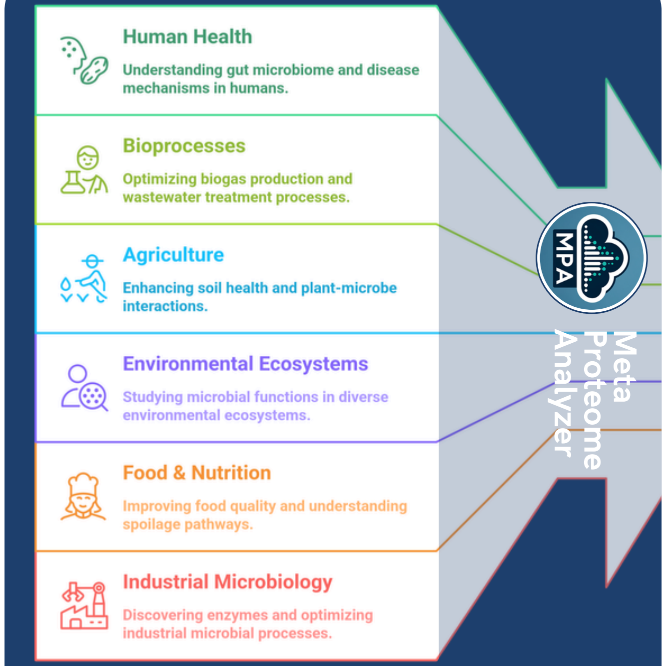
Metaproteomics Helps Understand:

Unveiling Microbial Roles



Human Health

Understanding gut microbiome and disease mechanisms in humans.

Bioprocesses

Optimizing biogas production and wastewater treatment processes.

Agriculture

Enhancing soil health and plant-microbe interactions.

Environmental Ecosystems

Studying microbial functions in diverse environmental ecosystems.

Food & Nutrition

Improving food quality and understanding spoilage pathways.

Industrial Microbiology

Discovering enzymes and optimizing industrial microbial processes.

This flyer shows how the de.NBI Service MPA helps you answer research questions.

Example Success Stories:

Journal of Proteomics

Fecal metaproteomics enables functional characterization of remission in patients with inflammatory bowel disease

Microbiome

RESEARCH

Open Access

Metaproteome analysis reveals that syntrophy, competition, and phage-host interaction shape microbial communities in biogas plants

BMC

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

What We Offer

- ✓ Curated tools for genomics, pangenomics, metagenomics, proteomics and more
- ✓ 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 Access: www.cloud.denbi.de

www.denbi.de →
✉ contact@denbi.de

supported by
Federal Ministry of Research, Technology and Space

Follow us

de.NBI & ELIXIR Germany
@denbi@mastodon.science
@denbi.bsky.social

de.NBI is the German ELIXIR Node
elixir GERMANY

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

Metaproteomics: from Community to Function

– with de.NBI Tools & Training

Free for academic life scientists

de.NBI
GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE

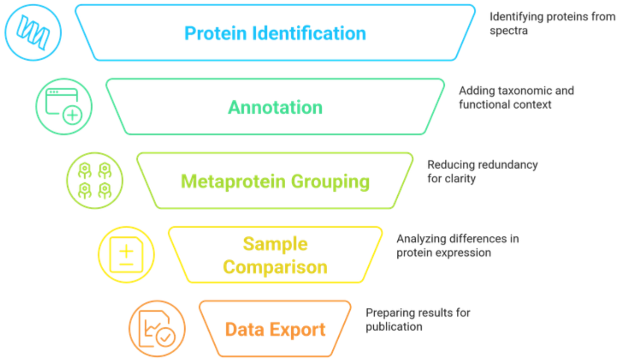
Meet: Meta Proteome Analyzer

What MPA offers:

- Load **MS/MS spectra** and search against protein databases → streamlined, cloud-based workflow
- **Functional & taxonomic annotation** including integrated re-annotation pipelines (e.g., Prophane) for deeper functional coverage
- Link proteins to **taxa, pathways & functions** for easy biological interpretation
- Grouping into **metaproteins** to reduce redundancy and highlight biologically meaningful units
- Rich **metadata integration** (e.g., UniProt, KEGG, NCBI taxonomy) and direct connections to KEGG Maps
- **Sample comparison & differential analysis** to identify shifts in protein expression or microbial function across conditions
- **Flexible exports** – full datasets or targeted subsets (e.g. all proteins linked to a specific taxonomy, pathway, or function)

From Data to Insight

Typical Workflow Steps



Protein Identification – Identifying proteins from spectra

Annotation – Adding taxonomic and functional context

Metaprotein Grouping – Reducing redundancy for clarity

Sample Comparison – Analyzing differences in protein expression

Data Export – Preparing results for publication

Why this workflow matters:
It combines reliability, reproducibility and ease-of-use – no need to assemble multiple tools manually.

Scan to launch MPA-Cloud in your browser. No installation – analyse your data instantly.

Great for researchers with limited bioinformatics background.

de.NBI Training

We offer a regular **Applied Metaproteomics Workshop** in Magdeburg, providing hands-on training across the entire metaproteomics workflow – from experimental design and sample preparation to high-resolution MS measurement and data analysis with the **MetaProteomeAnalyzer (MPA) Cloud**.

Ideal for researchers working on microbiomes, environmental samples, bioreactors, clinical material or functional microbiology.

Find the latest course here:

Core topics include:

- Sample preparation & protein extraction
- High-resolution MS data measurement
- Protein identification & database search
- Taxonomic & functional (re-)annotation
- Metaprotein grouping
- Comparative analyses in MPA

The workshop is held by **Prof. Dirk Benndorf** and **Prof. Robert Heyer**, offering direct interaction with experts who significantly contributed to establishing applied metaproteomics.