Resource Summary Report

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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

Funding:

Resource Name: Arpeggio

Resource ID: SCR_010876

Alternate IDs: OMICS_00476

Record Creation Time: 20220129T080301+0000

Record Last Update: 20250410T070027+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 63 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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).

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.

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

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

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.

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

Zhou Y, et al. (2024) DDMut-PPI: predicting effects of mutations on protein-protein interactions using graph-based deep learning. Nucleic acids research, 52(W1), W207.

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.

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.

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.

Ryu J, et al. (2023) Joint genotypic and phenotypic outcome modeling improves base editing variant effect quantification. medRxiv : the preprint server for health sciences.

Çiftci N, et al. (2023) Clinical Characteristics and Genetic Analyses of Patients with Idiopathic Hypogonadotropic Hypogonadism. Journal of clinical research in pediatric endocrinology, 15(2), 160.

Vales S, et al. (2023) Discovery and pharmacophoric characterization of chemokine network inhibitors using phage-display, saturation mutagenesis and computational modelling. Nature communications, 14(1), 5763.

Zhou Y, et al. (2023) DDMut: predicting effects of mutations on protein stability using deep learning. Nucleic acids research, 51(W1), W122.

Pan Q, et al. (2023) Characterization on the oncogenic effect of the missense mutations of p53 via machine learning. Briefings in bioinformatics, 25(1).

Ejaz S, et al. (2023) Antibody designing against IIIabc junction (JIIIabc) of HCV IRES through affinity maturation; RNA-Antibody docking and interaction analysis. PloS one, 18(9), e0291213.

MacGowan SA, et al. (2022) Missense variants in human ACE2 strongly affect binding to SARS-CoV-2 Spike providing a mechanism for ACE2 mediated genetic risk in Covid-19: A case study in affinity predictions of interface variants. PLoS computational biology, 18(3), e1009922.

Periwal N, et al. (2022) In silico characterization of mutations circulating in SARS-CoV-2 structural proteins. Journal of biomolecular structure & dynamics, 40(18), 8216.

Ahsan T, et al. (2022) Missense variants in the TNFA epitopes and their effects on interaction with therapeutic antibodies-in silico analysis. Journal, genetic engineering & biotechnology, 20(1), 7.