

# Resource Summary Report

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## OncoboxPD

RRID:SCR\_023723

Type: Tool

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### Proper Citation

OncoboxPD (RRID:SCR\_023723)

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### Resource Information

**URL:** <https://open.oncobox.com/>

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**Description:** Structured curated collection of protein based and of metabolic human molecular pathways. Human molecular pathways database with tools for activity calculating and visualization. All pathways are functionally classified according to GO terms enrichment patterns. All pathway participants, their interactions and reactions are uniformly processed and annotated, and are ready for numeric analysis of experimental expression data. For every comparison graph is generated summarizing top up and down regulated pathways.

**Synonyms:** Oncobox Pathway Databank

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

**Defining Citation:** [PMID:35615022](#)

**Keywords:** Gene Ontology terms enrichment patterns, human molecular pathways, curated collection, GO terms enrichment patterns, experimental expression data analysis,

**Funding:** National Natural Science Foundation of China ;  
Qingdao Key Health Discipline Development Fund ;  
Qingdao Key Research Project ;  
Russian Science Foundation

**Availability:** Free, Freely available

**Resource Name:** OncoboxPD

**Resource ID:** SCR\_023723

**Record Creation Time:** 20230628T050216+0000

**Record Last Update:** 20260919T195739+0000

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## Ratings and Alerts

No rating or validation information has been found for OncoboxPD.

No alerts have been found for OncoboxPD.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Tan Z, et al. (2025) Construction of a gene-metabolite-microbiome regulatory network reveals novel therapeutic targets in bladder cancer through multi-omics analysis. *Annals of medicine*, 57(1), 2553220.

Liao H, et al. (2023) Mannose-Binding Lectin 2 as a Potential Therapeutic Target for Hepatocellular Carcinoma: Multi-Omics Analysis and Experimental Validation. *Cancers*, 15(19).

Chiou KL, et al. (2023) A single-cell multi-omic atlas spanning the adult rhesus macaque brain. *Science advances*, 9(41), eadh1914.

Zolotovskaia M, et al. (2023) Algorithmically Reconstructed Molecular Pathways as the New Generation of Prognostic Molecular Biomarkers in Human Solid Cancers. *Proteomes*, 11(3).

Sorokin M, et al. (2023) Large-scale assessment of pros and cons of autopsy-derived or tumor-matched tissues as the norms for gene expression analysis in cancers. *Computational and structural biotechnology journal*, 21, 3964.

Wang Y, et al. (2022) Comprehensive Pan-Cancer Analyses of Immunogenic Cell Death as a Biomarker in Predicting Prognosis and Therapeutic Response. *Cancers*, 14(23).

Zolotovskaia MA, et al. (2022) OncoboxPD: human 51 672 molecular pathways database with tools for activity calculating and visualization. *Computational and structural biotechnology journal*, 20, 2280.

Zhu Y, et al. (2022) Identification of oncogenes and tumor-suppressor genes with hepatocellular carcinoma: A comprehensive analysis based on TCGA and GEO datasets. *Frontiers in genetics*, 13, 934883.