Resource Summary Report

Generated by Kravitz on Sep 10, 2026

Edtsurf

RRID:SCR_016083
Type: Tool

Proper Citation

Edtsurf (RRID:SCR_016083)

Resource Information

URL: http://zhanglab.ccmb.med.umich.edu/EDTSurf/

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Description: Software that constructs triangulated surfaces for macromolecules. It generates three major macromolecular surfaces: van der Waals surface, solvent-accessible surface and molecular surface (solvent-excluded surface) and also identifies cavities which are inside of macromolecules. Used in accurate calculation of protein surfaces in the protein structural and functional studies including ligand-protein docking and virtual screening.

Synonyms: EDTSurf: Quick and accurate construction of macromolecular surfaces

Resource Type: data processing software, data visualization software, software application, software resource, source code

Defining Citation: PMID:19956577

Keywords: construct, triangulate, surface, macromolecule, van der Waals, solvent, accessible, molecular, cavities, program

Funding: NIGMS GM083107;
NIGMS GM084222;
NSF 0746198;
the Alfred P. Sloan Foundation

Availability: Free, Available for download, Freely available

Resource Name: Edtsurf

Resource ID: SCR_016083

Alternate IDs: OMICS_16795

Alternate URLs: https://sources.debian.org/src/edtsurf/

License: Apache 2.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260905T132803+0000

Ratings and Alerts

No rating or validation information has been found for Edtsurf.

No alerts have been found for Edtsurf.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at Kravitz .

Maksymenko K, et al. (2025) A Complementarity-Based Approach to De Novo Binder Design. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(33), e02015.

Liao KJ, et al. (2025) Using AlphaFold and Symmetrical Docking to Predict Protein-Protein Interactions for Exploring Potential Crystallization Conditions. Proteins, 93(10), 1747.

Machat M, et al. (2021) Comparative evaluation of shape retrieval methods on macromolecular surfaces: an application of computer vision methods in structural bioinformatics. Bioinformatics (Oxford, England), 37(23), 4375.

Gui S, et al. (2018) Frontiers in biomolecular mesh generation and molecular visualization systems. Visual computing for industry, biomedicine, and art, 1(1), 7.