Resource Summary Report

Generated by dkNET on Apr 15, 2025

TPA

RRID:SCR_003593

Type: Tool

Proper Citation

TPA (RRID:SCR_003593)

Resource Information

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

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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: database, data or information resource

Defining Citation: PMID:16901214

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

Funding:

Resource Name: TPA

Resource ID: SCR 003593

Alternate IDs: nlx_157738

Record Creation Time: 20220129T080219+0000

Record Last Update: 20250412T054848+0000

Ratings and Alerts

No rating or validation information has been found for TPA.

No alerts have been found for TPA.

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 dkNET.

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.