

Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

MagicBlast

RRID:SCR_015513

Type: Tool

Proper Citation

MagicBlast (RRID:SCR_015513)

Resource Information

URL:

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: data analysis software, data processing software, sequence analysis software, software application, software resource

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: 20260912T195827+0000

Ratings and Alerts

No rating or validation information has been found for MagicBlast.

No alerts have been found for MagicBlast.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Swift SZ, et al. (2026) Integration of Short- and Long-Read RNA Sequencing Enables the Discovery of Circular RNAs. *Cancer research*, 86(5), 1300.

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 CO₂ 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).