

# Resource Summary Report

Generated by [kravitz2](#) on Sep 17, 2026

## piNET

RRID:SCR\_018693

Type: Tool

---

### Proper Citation

piNET (RRID:SCR\_018693)

---

### Resource Information

**URL:** <http://pinet-server.org>

**Proper Citation:** piNET (RRID:SCR\_018693)

**Description:** Web platform for downstream analysis and visualization of proteomics data. Server that facilitates integrated annotation, analysis and visualization of quantitative proteomics data, with emphasis on PTM networks and integration with LINCS library of chemical and genetic perturbation signatures in order to provide further mechanistic and functional insights. Primary input for server consists of set of peptides or proteins, optionally with PTM sites, and their corresponding abundance values.

**Resource Type:** analysis service resource, data access protocol, production service resource, service resource, software resource, web service

**Defining Citation:** [DOI:10.1093/nar/gkaa436](https://doi.org/10.1093/nar/gkaa436)

**Keywords:** Analysis, visualization, proteomics data, integrated annotation, quantitative proteomics data, PTM network, LINCS library integration, genetic perturbation signature, peptide, protein, post translational modification site, PTM site, data

**Funding:** NCATS UL1 TR001425;  
NCI T32 CA236764;  
NHLBI U54 HL127624;  
NIEHS P30 ES006096;  
NIGMS U01 GM120953;  
NIMH R01 MH107487

**Availability:** Free, Freely available

**Resource Name:** piNET

**Resource ID:** SCR\_018693

**Record Creation Time:** 20220129T080341+0000

**Record Last Update:** 20260912T195904+0000

---

## Ratings and Alerts

No rating or validation information has been found for piNET.

No alerts have been found for piNET.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Yang L, et al. (2023) From single- to multi-omics: future research trends in medicinal plants. Briefings in bioinformatics, 24(1).

Liu X, et al. (2022) ExpressVis: a biologist-oriented interactive web server for exploring multi-omics data. Nucleic acids research, 50(W1), W312.

Shamsaei B, et al. (2020) piNET: a versatile web platform for downstream analysis and visualization of proteomics data. Nucleic acids research, 48(W1), W85.

Dowling P, et al. (2020) Protocol for the Bottom-Up Proteomic Analysis of Mouse Spleen. STAR protocols, 1(3), 100196.