

Resource Summary Report

Generated by [dkNET](#) on Aug 29, 2026

[neXtProt](#)

RRID:SCR_008911

Type: Tool

Proper Citation

neXtProt (RRID:SCR_008911)

Resource Information

URL: <http://www.nextprot.org/>

Proper Citation: neXtProt (RRID:SCR_008911)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on April 15, 2025. Human protein knowledge platform. Knowledge platform for human proteins selects and filters high throughput data pertinent to human proteins from UniProtKB. Extends UniProtKB/Swiss-Prot annotations for human proteins to include several new data types.

Resource Type: data or information resource, database, portal, topical portal

Defining Citation: [PMID:22139911](#)

Keywords: Protein, proteomics, sirna, 3d, pathway, variant, protein-protein interaction, protein-drug interaction, bio.tools, FASEB list

Funding: SIB ;
Swiss Commission for Technology and Innovation

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: neXtProt

Resource ID: SCR_008911

Alternate IDs: biotools:nextprot, nlx_151482

Alternate URLs: <https://bio.tools/nextprot>

License URLs: <https://www.nextprot.org/legal-disclaimer>

Record Creation Time: 20220129T080250+0000

Record Last Update: 20260829T182757+0000

Ratings and Alerts

No rating or validation information has been found for neXtProt.

No alerts have been found for neXtProt.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 177 mentions in open access literature.

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

Scala M, et al. (2026) ASAH2 deficiency affects sphingolipid homeostasis and neuromotor control, causing a progressive neurological disorder. HGG advances, 7(2), 100587.

Kemunto G, et al. (2026) Advancing Extracellular Vesicle Research: A Review of Systems Biology and Multiomics Perspectives. Proteomics, 26(2-3), 33.

Zhou N, et al. (2025) Proteomic patterns associated with ketamine response in major depressive disorders. Cell biology and toxicology, 41(1), 26.

Nezvedová M, et al. (2025) Non-standardized protein background in IVF media linked to serum-derived albumin supplementation. Journal of assisted reproduction and genetics, 42(10), 3535.

Wagt M, et al. (2025) PredLyP: A computational tool for predicting tissue-specific (phago-)lysosomal post-digestion peptides. Computational and structural biotechnology journal, 27, 4645.

Scala M, et al. (2024) De novo variants in DENND5B cause a neurodevelopmental disorder. American journal of human genetics, 111(3), 529.

Silvestri R, et al. (2024) Polymorphism Pro64His within galectin-3 has functional consequences at proteome level in thyroid cells. Frontiers in genetics, 15, 1380495.

Jiang Y, et al. (2024) Comprehensive Overview of Bottom-Up Proteomics Using Mass Spectrometry. ACS measurement science au, 4(4), 338.

Lan N, et al. (2024) MECOM Locus classical transcript isoforms affect tumor immune microenvironment and different targets in ovarian cancer. Journal of ovarian research, 17(1), 207.

Zhou Q, et al. (2024) Mitochondrial respiratory chain component NDUFA4: a promising therapeutic target for gastrointestinal cancer. Cancer cell international, 24(1), 97.

Gracia B, et al. (2024) Protein-folding chaperones predict structure-function relationships and cancer risk in BRCA1 mutation carriers. Cell reports, 43(2), 113803.

Richardson R, et al. (2024) Meta-Research: Understudied genes are lost in a leaky pipeline between genome-wide assays and reporting of results. *eLife*, 12.

Raj A, et al. (2024) PgxSAVy: A tool for comprehensive evaluation of variant peptide quality in proteogenomics - catching the (un)usual suspects. *Computational and structural biotechnology journal*, 23, 711.

Lee YS, et al. (2024) New Function Annotation of PROSER2 in Pancreatic Ductal Adenocarcinoma. *Journal of proteome research*, 23(3), 905.

Pirone A, et al. (2023) Proteomic Profiling Reveals Specific Molecular Hallmarks of the Pig Claustrium. *Molecular neurobiology*, 60(8), 4336.

Garcia-Del Rio DF, et al. (2023) Protocol to identify human subcellular alternative protein interactions using cross-linking mass spectrometry. *STAR protocols*, 4(3), 102380.

Casella C, et al. (2023) Methylomic, Proteomic, and Metabolomic Correlates of Traffic-Related Air Pollution in the Context of Cardiorespiratory Health: A Systematic Review, Pathway Analysis, and Network Analysis. *Toxics*, 11(12).

Jiang Y, et al. (2023) Comprehensive Overview of Bottom-Up Proteomics using Mass Spectrometry. *ArXiv*.

Rusilowicz M, et al. (2023) AlacatDesigner?Computational Design of Peptide Concatamers for Protein Quantitation. *Journal of proteome research*, 22(2), 594.

Nezvedová M, et al. (2023) Single Cerebral Organoid Mass Spectrometry of Cell-Specific Protein and Glycosphingolipid Traits. *Analytical chemistry*, 95(6), 3160.