

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

Edtsurf

RRID:SCR_016083

Type: Tool

Proper Citation

Edtsurf (RRID:SCR_016083)

Resource Information

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

Proper Citation: Edtsurf (RRID:SCR_016083)

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 visualization software, source code, software application, data processing software, software resource

Defining Citation: [PMID:19956577](#)

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

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

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: 20260801T190525+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 [RRID](#) .

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

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

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.