

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

IgBLAST

RRID:SCR_002873

Type: Tool

Proper Citation

IgBLAST (RRID:SCR_002873)

Resource Information

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

Proper Citation: IgBLAST (RRID:SCR_002873)

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 application, software resource

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: 20260727T040323+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 [kravitz2](#).

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.

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.

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.

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.

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

Wilbrink R, et al. (2025) B Cell Receptor Repertoire Analysis of the CD21^{lo} 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.

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

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.

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.

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

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.