

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

## PEPPER

RRID:SCR\_000431

Type: Tool

### Proper Citation

PEPPER (RRID:SCR\_000431)

### Resource Information

**URL:** <http://apps.cytoscape.org/apps/pepper>

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**Description:** A Cytoscape app designed to identify protein pathways / complexes as densely connected subnetworks from seed lists of proteins derived from pull-down assays (i.e AP-MS...).

**Abbreviations:** PEPPER

**Synonyms:** Protein complex Expansion using Protein-Protein intERaction networks, Protein complex Expansion using Protein-Protein intERactions

**Resource Type:** software resource, software application

**Defining Citation:** [PMID:25138169](#)

**Keywords:** plugin, protein-protein interaction, network, bio.tools

**Availability:** Free, Available for download, Freely available

**Resource Name:** PEPPER

**Resource ID:** SCR\_000431

**Alternate IDs:** biotools:pepper, OMICS\_05485

**Alternate URLs:** <https://bio.tools/pepper>

**Record Creation Time:** 20220129T080201+0000

**Record Last Update:** 20260808T190437+0000

### Ratings and Alerts

No rating or validation information has been found for PEPPER.

No alerts have been found for PEPPER.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Wang YS, et al. (2024) Chromosome-level genome assemblies of two littorinid marine snails indicate genetic basis of intertidal adaptation and ancient karyotype evolved from bilaterian ancestors. GigaScience, 13.