Resource Summary Report

Generated by RRID on Apr 28, 2025

Integrated Proteome Resources

RRID:SCR_026109
Type: Tool

Proper Citation

Integrated Proteome Resources (RRID:SCR_026109)

Resource Information

URL: https://www.iprox.cn/

Proper Citation: Integrated Proteome Resources (RRID:SCR_026109)

Description: Integrated proteome resources center in China to accelerate data sharing in proteomics. Composed of data submission system and proteome database. Submission system is established under the guidance of data-sharing policy made by ProteomeXchange consortium. Registered users can submit their proteomic datasets to iProX in public or private modes. Once associated manuscript has been published, dataset becomes automatically public.

Abbreviations: iProX

Resource Type: database, data or information resource

Defining Citation: PMID:34871441

Keywords: data sharing, proteomics, proteome database,

Funding:

Availability: Free, Freely available

Resource Name: Integrated Proteome Resources

Resource ID: SCR_026109

Record Creation Time: 20241203T053255+0000

Record Last Update: 20250423T061423+0000

Ratings and Alerts

No rating or validation information has been found for Integrated Proteome Resources.

No alerts have been found for Integrated Proteome Resources.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Zhang Q, et al. (2025) Integrated proteogenomic characterization of ampullary adenocarcinoma. Cell discovery, 11(1), 2.

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

Huang X, et al. (2025) Proteomic analysis of egg production peak and senescence in the ovaries of Taihe black-boned silky fowl (Gallus gallus domesticus Brisson). BMC genomics, 26(1), 17.

Wang Y, et al. (2025) Establishment and characterization of a new mouse gastric carcinoma cell line, MCC. Cancer cell international, 25(1), 9.

Li H, et al. (2024) Quantitative proteomics reveals the mechanism of endoplasmic reticulum stress-mediated pulmonary fibrosis in mice. Heliyon, 10(20), e39150.

Lin Q, et al. (2024) Plasma biomarkers in patients with age-related sarcopenia: a proteomic exploration and experimental validation. Aging clinical and experimental research, 37(1), 13.

Price E, et al. (2024) What is the real value of omics data? Enhancing research outcomes and securing long-term data excellence. Nucleic acids research, 52(20), 12130.

Guo H, et al. (2024) Physiological traits, gene expression responses, and proteomics of rice varieties varying in heat stress tolerance at the flowering stage. Frontiers in plant science, 15, 1489331.

Chen J, et al. (2024) Lnc-H19-derived protein shapes the immunosuppressive microenvironment of glioblastoma. Cell reports. Medicine, 5(11), 101806.

Rosani U, et al. (2024) Long-read transcriptomics of Ostreid herpesvirus 1 uncovers a conserved expression strategy for the capsid maturation module and pinpoints a mechanism

for evasion of the ADAR-based antiviral defence. Virus evolution, 10(1), veae088.

Ben Diouf O, et al. (2024) Phospho-Proteomics Analysis of Early Response to X-Ray Irradiation Reveals Molecular Mechanism Potentially Related to U251 Cell Radioresistance. Proteomes, 13(1).