Resource Summary Report

Generated by RRID on Aug 2, 2026

IgBLAST

RRID:SCR_002873
Type: Tool

Proper Citation

IgBLAST (RRID:SCR_002873)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/igblast/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE.Documented on January 4,2023. IgBLAST was developed at NCBI to facilitate analysis of immunoglobulin V region sequences in GenBank. In addition to performing a regular BLAST search, IgBLAST has several additional functions: - Reports the germline V, D and J gene matches to the query sequence. - Annotates the immunoglobulin domains (FWR1 through FWR3). - Matches the returned hits (for databases other than germline genes) to the closest germline V genes, making it easier to identify related sequences. - Reveals the V(D)J junction details such as nucleotide homology between the ends of V(D)J segments and N nucleotide insertions. D and J gene reporting is only for nucleotide sequence search and requires a stretch of five or more nucleotide identity between the query and D or J genes. Sponsors: This resource is supported by the National Center for Biotechnology Information, a division of the U.S. National Library of Medicine.

Synonyms: IgBLAST

Resource Type: software resource, software application

Defining Citation: PMID:23671333

Keywords: gene, analysis, domain, homology, immunoglobulin v, nucleotide, sequence, bio.tools

Availability: Free, Freely available

Resource Name: IgBLAST

Resource ID: SCR_002873

Alternate IDs: nif-0000-25554, biotools:igblast, OMICS_06083

Alternate URLs: https://bio.tools/igblast, https://sources.debian.org/src/ncbi-igblast/

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260801T191034+0000

Ratings and Alerts

No rating or validation information has been found for IgBLAST.

No alerts have been found for IgBLAST.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 609 mentions in open access literature.

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

Halfmann PJ, et al. (2025) Multivalent S2 subunit vaccines provide broad protection against Clade 1 sarbecoviruses in female mice. Nature communications, 16(1), 462.

Kochayoo P, et al. (2025) Atypical memory B cells from natural malaria infection produced broadly neutralizing antibodies against Plasmodium vivax variants. PLoS pathogens, 21(1), e1012866.

Hanna SJ, et al. (2025) The Type 1 Diabetes T Cell Receptor and B Cell Receptor Repository in the AIRR Data Commons: a practical guide for access, use and contributions through the Type 1 Diabetes AIRR Consortium. Diabetologia, 68(1), 186.

Ryback AA, et al. (2025) Deep sequencing of BCR heavy chain repertoires in myalgic encephalomyelitis/chronic fatigue syndrome. Frontiers in immunology, 16, 1489312.

Rosenfeld R, et al. (2025) Efficient Identification of Monoclonal Antibodies Against Rift Valley Fever Virus Using High-Throughput Single Lymphocyte Transcriptomics of Immunized Mice. Antibodies (Basel, Switzerland), 14(1).

Siu JHY, et al. (2025) Early lymph node T follicular helper cell signalling hub drives influenza vaccine response in an ancestrally diverse cohort. EBioMedicine, 122, 106036.

Merico D, et al. (2025) Pre-T cell receptor-? immunodeficiency detected exclusively using whole genome sequencing. NPJ genomic medicine, 10(1), 2.

McGrath JJC, et al. (2025) Mutability and hypermutation antagonize immunoglobulin codon optimality. Molecular cell, 85(2), 430.

Çakan E, et al. (2025) CTLA-4 blockade shifts the B cell repertoire toward autoimmunity. The Journal of clinical investigation, 135(22).

Wilbrink R, et al. (2025) B Cell Receptor Repertoire Analysis of the CD21lo B Cell Compartment in Healthy Individuals, Patients With Sjögren's Disease, and Patients With Radiographic Axial Spondyloarthritis. European journal of immunology, 55(2), e202451398.

Chen S, et al. (2025) Combination of spatial transcriptomics analysis and retrospective study reveals liver infection of SARS-COV-2 is associated with clinical outcomes of COVID-19. EBioMedicine, 111, 105517.

Jian F, et al. (2025) Evolving antibody response to SARS-CoV-2 antigenic shift from XBB to JN.1. Nature, 637(8047), 921.

Huang X, et al. (2025) Protocol to isolate broadly neutralizing monoclonal antibodies against SARS-CoV-2 from human B cells. STAR protocols, 7(1), 104275.

Amisaki M, et al. (2025) IL-33-activated ILC2s induce tertiary lymphoid structures in pancreatic cancer. Nature, 638(8052), 1076.

Camus V, et al. (2025) Identification of primary mediastinal B-cell lymphomas with higher clonal dominance and poorer outcome using 5'RACE. Blood advances, 9(1), 101.

Abdullah L, et al. (2025) The endogenous antigen-specific CD8+ T cell repertoire is composed of unbiased and biased clonotypes with differential fate commitments. Immunity, 58(3), 601.

Guthmiller JJ, et al. (2025) Long-lasting B cell convergence to distinct broadly reactive epitopes following vaccination with chimeric influenza virus hemagglutinins. Immunity, 58(4), 980.

Yisimayi A, et al. (2024) Repeated Omicron exposures override ancestral SARS-CoV-2 immune imprinting. Nature, 625(7993), 148.

Balashova D, et al. (2024) Systematic evaluation of B-cell clonal family inference approaches. BMC immunology, 25(1), 13.

Tuan Duong B, et al. (2024) Identification of specific neutralizing antibodies for highly pathogenic avian influenza H5 2.3.4.4b clades to facilitate vaccine design and therapeutics. Emerging microbes & infections, 13(1), 2302106.