

# Resource Summary Report

Generated by [NIF](#) on Aug 26, 2026

## TPA

RRID:SCR\_003593

Type: Tool

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### Proper Citation

TPA (RRID:SCR\_003593)

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### Resource Information

**URL:** <http://www.ncbi.nlm.nih.gov/genbank/tpa/>

**Proper Citation:** TPA (RRID:SCR\_003593)

**Description:** Database designed to capture experimental or inferential results that support submitter-provided annotation for sequence data that the submitter did not directly determine but derived from GenBank primary data. Records are divided into two categories: \* TPA:experimental: Annotation of sequence data is supported by peer-reviewed wet-lab experimental evidence. \* TPA:inferential: Annotation of sequence data by inference (where the source molecule or its product(s) have not been the subject of direct experimentation) TPA records are retrieved through the Nucleotide Database and feature information on the sequence, how it was cataloged, and proper way to cite the sequence information.

**Abbreviations:** TPA

**Synonyms:** Third Party Annotation, NCBI TPA, NCBI Third Party Annotation

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

**Defining Citation:** [PMID:16901214](#)

**Keywords:** gene, gene expression, nucleotide sequence, annotation, sequence

**Resource Name:** TPA

**Resource ID:** SCR\_003593

**Alternate IDs:** nlx\_157738, r3d100010506

**Alternate URLs:** <https://doi.org/10.17616/R3KS4H>

**Record Creation Time:** 20220129T080219+0000

**Record Last Update:** 20260821T193713+0000

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## Ratings and Alerts

No rating or validation information has been found for TPA.

No alerts have been found for TPA.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Sayers EW, et al. (2019) GenBank. Nucleic acids research, 47(D1), D94.

Clark K, et al. (2016) GenBank. Nucleic acids research, 44(D1), D67.

Benson DA, et al. (2015) GenBank. Nucleic acids research, 43(Database issue), D30.

Peterson ES, et al. (2012) VESPA: software to facilitate genomic annotation of prokaryotic organisms through integration of proteomic and transcriptomic data. BMC genomics, 13, 131.