

Resource Summary Report

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HUPO - Human Proteome Organisation

RRID:SCR_010707

Type: Tool

Proper Citation

HUPO - Human Proteome Organisation (RRID:SCR_010707)

Resource Information

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

Proper Citation: HUPO - Human Proteome Organisation (RRID:SCR_010707)

Description: The Human Proteome Organisation (HUPO) is an international scientific organization representing and promoting proteomics through international cooperation and collaborations by fostering the development of new technologies, techniques and training.

Abbreviations: HUPO

Synonyms: Human Proteome Organisation

Resource Type: data or information resource, journal article, knowledge environment, meeting resource, organization portal, portal, training resource

Resource Name: HUPO - Human Proteome Organisation

Resource ID: SCR_010707

Alternate IDs: nlx_85721

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260905T132645+0000

Ratings and Alerts

No rating or validation information has been found for HUPO - Human Proteome Organisation.

No alerts have been found for HUPO - Human Proteome Organisation.

Data and Source Information

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

Díez P, et al. (2025) Tonic signaling of the B-cell antigen-specific receptor is a common functional hallmark in chronic lymphocytic leukemia cell phosphoproteomes at early disease stages. *Molecular oncology*, 19(12), 3706.

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

Hoppstock G, et al. (2024) DNA-Binding Protein A Is Actively Secreted in a Calcium-and Inflammasome-Dependent Manner and Negatively Influences Tubular Cell Survival. *Cells*, 13(20).

Feser R, et al. (2023) Breast cancer cell secretome analysis to decipher miRNA regulating the tumor microenvironment and discover potential biomarkers. *Heliyon*, 9(4), e15421.

Naryzhny S, et al. (2023) Quantitative Aspects of the Human Cell Proteome. *International journal of molecular sciences*, 24(10).

Łyszczak A, et al. (2021) Survival analysis in breast cancer using proteomic data from four independent datasets. *Scientific reports*, 11(1), 16787.

Barba-Vicente V, et al. (2020) Detection of Human p53 In-Vitro Expressed in a Transcription-Translation Cell-Free System by a Novel Conjugate Based on Cadmium Sulphide Nanoparticles. *Nanomaterials (Basel, Switzerland)*, 10(5).

Hübel C, et al. (2019) Body composition in anorexia nervosa: Meta-analysis and meta-regression of cross-sectional and longitudinal studies. *The International journal of eating disorders*, 52(11), 1205.

Murnyák B, et al. (2017) PARP1 expression and its correlation with survival is tumour molecular subtype dependent in glioblastoma. *Oncotarget*, 8(28), 46348.

Alm T, et al. (2016) Introducing the Affinity Binder Knockdown Initiative? A public-private partnership for validation of affinity reagents. *EuPA open proteomics*, 10, 56.

Boi M, et al. (2016) Therapeutic efficacy of the bromodomain inhibitor OTX015/MK-8628 in ALK-positive anaplastic large cell lymphoma: an alternative modality to overcome resistant phenotypes. *Oncotarget*, 7(48), 79637.

Gaudet P, et al. (2015) The neXtProt knowledgebase on human proteins: current status. *Nucleic acids research*, 43(Database issue), D764.

López-Villar E, et al. (2015) A proteomic approach to obesity and type 2 diabetes. *Journal of cellular and molecular medicine*, 19(7), 1455.

Colangelo CM, et al. (2015) YPED: an integrated bioinformatics suite and database for mass spectrometry-based proteomics research. *Genomics, proteomics & bioinformatics*, 13(1), 25.

Nishimura T, et al. (2014) Clinical initiatives linking Japanese and Swedish healthcare resources on cancer studies utilizing Biobank Repositories. *Clinical and translational medicine*, 3(1), 61.

Deibel E, et al. (2014) Open Genetic Code: on open source in the life sciences. *Life sciences, society and policy*, 10, 2.

Colangelo CM, et al. (2013) Review of software tools for design and analysis of large scale MRM proteomic datasets. *Methods (San Diego, Calif.)*, 61(3), 287.

Furczyk K, et al. (2013) The neurobiology of suicide - A Review of post-mortem studies. *Journal of molecular psychiatry*, 1(1), 2.

Aretz S, et al. (2013) In-depth mass spectrometric mapping of the human vitreous proteome. *Proteome science*, 11(1), 22.

Welinder C, et al. (2013) Establishing a Southern Swedish Malignant Melanoma OMICS and biobank clinical capability. *Clinical and translational medicine*, 2(1), 7.