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 resource, software application

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: 20260812T044318+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 dkNET .

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.