

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

Structural Antibody Database

RRID:SCR_022096

Type: Tool

Proper Citation

Structural Antibody Database (RRID:SCR_022096)

Resource Information

URL: <http://opig.stats.ox.ac.uk/webapps/newsabdab/sabdab/>

Proper Citation: Structural Antibody Database (RRID:SCR_022096)

Description: Database containing all antibody structures available in the PDB, annotated and presented in consistent fashion. Each structure is annotated with number of properties including experimental details, antibody nomenclature (e.g. heavy-light pairings), curated affinity data and sequence annotations. You can use the database to inspect individual structures, create and download datasets for analysis, search the database for structures with similar sequences to your query, monitor the known structural repertoire of antibodies.

Abbreviations: SAbDab

Resource Type: data or information resource, database

Defining Citation: [DOI:10.1093/nar/gkt1043](https://doi.org/10.1093/nar/gkt1043)

Keywords: antibody structure, annotated structure, Protein Data Bank

Funding: Engineering and Physical Sciences Research Council ;
Roche GmbH ;
UCB Pharma

Availability: Free, Freely available

Resource Name: Structural Antibody Database

Resource ID: SCR_022096

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260905T133218+0000

Ratings and Alerts

No rating or validation information has been found for Structural Antibody Database .

No alerts have been found for Structural Antibody Database .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Mokhtari O, et al. (2026) DynaRepo: the repository of macromolecular conformational dynamics. Nucleic acids research, 54(D1), D393.

Dreyer FA, et al. (2026) Conformation-aware structure prediction of antigen-recognizing immune proteins. mAbs, 18(1), 2602217.

Czerwiński A, et al. (2026) ASD: antigen-specific antibody database. mAbs, 18(1), 2623330.

Shrock EL, et al. (2026) Systems-Scale Structural Modeling Reveals the Germline Architecture of Immunodominance. bioRxiv : the preprint server for biology.

Gordon GL, et al. (2025) PLaBAb-nano: a database of camelid and shark nanobodies from patents and literature. Nucleic acids research, 53(D1), D535.

Loreti G, et al. (2025) Delineating SARS-CoV-2 spike protein and antibodies interaction interfaces via siamese neural networks: A geometric and image-based analysis. PloS one, 20(11), e0335270.

Hu J, et al. (2025) RLEAAI: improving antibody-antigen interaction prediction using protein language model and sequence order information. Briefings in bioinformatics, 26(3).

Shrestha P, et al. (2025) NanoBinder: a machine learning assisted nanobody binding prediction tool using Rosetta energy scores. Journal of cheminformatics, 17(1), 96.

Joubbi S, et al. (2025) Enhancing antibody-antigen interaction prediction with atomic flexibility. PLoS computational biology, 21(10), e1013576.

Wu F, et al. (2025) De novo design of epitope-specific antibodies via a structure-driven computational workflow. Nature communications, 17(1), 625.

Atkinson T, et al. (2025) Protein sequence modelling with Bayesian flow networks. Nature communications, 16(1), 3197.

Wang X, et al. (2025) NanoAbLLaMA: construction of nanobody libraries with protein large language models. Frontiers in chemistry, 13, 1545136.

Baselga M, et al. (2025) Species-Dependent Structural Variations in Single-Domain Antibodies. *Antibodies* (Basel, Switzerland), 14(4).

Xie J, et al. (2025) DeepProtein: deep learning library and benchmark for protein sequence learning. *Bioinformatics* (Oxford, England), 41(10).

Seidler CA, et al. (2025) Data-driven analyses of human antibody variable domain germlines: pairings, sequences and structural features. *mAbs*, 17(1), 2507950.

Lee M, et al. (2024) HIV-1-envelope trimer transitions from prefusion-closed to CD4-bound-open conformations through an occluded-intermediate state. *Computational and structural biotechnology journal*, 23, 4192.

Wang X, et al. (2024) WUREN: Whole-modal union representation for epitope prediction. *Computational and structural biotechnology journal*, 23, 2122.

Abanades B, et al. (2024) The Patent and Literature Antibody Database (PLAbDab): an evolving reference set of functionally diverse, literature-annotated antibody sequences and structures. *Nucleic acids research*, 52(D1), D545.

Zheng F, et al. (2024) Systematic investigation of machine learning on limited data: A study on predicting protein-protein binding strength. *Computational and structural biotechnology journal*, 23, 460.

Zhao N, et al. (2024) ABAG-docking benchmark: a non-redundant structure benchmark dataset for antibody-antigen computational docking. *Briefings in bioinformatics*, 25(2).