

Resource Summary Report

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T3DB

RRID:SCR_002672

Type: Tool

Proper Citation

T3DB (RRID:SCR_002672)

Resource Information

URL: <http://t3db.org/>

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Description: Database that combines detailed toxin data with comprehensive toxin target information. The database currently houses 3,053 toxins described by 32,276 synonyms, including pollutants, pesticides, drugs, and food toxins, which are linked to 1,670 corresponding toxin target records. Altogether there are 37,084 toxin, toxin target associations. (March 2014) Each toxin record (ToxCard) contains over 50 data fields and holds information such as chemical properties and descriptors, toxicity values, molecular and cellular interactions, and medical information. This information has been extracted from over 5,454 sources, which include other databases, government documents, books, and scientific literature. The focus of the T3DB is on providing mechanisms of toxicity and target proteins for each toxin. This dual nature of the T3DB, in which toxin and toxin target records are interactively linked in both directions, makes it unique from existing databases. It is also fully searchable and supports extensive text, sequence, chemical structure, and relational query searches

Abbreviations: T3DB

Synonyms: Toxin-Target Database, Toxin Toxin-Target Database, Toxin and Toxin Target Database, Toxin, Toxin Toxin Target Database

Resource Type: data or information resource, database

Defining Citation: [PMID:19897546](#)

Keywords: toxicology, toxin, pollutant, pesticide, drug, food, gene-drug, interaction, gene, phenotype, mechanism, bio.tools

Funding: Alberta Advanced Education and Technology ;
Canadian Institutes of Health Research ;
Genome Alberta ;

Genome Canada

Availability: Free, Available for download, Freely available

Resource Name: T3DB

Resource ID: SCR_002672

Alternate IDs: r3d100012189, nif-0000-22933, biotools:t3db, OMICS_01592

Alternate URLs: <https://bio.tools/t3db>, <https://doi.org/10.17616/R3VM0R>

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260904T000100+0000

Ratings and Alerts

No rating or validation information has been found for T3DB.

No alerts have been found for T3DB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Wang X, et al. (2026) TidyMass2: advancing LC-MS untargeted metabolomics through metabolite origin inference and metabolic feature-based functional module analysis. Nature communications, 17(1), 1755.

Delgado LF, et al. (2026) PathoFact 2.0: an integrative pipeline for the prediction of antimicrobial resistance genes, virulence factors, toxins and toxin-associated proteins, and biosynthetic gene clusters in metagenomes. GigaScience, 15.

Tian X, et al. (2025) Multiomics analyses of gut microbiota and metabolites in people living with HIV before and during SARS-COV-2 infection. Scientific reports, 15(1), 22144.

Niu XY, et al. (2025) Chromosome-level genome assembly of the wasp *Vespa mandarinia* (Hymenoptera: Vespidae). Scientific data, 12(1), 1404.

Zhu Y, et al. (2025) A Transformer-Based Deep Learning Approach to Predicting Air Organic Pollutant-Human Protein Interactions. Environmental science & technology, 59(50), 27425.

- Ranjit S, et al. (2024) In vitro, in planta, and comparative genomic analyses of *Pseudomonas syringae* pv. *syringae* strains of pepper (*Capsicum annuum* var. *annuum*). *Microbiology spectrum*, 12(6), e0006424.
- Setiya A, et al. (2024) MolToxPred: small molecule toxicity prediction using machine learning approach. *RSC advances*, 14(6), 4201.
- Ibrahim MAA, et al. (2023) In-Silico Mining of the Toxins Database (T3DB) towards Hunting Prospective Candidates as ABCB1 Inhibitors: Integrated Molecular Docking and Lipid Bilayer-Enhanced Molecular Dynamics Study. *Pharmaceuticals (Basel, Switzerland)*, 16(7).
- Liu Y, et al. (2023) Integrative network pharmacology and in silico analyses identify the anti-omicron SARS-CoV-2 potential of eugenol. *Heliyon*, 9(3), e13853.
- Limbu S, et al. (2022) Predicting Dose-Range Chemical Toxicity using Novel Hybrid Deep Machine-Learning Method. *Toxics*, 10(11).
- Santos JX, et al. (2022) A Role for Gene-Environment Interactions in Autism Spectrum Disorder Is Supported by Variants in Genes Regulating the Effects of Exposure to Xenobiotics. *Frontiers in neuroscience*, 16, 862315.
- Sostare E, et al. (2022) Knowledge-Driven Approaches to Create the MTox700+ Metabolite Panel for Predicting Toxicity. *Toxicological sciences : an official journal of the Society of Toxicology*, 186(2), 208.
- Llorach-Pares L, et al. (2022) Computer-Aided Drug Design (CADD) to De-Orphanize Marine Molecules: Finding Potential Therapeutic Agents for Neurodegenerative and Cardiovascular Diseases. *Marine drugs*, 20(1).
- Gao P, et al. (2022) Precision environmental health monitoring by longitudinal exposome and multi-omics profiling. *Genome research*, 32(6), 1199.
- Yang Q, et al. (2021) MMEASE: Online meta-analysis of metabolomic data by enhanced metabolite annotation, marker selection and enrichment analysis. *Journal of proteomics*, 232, 104023.
- Wetherbee O, et al. (2020) WellExplorer: an integrative resource linking hydraulic fracturing chemicals with hormonal pathways and geographic location. *Database : the journal of biological databases and curation*, 2020.
- Li L, et al. (2019) Comparative genomic analysis of *Pectobacterium carotovorum* subsp. *brasiliense* SX309 provides novel insights into its genetic and phenotypic features. *BMC genomics*, 20(1), 486.
- Eissa HF, et al. (2017) Developing transgenic wheat to encounter rusts and powdery mildew by overexpressing barley chi26 gene for fungal resistance. *Plant methods*, 13, 41.
- Katsila T, et al. (2016) Computational approaches in target identification and drug discovery. *Computational and structural biotechnology journal*, 14, 177.
- Dhanani AS, et al. (2015) Genomic Comparison of Non-Typhoidal *Salmonella enterica* Serovars Typhimurium, Enteritidis, Heidelberg, Hadar and Kentucky Isolates from Broiler

Chickens. PloS one, 10(6), e0128773.