

# Resource Summary Report

Generated by [Kravitz](#) on Sep 18, 2026

## Parasite Databases of Clustered ESTs

RRID:SCR\_002262

Type: Tool

### Proper Citation

Parasite Databases of Clustered ESTs (RRID:SCR\_002262)

### Resource Information

**URL:** <http://www.cbil.upenn.edu/ParaDBs/>

**Proper Citation:** Parasite Databases of Clustered ESTs (RRID:SCR\_002262)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on October 28, 2025. These databases were constructed by extracting the organism specific ESTs from dbEST, removing polyA sequences from the ends and trimming 5' and 3' regions with greater than 25% N's in a 20 base pair window. These quality sequences were then aligned using the cap2 program and the consensus sequences thus generated put into a database that is available on the web. A number of parasitic organisms were chosen that have between 3000 and 15000 ESTs. The attempt here is to provide useful information and analyses to the scientific community without curating the results in any way. A total of 55192 ESTs, deposited into dbEST/GenBank, were included in the analyses. The resulting sequences have been clustered into nonredundant gene assemblies and deposited into a relational database that supports a variety of sequence and text searches. This database has been used to compare the gene assemblies using BLAST similarity comparisons to the public protein databases to identify putative genes. Of these new entries, approximately 15%-20% represent putative homologs with a conservative cutoff of  $p < 10^{-9}$ , thus identifying many conserved genes that are likely to share common functions with other well-studied organisms. Gene assemblies were also used to identify strain polymorphisms, examine stage-specific expression, and identify gene families. An interesting class of genes that are confined to members of this phylum and not shared by plants, animals, or fungi, was identified. These genes likely mediate the novel biological features of members of the Apicomplexa and hence offer great potential for biological investigation and as possible therapeutic targets.

**Synonyms:** PDCEST

**Resource Type:** data or information resource, database

**Keywords:** est, expression, fungus, gene, animal, apicomplexa, biological, organism, parasitic, phylum, plants, polyA, protein, sequence, therapeutic

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Parasite Databases of Clustered ESTs

**Resource ID:** SCR\_002262

**Alternate IDs:** nif-0000-20980

**Record Creation Time:** 20220129T080212+0000

**Record Last Update:** 20260912T200125+0000

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## Ratings and Alerts

No rating or validation information has been found for Parasite Databases of Clustered ESTs.

No alerts have been found for Parasite Databases of Clustered ESTs.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Delbac F, et al. (2001) Toxoplasma gondii myosins B/C: one gene, two tails, two localizations, and a role in parasite division. The Journal of cell biology, 155(4), 613.

Carey KL, et al. (2000) Identification and molecular characterization of GRA8, a novel, proline-rich, dense granule protein of Toxoplasma gondii. Molecular and biochemical parasitology, 105(1), 25.