

# Resource Summary Report

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## 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:** 20260821T194101+0000

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## Ratings and Alerts

No rating or validation information has been found for Edtsurf.

No alerts have been found for Edtsurf.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

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.