Resource Summary Report

Generated by dkNET on May 19, 2025

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

Funding:

Resource Name: HUPO - Human Proteome Organisation

Resource ID: SCR_010707

Alternate IDs: nlx_85721

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250519T203620+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 35 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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).

?sz Á, 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.

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

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

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.

Kelleher NL, et al. (2012) A cell-based approach to the human proteome project. Journal of the American Society for Mass Spectrometry, 23(10), 1617.

Gilany K, et al. (2011) The Profile of Human Sperm Proteome; A Mini-review. Journal of reproduction & infertility, 12(3), 193.

Higdon R, et al. (2011) IPM: An integrated protein model for false discovery rate estimation and identification in high-throughput proteomics. Journal of proteomics, 75(1), 116.