

Resource Summary Report

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

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: 20260805T044358+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 1 mentions in open access literature.

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

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