

Resource Summary Report

Generated by [Kravitz](#) on Sep 13, 2026

Voronoia

RRID:SCR_006005

Type: Tool

Proper Citation

Voronoia (RRID:SCR_006005)

Resource Information

URL: <http://bioinformatics.charite.de/voronoia/>

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Description: Voronoia is a program suite to analyse and visualize the atomic packing of protein structures. It is based on the Voronoi Cell method and can be used to estimate the quality of a protein structure, e.g. by comparing the packing density of buried atoms to a reference data set or by highlighting protein regions with large packing defects. Voronoia is also targeted to detect locations of putative internal water or binding sites for ligands. Accordingly, Voronoia is beneficial for a broad range of protein structure approaches. It is applicable as a standalone version coming with a user friendly GUI or, alternatively, as a Pymol Plugin. Finally, Voronoia is also available as an easy to use webtool to process user defined PDB-files or to asses precalculated packing files from DOPP, the regularly updated Dictionary of Packing in Proteins.

Synonyms: Voronoia

Resource Type: data or information resource, database, software resource, software toolkit

Resource Name: Voronoia

Resource ID: SCR_006005

Alternate IDs: nif-0000-03641

Old URLs: <http://141.42.202.21/voronoia/index.php>

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260912T195634+0000

Ratings and Alerts

No rating or validation information has been found for Voronoia.

No alerts have been found for Voronoia.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Wasilewski T, et al. (2026) Enhancing the Detection of Long-Chain Aldehydes by Peptide-Based Biosensors Through Counter-Ion Exchange. *Biosensors*, 16(3).

Flores-Lagunes L, et al. (2024) First family with Perry syndrome from Mexico. *Biomedical reports*, 21(2), 120.

Philipp M, et al. (2024) MUTATIONEXPLORER- A WEBSERVER FOR MUTATION OF PROTEINS AND 3D VISUALIZATION OF ENERGETIC IMPACTS. *bioRxiv : the preprint server for biology*.

Dhara P, et al. (2024) Influence of protein nativity on the stability of bovine serum albumin coated microbubbles. *iScience*, 27(3), 109286.

Kim S, et al. (2024) Hidden route of protein damage through oxygen-confined photooxidation. *Nature communications*, 15(1), 10873.

Chakraborty C, et al. (2022) Structural Landscape of nsp Coding Genomic Regions of SARS-CoV-2-ssRNA Genome: A Structural Genomics Approach Toward Identification of Druggable Genome, Ligand-Binding Pockets, and Structure-Based Druggability. *Molecular biotechnology*, 1.

Staritzbichler R, et al. (2021) Voronoia 4-ever. *Nucleic acids research*, 49(W1), W685.

Chakraborti S, et al. (2021) 'All That Glitters Is Not Gold': High-Resolution Crystal Structures of Ligand-Protein Complexes Need Not Always Represent Confident Binding Poses. *International journal of molecular sciences*, 22(13).

Percival CJ, et al. (2017) The Interaction of Genetic Background and Mutational Effects in Regulation of Mouse Craniofacial Shape. *G3 (Bethesda, Md.)*, 7(5), 1439.

Ayres CM, et al. (2016) Differential utilization of binding loop flexibility in T cell receptor ligand selection and cross-reactivity. *Scientific reports*, 6, 25070.