

Resource Summary Report

Generated by [dkNET](#) on Aug 4, 2026

Unipept

RRID:SCR_024987

Type: Tool

Proper Citation

Unipept (RRID:SCR_024987)

Resource Information

URL: <https://unipept.ugent.be/>

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Description: Web application for metaproteome data analysis, with initial focus on tryptic-peptide-based biodiversity analysis of MS/MS samples. Designed for metaproteomics data analysis with focus on interactive data visualizations. Unipept 4.0 introduces complementary functional analysis based on GO terms and EC numbers.

Synonyms: Unipept 4.0

Resource Type: software resource, web application

Defining Citation: [PMID:30465426](#)

Keywords: metaproteomics data analysis, interactive data visualizations, biodiversity analysis of large and complex metaproteome samples,

Availability: Free, Freely available

Resource Name: Unipept

Resource ID: SCR_024987

Record Creation Time: 20240202T050227+0000

Record Last Update: 20260804T043856+0000

Ratings and Alerts

No rating or validation information has been found for Unipept.

No alerts have been found for Unipept.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Bao D, et al. (2025) Precise mycobacterial species and subspecies identification using the PEP-TORCH peptidome algorithm. EMBO molecular medicine, 17(4), 841.

Kontopodis E, et al. (2025) Uniquome: Construction and decoding of a novel proteomic atlas that contains new peptide entities. Computational and structural biotechnology journal, 27, 2123.

Griffiths JA, et al. (2024) Peripheral neuronal activation shapes the microbiome and alters gut physiology. Cell reports, 43(4), 113953.

M??ndez A, et al. (2024) Environmental Proteomics Elucidates Phototrophic Biofilm Responses to Ornamental Lighting on Stone-built Heritage. Microbial ecology, 87(1), 147.

Wu EH, et al. (2024) [Microbial metaproteomics--From sample processing to data acquisition and analysis]. Se pu = Chinese journal of chromatography, 42(7), 658.

Nasr E, et al. (2024) microGalaxy: A gateway to tools, workflows, and training for reproducible and FAIR analysis of microbial data. bioRxiv : the preprint server for biology.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. GigaScience, 13.

Zhang T, et al. (2024) Core microbiome-associated proteins associated with ulcerative colitis interact with cytokines for synergistic or antagonistic effects on gut bacteria. The ISME journal, 18(1).