

# Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

## PASSer

RRID:SCR\_027790

Type: Tool

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### Proper Citation

PASSer (RRID:SCR\_027790)

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### Resource Information

**URL:** <https://passer.smu.edu/>

**Proper Citation:** PASSer (RRID:SCR\_027790)

**Description:** Web allosteric site prediction tool. Web server designed for prediction and visualization of protein allosteric sites, which are crucial locations on proteins for regulating their function and key targets for drug development. Helps researchers identify these regulatory sites on proteins, supporting efforts in allosteric drug discovery by analyzing protein structures from Protein Data Bank.

**Synonyms:** Protein Allosteric Sites Server

**Resource Type:** data access protocol, software resource, web application, web service

**Keywords:** allosteric site prediction, identify regulatory sites, identify regulatory sites on proteins, proteins, allosteric drug discovery, analyzing protein structures,

**Availability:** Free, Freely available

**Resource Name:** PASSer

**Resource ID:** SCR\_027790

**Record Creation Time:** 20251216T055148+0000

**Record Last Update:** 20260904T001149+0000

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### Ratings and Alerts

No rating or validation information has been found for PASSer.

No alerts have been found for PASSer.

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### Data and Source Information

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

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Yadalam PK, et al. (2023) Prediction of Druggable Allosteric Sites of Undruggable Multidrug Resistance Efflux Pump P. Gingivalis Proteins. Biomedical engineering and computational biology, 14, 11795972231202394.

Zhao H, et al. (2022) Virtual screening and molecular dynamics simulation for identification of natural antiviral agents targeting SARS-CoV-2 NSP10. Biochemical and biophysical research communications, 626, 114.

Faisal S, et al. (2022) Identification and Inhibition of the Druggable Allosteric Site of SARS-CoV-2 NSP10/NSP16 Methyltransferase through Computational Approaches. Molecules (Basel, Switzerland), 27(16).