

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 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: 20260801T190417+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 73 mentions in open access literature.

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

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.

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).

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.

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

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

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? signaling. *Nature communications*, 16(1), 3499.

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

Serghini A, et al. (2024) Characterizing and predicting ccRCC-causing missense mutations in Von Hippel-Lindau disease. *Human molecular genetics*, 33(3), 224.

Kandoor A, et al. (2024) CoDIAC: A comprehensive approach for interaction analysis reveals novel insights into SH2 domain function and regulation. *bioRxiv : the preprint server for biology*.

Mahmood HR, et al. (2024) Epidemiological trends, antifungal drug susceptibility and SQLE point mutations in etiologic species of human dermatophytosis in Al-Diwaneyah, Iraq. *Scientific reports*, 14(1), 12669.

Smorodina E, et al. (2024) Computational engineering of water-soluble human potassium ion channels through QTY transformation. *Scientific reports*, 14(1), 28159.

de Abreu AP, et al. (2024) An Approach for Engineering Peptides for Competitive Inhibition of the SARS-COV-2 Spike Protein. *Molecules (Basel, Switzerland)*, 29(7).

Tahir A, et al. (2024) Structure-guided computational insecticide discovery targeting β -N-acetyl-D-hexosaminidase of *Ostrinia furnacalis*. *Journal of biomolecular structure & dynamics*, 42(21), 11717.

Schulte T, et al. (2024) Helical superstructures between amyloid and collagen in cardiac fibrils from a patient with AL amyloidosis. *Nature communications*, 15(1), 6359.

Bashour H, et al. (2024) Biophysical cartography of the native and human-engineered antibody landscapes quantifies the plasticity of antibody developability. *Communications biology*, 7(1), 922.

Ling Y, et al. (2024) Exploration of the biological mechanisms of CENPA as an oncogene in glioma: Screening based on cancer functional status. *Journal of cellular and molecular medicine*, 28(23), e70181.

Pan Q, et al. (2024) AlzDiscovery: A computational tool to identify Alzheimer's disease-causing missense mutations using protein structure information. *Protein science : a publication of the Protein Society*, 33(10), e5147.