI – Tools and Training for Life Science Data Analysis

What We Offer

- ✓ Curated tools for proteomics and complementary omics, from genomics to transcriptomics and metabolomics
- ✓ Training, documentation and expert support
- ✓ Access to the de.NBI Cloud
- ✓ Free of charge for academic users

Get Started

Explore Tools: www.denbi.de/services

Find Training: www.denbi.de/training

Apply for Cloud Grant: www.cloud.denbi.de

www.denbi.de
✉ contact@denbi.de



supported by
 Federal Ministry of Research, Technology and Space

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de.NBI – German Network for Bioinformatics Infrastructure
Coordination Office: Forschungszentrum Jülich (FZJ)

From Mass Spectra to Meaning

Reproducible Proteomics with de.NBI
Tools & Training

Free for academic life scientists



de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

From Data to Insight – with de.NBI Tools

Data Processing with OpenMS



- LC-MS data processing
- Feature detection
- Quantification

Metaproteomics Pipeline



with MPA Cloud

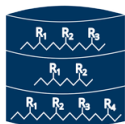
- Protein identification
- Spectra to protein groups

Calibration with CalibraCurve



- Improved quantitative accuracy

Peptide Lookup with MacPepDB



- Peptide lookup
- Fast validation

Functional Interpretation with BRENDA



- Enzymes, pathways
- Biological context

30+ proteomics
tools & databases

Consulting and Expert Support

Proteomics projects often require tailored bioinformatics expertise. From study design and statistical analysis to machine learning and biological interpretation, de.NBI experts support researchers throughout the entire analysis workflow. Expert consulting is available to academic researchers through de.NBI.

What we support you with:



Experimental Design

Strategy for your research question



Proteomics Data Analysis

Raw MS data to interpretable results



Statistical Evaluation

Robust quantification and validation



Machine Learning

Advanced methods for pattern detection

Why it matters:

- Avoid common pitfalls in analysis
- Get reliable and reproducible results
- Save time and resources

Work directly with
experts who develop
and apply these tools.

Scan to learn more →



de.NBI Training

We offer regular **hands-on training courses** on proteomics tools and workflows, covering the full analysis pipeline – from experimental design and data acquisition to processing, quantification and biological interpretation.

Ideal for researchers working in areas such as molecular biology, microbiology, clinical research, environmental studies or systems biology.



Explore
upcoming
trainings:



Your Proteomics Workflow – supported by de.NBI



- Experimental design
- Processing & identification
- Statistical analysis
- Biological interpretation

