

# Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

## MOLE-BLAST

RRID:SCR\_016644

Type: Tool

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### Proper Citation

MOLE-BLAST (RRID:SCR\_016644)

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### Resource Information

**URL:** <https://blast.ncbi.nlm.nih.gov/moleblast/moleblast.cgi>

**Proper Citation:** MOLE-BLAST (RRID:SCR\_016644)

**Description:** Software tool that helps taxonomists find closest database neighbors of submitted query sequences by generating a phylogenetic tree from BLAST results.

**Abbreviations:** moleblast, Mole Blast, MOLE BLAST

**Resource Type:** data processing software, sequence analysis software, data access protocol, data analysis software, software resource, web service, software application

**Keywords:** taxonomist, find, close, database, submitted, query, sequence, generate, phylogenetic, tree, nucleotide

**Availability:** Free, Freely available

**Resource Name:** MOLE-BLAST

**Resource ID:** SCR\_016644

**Record Creation Time:** 20220129T080331+0000

**Record Last Update:** 20260731T043004+0000

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### Ratings and Alerts

No rating or validation information has been found for MOLE-BLAST.

No alerts have been found for MOLE-BLAST.

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### Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Cusc?? A, et al. (2021) Long-read metagenomics retrieves complete single-contig bacterial genomes from canine feces. BMC genomics, 22(1), 330.