

# Resource Summary Report

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## TOPSAN

RRID:SCR\_005758

Type: Tool

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### Proper Citation

TOPSAN (RRID:SCR\_005758)

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### Resource Information

**URL:** <http://www.topsan.org/>

**Proper Citation:** TOPSAN (RRID:SCR\_005758)

**Description:** Collect, share, and distribute information about protein three-dimensional structures. It serves as a portal for the scientific community to learn about protein structures solved by SG centers, and also to contribute their expertise in annotating protein function. The premise of the TOPSAN project is that, no matter how much any individual knows about a particular protein, there are other members of the scientific community who know more about certain aspects of the same protein, and that the collective analyses from experts will be far more informative than any local group, let alone individual, could contribute. They believe that, if the members of the biological community are given the opportunity, authorship incentives, and an easy way to contribute their knowledge to the structure annotation, they would do so. Therefore, borrowing elements from successful, distributed, collaborative projects, such as Wikipedia (the free encyclopedia anyone can edit) and from other open source software development projects, TOPSAN will be a broad, collaborative effort to annotate protein structures, initially, those determined at the JCSG. They believe that the annotation of proteins solved by structural genomics consortia offers a unique opportunity to challenge the extant paradigm of how biological data is collected and distributed, and to connect structural genomics and structural biology to the entire biological research community. TOPSAN is designed to be scalable, modular and extensible. Furthermore, it is intended to be immediately useful in a simplistic way and will accommodate incremental improvements to functionality as usage becomes more sophisticated. Their annotation pages will offer the end user a combination of automatically generated as well as expert-curated annotations of protein structures. They will use available technology to increase the speed and granularity of the exchange of scientific ideas, and use incentive mechanisms that will encourage collaborative participation.

**Abbreviations:** TOPSAN

**Synonyms:** he Open Protein Structure Annotation Network, TOPSAN Project, TOPSAN - The Open Protein Structure Annotation Network

**Resource Type:** data or information resource, data repository, image collection, database, storage service resource, service resource

**Defining Citation:** [PMID:20961957](#), [PMID:20716366](#), [PMID:20944203](#), [PMID:20961957](#)

**Keywords:** protein, structure, 3d, protein structure, protein function, annotate, crowd sourcing, image, annotation, genomics, collaboration

**Funding:** NIGMS U54 GM074898;  
NIGMS P20 GM076221

**Availability:** Creative Commons Attribution v3 License, The community can contribute to this resource

**Resource Name:** TOPSAN

**Resource ID:** SCR\_005758

**Alternate IDs:** nlx\_149221

**Record Creation Time:** 20220129T080232+0000

**Record Last Update:** 20260806T054420+0000

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## Ratings and Alerts

No rating or validation information has been found for TOPSAN.

No alerts have been found for TOPSAN.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Tanoli Z, et al. (2021) Exploration of databases and methods supporting drug repurposing: a comprehensive survey. Briefings in bioinformatics, 22(2), 1656.

Kumar R, et al. (2019) Exploring the new horizons of drug repurposing: A vital tool for turning hard work into smart work. European journal of medicinal chemistry, 182, 111602.

Gray C, et al. (2015) Known structure, unknown function: An inquiry-based undergraduate biochemistry laboratory course. Biochemistry and molecular biology education : a

bimonthly publication of the International Union of Biochemistry and Molecular Biology, 43(4), 245.

Seiler CY, et al. (2014) DNASU plasmid and PSI: Biology-Materials repositories: resources to accelerate biological research. *Nucleic acids research*, 42(Database issue), D1253.

Farelli JD, et al. (2014) Structure of the trehalose-6-phosphate phosphatase from *Brugia malayi* reveals key design principles for anthelmintic drugs. *PLoS pathogens*, 10(7), e1004245.

Krishna SS, et al. (2010) TOPSAN: use of a collaborative environment for annotating, analyzing and disseminating data on JCSG and PSI structures. *Acta crystallographica. Section F, Structural biology and crystallization communications*, 66(Pt 10), 1143.

Weekes D, et al. (2010) TOPSAN: a collaborative annotation environment for structural genomics. *BMC bioinformatics*, 11, 426.

Kumar A, et al. (2010) Ligands in PSI structures. *Acta crystallographica. Section F, Structural biology and crystallization communications*, 66(Pt 10), 1309.

Elslinger MA, et al. (2010) The JCSG high-throughput structural biology pipeline. *Acta crystallographica. Section F, Structural biology and crystallization communications*, 66(Pt 10), 1137.

Hodis E, et al. (2008) Proteopedia - a scientific 'wiki' bridging the rift between three-dimensional structure and function of biomacromolecules. *Genome biology*, 9(8), R121.