

# Resource Summary Report

Generated by SPARC SAWG on Aug 10, 2026

## LIGand Attachment SITE Database

RRID:SCR\_013172

Type: Tool

### Proper Citation

LIGand Attachment SITE Database (RRID:SCR\_013172)

### Resource Information

**URL:** <http://www.scmdbb.ulb.ac.be/Users/benoit/LigASite>

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**Description:** A gold-standard dataset of biologically relevant binding sites in protein structures. It consists of proteins with one unbound structure and at least one structure of the protein-ligand complex. Both a redundant and a non-redundant (sequence identity lower than 25) version is available. Quaternary structures proposed by PQS (2) are used for all structures in the dataset. The availability of both unbound and bound structures for each protein guarantees that our dataset can be used to benchmark binding site prediction methods, in conditions that mimic cases where the binding site is truly unknown. In cases where several different bound structures are available for a given protein, all are used to define the binding sites.

**Synonyms:** LigASite

**Resource Type:** database, data or information resource

**Resource Name:** LIGand Attachment SITE Database

**Resource ID:** SCR\_013172

**Alternate IDs:** nif-0000-03083

**Record Creation Time:** 20220129T080314+0000

**Record Last Update:** 20260808T190425+0000

### Ratings and Alerts

No rating or validation information has been found for LIGand Attachment SITE Database.

No alerts have been found for LIGand Attachment SITE Database.

## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Tsujikawa H, et al. (2016) Development of a protein-ligand-binding site prediction method based on interaction energy and sequence conservation. Journal of structural and functional genomics, 17(2-3), 39.

Hu X, et al. (2016) Protein ligand-specific binding residue predictions by an ensemble classifier. BMC bioinformatics, 17(1), 470.