

Resource Summary Report

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Antibody Prediction Toolbox

RRID:SCR_022094

Type: Tool

Proper Citation

Antibody Prediction Toolbox (RRID:SCR_022094)

Resource Information

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

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Description: Web tool as structure based antibody prediction server. Collection of computational tools that make predictions about properties of antibodies, focusing on their structures. Single platform containing multiple applications which can: number and align sequences; automatically generate antibody variable fragment homology models; annotate such models with estimated accuracy alongside sequence and structural properties including potential developability issues; predict paratope residues; and predict epitope patches on protein antigens.

Abbreviations: SAbPred

Synonyms: The Antibody Prediction Toolbox

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

Defining Citation: [DOI:10.1093/nar/gkw361](https://doi.org/10.1093/nar/gkw361)

Keywords: structure based antibody prediction server, antibody prediction server, antibodies properties prediction

Funding: Engineering and Physical Research council

Availability: Free, Freely available

Resource Name: Antibody Prediction Toolbox

Resource ID: SCR_022094

Record Creation Time: 20220421T050138+0000

Record Last Update: 20260905T132950+0000

Ratings and Alerts

No rating or validation information has been found for Antibody Prediction Toolbox.

No alerts have been found for Antibody Prediction Toolbox.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Zost SJ, et al. (2026) Epitope-focused discovery of SARS-CoV-2 antibodies that potently neutralize Omicron variants. *Nature microbiology*, 11(4), 1113.

Huang J, et al. (2025) CryoEM Structures of Antibodies Elicited by Germline-Targeting HIV MPER Epitope-Scaffolds. *bioRxiv : the preprint server for biology*.

Peng W, et al. (2025) Structural Basis for Postfusion-Specific Binding to the Respiratory Syncytial Virus F Protein by the Canonical Antigenic Site I Antibody 131-2a. *ACS infectious diseases*, 11(8), 2357.

Tang WK, et al. (2024) Multistage protective anti-CeLTOS monoclonal antibodies with cross-species sterile protection against malaria. *Nature communications*, 15(1), 7487.

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).

Mitchell KG, et al. (2023) High-volume hybridoma sequencing on the NeuroMabSeq platform enables efficient generation of recombinant monoclonal antibodies and scFvs for neuroscience research. *Scientific reports*, 13(1), 16200.

Mitchell KG, et al. (2023) NeuroMabSeq: high volume acquisition, processing, and curation of hybridoma sequences and their use in generating recombinant monoclonal antibodies and scFvs for neuroscience research. *bioRxiv : the preprint server for biology*.

Luo M, et al. (2023) Structural insights into broadly neutralizing antibodies elicited by hybrid immunity against SARS-CoV-2. *Emerging microbes & infections*, 12(1), 2146538.

Abanades B, et al. (2023) ImmuneBuilder: Deep-Learning models for predicting the structures of immune proteins. *Communications biology*, 6(1), 575.

Dibrov A, et al. (2022) Molecular dynamics modeling of the *Vibrio cholera* Na⁺-translocating NADH:quinone oxidoreductase NqrB-NqrD subunit interface. *Molecular and cellular biochemistry*, 477(1), 153.

Wong SWK, et al. (2022) Conformational variability of loops in the SARS-CoV-2 spike protein. *Proteins*, 90(3), 691.

Chang MR, et al. (2022) IgG-like bispecific antibodies with potent and synergistic neutralization against circulating SARS-CoV-2 variants of concern. *Nature communications*, 13(1), 5814.

Liu L, et al. (2022) An antibody class with a common CDRH3 motif broadly neutralizes sarbecoviruses. *Science translational medicine*, 14(646), eabn6859.

Gao N, et al. (2022) Development of Neutralization Breadth against Diverse HIV-1 by Increasing Ab-Ag Interface on V2. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 9(15), e2200063.

Doyle MP, et al. (2021) Cooperativity mediated by rationally selected combinations of human monoclonal antibodies targeting the henipavirus receptor binding protein. *Cell reports*, 36(9), 109628.

Moreira M, et al. (2021) A structure-based approach for the development of a bicyclic peptide acting as a miniaturized anti-CD55 antibody. *International journal of biological macromolecules*, 182, 1455.

Cerutti G, et al. (2021) Potent SARS-CoV-2 neutralizing antibodies directed against spike N-terminal domain target a single supersite. *Cell host & microbe*, 29(5), 819.

Ahmad B, et al. (2021) Computational-Driven Epitope Verification and Affinity Maturation of TLR4-Targeting Antibodies. *International journal of molecular sciences*, 22(11).

Cannon DA, et al. (2019) Experimentally guided computational antibody affinity maturation with de novo docking, modelling and rational design. *PLoS computational biology*, 15(5), e1006980.