Resource Summary Report

Generated by dkNET on Aug 15, 2026

OpenCell

RRID:SCR_021870
Type: Tool

Proper Citation

OpenCell (RRID:SCR_021870)

Resource Information

URL: https://opencell.czbiohub.org/

Proper Citation: OpenCell (RRID:SCR_021870)

Description: Proteome scale collection of protein localization and interaction measurements in human cells. Proteome scale endogenous tagging enables cartography of human cellular organization.

Resource Type: data or information resource, portal, project portal

Defining Citation: DOI:10.1101/2021.03.29.437450

Keywords: Proteome scale collection, protein localization, interaction measurements, human cells

Availability: Free, Freely available

Resource Name: OpenCell

Resource ID: SCR_021870

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260815T182818+0000

Ratings and Alerts

No rating or validation information has been found for OpenCell.

No alerts have been found for OpenCell.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Gribkova AK, et al. (2026) (Re)defining the human chromatome: an integrated meta-analysis of localization, function, abundance, physical properties, and domain composition of chromatin proteins. Nucleic acids research, 54(2).

Monziani A, et al. (2025) BAHCC1 promotes gene expression in neuronal cells by antagonizing SIN3A-HDAC1. Nucleic acids research, 53(14).

Schaffer LV, et al. (2025) Unifying proteomic technologies with ProteinProjector. Bioinformatics advances, 5(1), vbaf266.

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1 charts the structural landscape of human early endosome complexes. Nature, 643(8070), 252.

Ricci MMC, et al. (2024) Actin-binding protein profilin1 is an important determinant of cellular phosphoinositide control. The Journal of biological chemistry, 300(1), 105583.

Carr A, et al. (2024) AI: A transformative opportunity in cell biology. Molecular biology of the cell, 35(12), pe4.

Uhlmann V, et al. (2024) Making the most of bioimaging data through interdisciplinary interactions. Journal of cell science, 137(20).

Tateno K, et al. (2024) Different molecular recognition by three domains of the full-length GRB2 to SOS1 proline-rich motifs and EGFR phosphorylated sites. Chemical science, 15(38), 15858.

Hagiwara T, et al. (2023) Proteotoxic stresses stimulate dissociation of UBL4A from the tail-anchored protein recognition complex. The Biochemical journal, 480(19), 1583.

Filbeck S, et al. (2022) Ribosome-associated quality-control mechanisms from bacteria to humans. Molecular cell, 82(8), 1451.

Baldus M, et al. (2022) Biological solid-state NMR: Integrative across different scientific disciplines. Journal of structural biology: X, 6, 100075.

Kobayashi H, et al. (2022) Self-supervised deep learning encodes high-resolution features of protein subcellular localization. Nature methods, 19(8), 995.