

# Resource Summary Report

Generated by ASWG on Aug 3, 2026

## MagicBlast

RRID:SCR\_015513

Type: Tool

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### Proper Citation

MagicBlast (RRID:SCR\_015513)

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### Resource Information

**URL:**

[https://www.ncbi.nlm.nih.gov/IEB/ToolBox/CPP\\_DOC/lxr/source/scripts/projects/magicblast/](https://www.ncbi.nlm.nih.gov/IEB/ToolBox/CPP_DOC/lxr/source/scripts/projects/magicblast/)

**Proper Citation:** MagicBlast (RRID:SCR\_015513)

**Description:** Software tool for making a BLAST database from various data structures. It maps large sets of next-generation RNA or DNA sequencing runs against a whole genome or transcriptome.

**Synonyms:** Magic-Blast, Magic - Blast, Magic Blast

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

**Keywords:** blast database, blast, next generation rna sequencing, next generation dna sequencing

**Availability:** Public, Free, Acknowledgement requested, Available for download, Available for LINUX, Available for MacOSX, Available for Windows

**Resource Name:** MagicBlast

**Resource ID:** SCR\_015513

**Alternate URLs:** <https://ncbiinsights.ncbi.nlm.nih.gov/tag/magic-blast/>

**License:** GNU General Public License

**Record Creation Time:** 20220129T080326+0000

**Record Last Update:** 20260803T040707+0000

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### Ratings and Alerts

No rating or validation information has been found for MagicBlast.

No alerts have been found for MagicBlast.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Gleason C, et al. (2025) An integrated approach for the accurate detection of HERV-K HML-2 transcription and protein synthesis. *Nucleic acids research*, 53(2).

Davasaz Tabrizi E, et al. (2025) Bioinformatic strategies in metagenomics of chronic prostatitis. *World journal of urology*, 43(1), 188.

Cochetel N, et al. (2023) A super-pangenome of the North American wild grape species. *Genome biology*, 24(1), 290.

Xu Z, et al. (2022) Metabolism Interactions Promote the Overall Functioning of the Episymbiotic Chemosynthetic Community of *Shinkaia crosnieri* of Cold Seeps. *mSystems*, 7(4), e0032022.

Yoshida M, et al. (2022) Necessity of integrated genomic analysis to establish a designed knock-in mouse from CRISPR-Cas9-induced mutants. *Scientific reports*, 12(1), 20390.

Petit-Marty N, et al. (2021) Natural CO<sub>2</sub> seeps reveal adaptive potential to ocean acidification in fish. *Evolutionary applications*, 14(7), 1794.

Cochetel N, et al. (2021) Diploid chromosome-scale assembly of the *Muscadinia rotundifolia* genome supports chromosome fusion and disease resistance gene expansion during *Vitis* and *Muscadinia* divergence. *G3 (Bethesda, Md.)*, 11(4).

Morales-Cruz A, et al. (2021) Introgression among North American wild grapes (*Vitis*) fuels biotic and abiotic adaptation. *Genome biology*, 22(1), 254.

Poole TL, et al. (2020) Whole-Genome Sequence of *Aeromonas hydrophila* CVM861 Isolated from Diarrhetic Neonatal Swine. *Microorganisms*, 8(11).

Perlaza-Jimenez L, et al. (2020) Forensic genomics of a novel *Klebsiella quasipneumoniae* type from a neonatal intensive care unit in China reveals patterns of colonization, evolution and epidemiology. *Microbial genomics*, 6(10).

Chamings A, et al. (2019) An Emerging Human Parechovirus Type 5 Causing Sepsis-Like Illness in Infants in Australia. *Viruses*, 11(10).