

Resource Summary Report

Generated by [dkNET](#) on Sep 11, 2026

Arpeggio

RRID:SCR_010876

Type: Tool

Proper Citation

Arpeggio (RRID:SCR_010876)

Resource Information

URL: <http://sourceforge.net/p/arpeggio/wiki/Home/>

Proper Citation: Arpeggio (RRID:SCR_010876)

Description: Software for harmonic compression of ChIP-seq data reveals protein-chromatin interaction signatures.

Abbreviations: Arpeggio

Synonyms: Arpeggio - Harmonic analysis of ChIP-seq experiments

Resource Type: software resource

Defining Citation: [PMID:23873955](#)

Resource Name: Arpeggio

Resource ID: SCR_010876

Alternate IDs: OMICS_00476

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260905T132649+0000

Ratings and Alerts

No rating or validation information has been found for Arpeggio.

No alerts have been found for Arpeggio.

Data and Source Information

Usage and Citation Metrics

We found 83 mentions in open access literature.

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

Zhang W, et al. (2026) Deciphering DEL pocket patterns through contrastive learning. Nature communications, 17(1).

Caballero-Méndez LC, et al. (2026) Evaluation of Colombian silk fibroin hydrogels functionalized with recombinant LSEctin for intervertebral disc tissue engineering. PloS one, 21(5), e0349634.

Gu C, et al. (2026) CTMP-REV7 axis modulates MHC-I antigen presentation via CDK1-AKT crosstalk in MSI-L/MSS colorectal cancer. Cellular oncology (Dordrecht, Netherlands), 49(3).

Porav SA, et al. (2026) (-)-Englerin A binding to human TRPC5 exposes an aromatic interaction network in channel activation. Nature communications, 17(1).

You Y, et al. (2026) Zinc ions attenuates iridovirus infection through regulation of ferroptosis pathways. Cell death discovery, 12(1).

Ogawa C, et al. (2026) Phosphorylation of Runx protein controls helper CD4+ T cell versus cytotoxic CD8+ T cell lineage choice. Nature immunology, 27(4), 799.

Gordon GL, et al. (2026) Characterising nanobody developability to improve therapeutic design using the Therapeutic Nanobody Profiler. Communications biology, 9(1).

Utichi M, et al. (2026) Role of N-glycosylation as a determinant of ATG9A conformations and activity. Protein science : a publication of the Protein Society, 35(1), e70390.

Arnaudi M, et al. (2026) MAVISp: A modular structure-based framework for protein variant effects. Protein science : a publication of the Protein Society, 35(5), e70548.

He M, et al. (2026) AID and TET2 cooperate to demethylate Irf4 for plasma cell fate in germinal center B cells. The Journal of experimental medicine, 223(6).

Kabinger F, et al. (2025) Structural basis of SARS-CoV-2 polymerase inhibition by nonnucleoside inhibitor HeE1-2Tyr. Proceedings of the National Academy of Sciences of the United States of America, 122(10), e2419854122.

Zhang Y, et al. (2025) Systematic evaluation of predictors for binding free energy changes upon mutations in protein complexes. Briefings in bioinformatics, 26(6).

Redfern-Nichols T, et al. (2025) Loss-of-function Gs rare disease variants exert mutation-specific effects on GPCR signaling. Science signaling, 18(887), eado7543.

Conrad RJ, et al. (2025) NRF2 supports non-small cell lung cancer growth independently of CBP/p300-enhanced glutathione synthesis. *EMBO reports*, 26(12), 3106.

Sanchez Rocha AC, et al. (2025) Coenzyme-protein interactions since early life. *eLife*, 13.

Rahbar MR, et al. (2025) Stability and functional consequences of disulfide bond engineering in *Aspergillus flavus* uricase. *Scientific reports*, 15(1), 18419.

Waich S, et al. (2025) Altered chaperone-nonmuscle myosin II interactions drive pathogenicity of the UNC45A c.710T>C variant in osteo-oto-hepato-enteric syndrome. *JCI insight*, 10(6).

Smith CJ, et al. (2025) Drug resistance-associated mutations in *Plasmodium* UBP-1 disrupt its essential deubiquitinating activity. *The Journal of biological chemistry*, 301(3), 108266.

Jiang W, et al. (2025) Fibromodulin selectively accelerates myofibroblast apoptosis in cutaneous wounds by enhancing interleukin 1 β signaling. *Nature communications*, 16(1), 3499.

Zhou PJ, et al. (2025) LDLR variant classification through activity-normalized prime editing screening. *bioRxiv : the preprint server for biology*.