

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

Abysis Database

RRID:SCR_000756

Type: Tool

Proper Citation

Abysis Database (RRID:SCR_000756)

Resource Information

URL: <http://www.bioinf.org.uk/abs/>

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Description: A database of antibody structure containing sequences from Kabat, IMGT and the Protein Databank (PDB), as well as structure data from the PDB. It provides search of the sequence data on various criteria and display of results in different formats. For data from the PDB, sequence searches can be combined with structural constraints. For example, one can ask for all the antibodies with a 10-residue Kabat CDR-L1 with a serine at H23 and an arginine within 10A of H36. The site also has software for structure analysis and other information on antibody structure available.

Synonyms: Abysis

Resource Type: data or information resource, database

Keywords: antibody, protein structure, software

Resource Name: Abysis Database

Resource ID: SCR_000756

Alternate IDs: nif-0000-20947

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260905T133112+0000

Ratings and Alerts

No rating or validation information has been found for Abysis Database.

No alerts have been found for Abysis Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Chen F, et al. (2021) Functional convergence of a germline-encoded neutralizing antibody response in rhesus macaques immunized with HCV envelope glycoproteins. *Immunity*, 54(4), 781.

Amon R, et al. (2018) A combined computational-experimental approach to define the structural origin of antibody recognition of sialyl-Tn, a tumor-associated carbohydrate antigen. *Scientific reports*, 8(1), 10786.

He XX, et al. (2018) Humanization of fibroblast growth factor 1 single-chain antibody and validation for its antitumorigenic efficacy in breast cancer and glioma cells. *Journal of cellular and molecular medicine*, 22(6), 3259.

Lhuillier C, et al. (2018) Characterization of neutralizing antibodies reacting with the 213-224 amino-acid segment of human galectin-9. *PloS one*, 13(9), e0202512.

Kim S, et al. (2017) Generation, Diversity Determination, and Application to Antibody Selection of a Human Na⁺/K⁺ ATPase Fab Library. *Molecules and cells*, 40(9), 655.

Avril A, et al. (2015) Isolation of nanomolar scFvs of non-human primate origin, cross-neutralizing botulinum neurotoxins A1 and A2 by targeting their heavy chain. *BMC biotechnology*, 15, 86.

Griffin LM, et al. (2014) Analysis of heavy and light chain sequences of conventional camelid antibodies from *Camelus dromedarius* and *Camelus bactrianus* species. *Journal of immunological methods*, 405, 35.

Li L, et al. (2013) How to use not-always-reliable binding site information in protein-protein docking prediction. *PloS one*, 8(10), e75936.

Bourne Y, et al. (2013) Molecular characterization of monoclonal antibodies that inhibit acetylcholinesterase by targeting the peripheral site and backdoor region. *PloS one*, 8(10), e77226.

Zein CO, et al. (2010) Latest and emerging therapies for primary biliary cirrhosis and primary sclerosing cholangitis. *Current gastroenterology reports*, 12(1), 13.

Dantas-Barbosa C, et al. (2009) Isolation of osteosarcoma-associated human antibodies from a combinatorial Fab phage display library. *Journal of biomedicine & biotechnology*, 2009, 157531.

Rogers J, et al. (2008) Rapid discovery and optimization of therapeutic antibodies against emerging infectious diseases. Protein engineering, design & selection : PEDS, 21(8), 495.

Hong WW, et al. (2007) Enhanced antibody affinity to Japanese encephalitis virus E protein by phage display. Biochemical and biophysical research communications, 356(1), 124.

Schlessinger A, et al. (2006) Epitome: database of structure-inferred antigenic epitopes. Nucleic acids research, 34(Database issue), D777.

Cross SS, et al. (2002) New variation on a theme: structure and mechanism of action of hydrolytic antibody 7F11, an aspartate rich relation of catalytic antibodies 17E8 and 29G11. Journal of immunological methods, 269(1-2), 173.