

Resource Summary Report

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CATNAP

RRID:SCR_016170

Type: Tool

Proper Citation

CATNAP (RRID:SCR_016170)

Resource Information

URL: <https://www.hiv.lanl.gov/catnap>

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Description: Analyze a database of HIV-1 IC50 and IC80 neutralization data from publicly-available sources, in conjunction with HIV-1 Envelope sequences. Access to an extensive databases of information about neutralizing antibodies and viruses used in published neutralization studies. Tool interfaces also allow input and analysis of user data. PMID: 26044712, THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: CATNAP - Compile Analyze and Tally Neutralizing Antibody Panels

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: [PMID:26044712](#)

Keywords: database, analysis,

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CATNAP

Resource ID: SCR_016170

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260912T195836+0000

Ratings and Alerts

No rating or validation information has been found for CATNAP.

No alerts have been found for CATNAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

Sutar J, et al. (2025) Distinct region-specific neutralization profiles of contemporary HIV-1 clade C against best-in-class broadly neutralizing antibodies. *Journal of virology*, 99(6), e0000825.

Roark RS, et al. (2025) Structural and genetic basis of HIV-1 envelope V2 apex recognition by rhesus broadly neutralizing antibodies. *The Journal of experimental medicine*, 222(10).

Saini C, et al. (2025) Personalized MRI-based characterization of subcortical anomalies in Ataxia-Telangiectasia using deep-learning. *PloS one*, 20(8), e0328828.

David-Fung ES, et al. (2025) Defining criteria for broadly neutralizing HIV antibodies. *Frontiers in immunology*, 16, 1624020.

Shimagaki KS, et al. (2025) Predicting viral sensitivity to antibodies using genetic sequences and antibody similarities. *bioRxiv : the preprint server for biology*.

Perez L, et al. (2024) RAIN: a Machine Learning-based identification for HIV-1 bNAbs. *Research square*.

Juraska M, et al. (2024) Prevention efficacy of the broadly neutralizing antibody VRC01 depends on HIV-1 envelope sequence features. *Proceedings of the National Academy of Sciences of the United States of America*, 121(4), e2308942121.

Foglierini M, et al. (2024) RAIN: machine learning-based identification for HIV-1 bNAbs. *Nature communications*, 15(1), 5339.

Igiraneza AB, et al. (2024) Learning patterns of HIV-1 resistance to broadly neutralizing antibodies with reduced subtype bias using multi-task learning. *PLoS computational biology*, 20(11), e1012618.

Bai H, et al. (2024) Contemporary HIV-1 consensus Env with AI-assisted redesigned hypervariable loops promote antibody binding. *Nature communications*, 15(1), 3924.

Williamson BD, et al. (2024) Predicting neutralization susceptibility to combination HIV-1 monoclonal broadly neutralizing antibody regimens. *PloS one*, 19(9), e0310042.

Williamson BD, et al. (2023) Predicting neutralization susceptibility to combination HIV-1 monoclonal broadly neutralizing antibody regimens. *bioRxiv : the preprint server for*

biology.

Hora B, et al. (2023) Neonatal SHIV infection in rhesus macaques elicited heterologous HIV-1-neutralizing antibodies. *Cell reports*, 42(3), 112255.

Williamson BD, et al. (2023) Application of the SLAPNAP statistical learning tool to broadly neutralizing antibody HIV prevention research. *iScience*, 26(9), 107595.

Kreer C, et al. (2023) Probabilities of developing HIV-1 bNAb sequence features in uninfected and chronically infected individuals. *Nature communications*, 14(1), 7137.

Niu J, et al. (2023) Structures and immune recognition of Env trimers from two Asia prevalent HIV-1 CRFs. *Nature communications*, 14(1), 4676.

Waltari E, et al. (2022) AIRRscape: An interactive tool for exploring B-cell receptor repertoires and antibody responses. *PLoS computational biology*, 18(9), e1010052.

Mayer BT, et al. (2022) Optimizing clinical dosing of combination broadly neutralizing antibodies for HIV prevention. *PLoS computational biology*, 18(4), e1010003.

Sahoo A, et al. (2022) Structure-guided changes at the V2 apex of HIV-1 clade C trimer enhance elicitation of autologous neutralizing and broad V1V2-scaffold antibodies. *Cell reports*, 38(9), 110436.

Sutar J, et al. (2021) Geospatial HIV-1 subtype C gp120 sequence diversity and its predicted impact on broadly neutralizing antibody sensitivity. *PloS one*, 16(5), e0251969.