

Resource Summary Report

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Taxonomically Broad EST Database

RRID:SCR_007962

Type: Tool

Proper Citation

Taxonomically Broad EST Database (RRID:SCR_007962)

Resource Information

URL: <http://tbestdb.bcm.umontreal.ca/searches/welcome.php>

Proper Citation: Taxonomically Broad EST Database (RRID:SCR_007962)

Description: The taxonomically broad EST database TBestDB serves as a repository for EST data from a wide range of eukaryotes, many of which have previously not been thoroughly investigated. Users can search by annotated name, EC#, and view datasets that contain classification hierarchies for pathways, for reactions (the enzyme nomenclature system), for compounds, and for genes. Most of the data contained in TBestDB has been generated by the labs of the Protist EST Program located in six universities across Canada.

Synonyms: TBestDB

Resource Type: database, data or information resource

Resource Name: Taxonomically Broad EST Database

Resource ID: SCR_007962

Alternate IDs: r3d100012085, nif-0000-03538

Alternate URLs: <https://doi.org/10.17616/R3P92V>, <https://doi.org/10.17616/R3P92V>

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260803T040516+0000

Ratings and Alerts

No rating or validation information has been found for Taxonomically Broad EST Database.

No alerts have been found for Taxonomically Broad EST Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Lhee D, et al. (2021) Amoeba Genome Reveals Dominant Host Contribution to Plastid Endosymbiosis. *Molecular biology and evolution*, 38(2), 344.

Lee YR, et al. (2015) Essential Role for an M17 Leucine Aminopeptidase in Encystation of *Acanthamoeba castellanii*. *PloS one*, 10(6), e0129884.

Palfree RG, et al. (2015) The Evolution of the Secreted Regulatory Protein Progranulin. *PloS one*, 10(8), e0133749.

Postberg J, et al. (2010) The evolutionary history of histone H3 suggests a deep eukaryotic root of chromatin modifying mechanisms. *BMC evolutionary biology*, 10, 259.