Resource Summary Report

Generated by RRID on Apr 14, 2025

pFind Studio: pLink

RRID:SCR_000084
Type: Tool

Proper Citation

pFind Studio: pLink (RRID:SCR_000084)

Resource Information

URL: http://pfind.ict.ac.cn/software/pLink/index.html

Proper Citation: pFind Studio: pLink (RRID:SCR_000084)

Description: Software dedicated for the analysis of chemically cross-linked proteins or protein complexes using mass spectrometry.

Abbreviations: pLink

Synonyms: , pLink, pLink (pFind Studio), pLink2

Resource Type: software resource

Defining Citation: PMID:22772728

Keywords: mass spectrometry, proteomics, pFind Studio, bio.tools

Funding:

Availability: Free, Public

Resource Name: pFind Studio: pLink

Resource ID: SCR_000084

Alternate IDs: OMICS_02404, biotools:pLink-2

Alternate URLs: https://bio.tools/pLink-2

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250410T064509+0000

Ratings and Alerts

No rating or validation information has been found for pFind Studio: pLink.

No alerts have been found for pFind Studio: pLink.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Vergara-Cruces Á, et al. (2024) Structure of the plant plastid-encoded RNA polymerase. Cell, 187(5), 1145.

Wu XX, et al. (2024) Cryo-EM structures of the plant plastid-encoded RNA polymerase. Cell, 187(5), 1127.

Ballmer D, et al. (2024) Dynamic localization of the chromosomal passenger complex in trypanosomes is controlled by the orphan kinesins KIN-A and KIN-B. eLife, 13.

Oh J, et al. (2024) A dual role of the conserved PEX19 helix in safeguarding peroxisomal membrane proteins. iScience, 27(4), 109537.

Jin Z, et al. (2022) Structure of a TOC-TIC supercomplex spanning two chloroplast envelope membranes. Cell, 185(25), 4788.

Lu S, et al. (2018) Mapping disulfide bonds from sub-micrograms of purified proteins or micrograms of complex protein mixtures. Biophysics reports, 4(2), 68.

Wang Y, et al. (2018) Solution structure of extracellular loop of human ?4 subunit of BK channel and its biological implication on ChTX sensitivity. Scientific reports, 8(1), 4571.

Wei Y, et al. (2017) SUMO-Targeted DNA Translocase Rrp2 Protects the Genome from Top2-Induced DNA Damage. Molecular cell, 66(5), 581.

Bertram K, et al. (2017) Cryo-EM Structure of a Pre-catalytic Human Spliceosome Primed for Activation. Cell, 170(4), 701.

Schmidt C, et al. (2017) Acetylation and phosphorylation control both local and global

stability of the chloroplast F1 ATP synthase. Scientific reports, 7, 44068.

Hillen HS, et al. (2017) Mechanism of Transcription Anti-termination in Human Mitochondria. Cell, 171(5), 1082.

Gorasia DG, et al. (2016) Structural Insights into the PorK and PorN Components of the Porphyromonas gingivalis Type IX Secretion System. PLoS pathogens, 12(8), e1005820.

Trahan C, et al. (2016) Targeted cross-linking-mass spectrometry determines vicinal interactomes within heterogeneous RNP complexes. Nucleic acids research, 44(3), 1354.

Fernandez-Martinez J, et al. (2016) Structure and Function of the Nuclear Pore Complex Cytoplasmic mRNA Export Platform. Cell, 167(5), 1215.