

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

MOLE-BLAST

RRID:SCR_016644

Type: Tool

Proper Citation

MOLE-BLAST (RRID:SCR_016644)

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 access protocol, data analysis software, data processing software, sequence analysis software, software application, software resource, web service

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: 20260912T195842+0000

Ratings and Alerts

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

No alerts have been found for MOLE-BLAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Abumsimir B, et al. (2022) Molecular characterization of human papillomavirus and mouse mammary tumor virus-like infections in prostate cancer tissue and relevance with tumor characteristics. *Molecular and clinical oncology*, 16(5), 97.

Khalid A, et al. (2022) Morphological and molecular characterization of *Tatera indica* Hardwicke 1807 (Rodentia: Muridae) from Pothwar, Pakistan. *Open life sciences*, 17(1), 610.

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