Resource Summary Report

Generated by ASWG on Aug 2, 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/

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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 repetoire of antibodies.

Abbreviations: SAbDab

Resource Type: data or information resource, database

Defining Citation: DOI:10.1093/nar/gkt1043

Keywords: antibody structure, annotated structure, Protein Data Bank

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

Availability: Free, Freely available

Resource Name: Structural Antibody Database

Resource ID: SCR_022096

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260801T191024+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 33 mentions in open access literature.

Listed below are recent publications. The full list is available at ASWG .

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

Gordon GL, et al. (2025) PLAbDab-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.

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).

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

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

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

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.

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).

Chen H, et al. (2024) Accurate prediction of CDR-H3 loop structures of antibodies with deep learning. eLife, 12.

Rossmueller G, et al. (2024) Integrating In Silico and In Vitro Tools for Optimized Antibody Development-Design of Therapeutic Anti-oxMIF Antibodies. Antibodies (Basel, Switzerland), 13(4).

Yi L, et al. (2024) Single-cell 5' RNA sequencing of camelid peripheral B cells provides insights into cellular basis of heavy-chain antibody production. Computational and structural biotechnology journal, 23, 1705.

Liu H, et al. (2024) PPB-Affinity: Protein-Protein Binding Affinity dataset for AI-based protein drug discovery. Scientific data, 11(1), 1316.