

Resource Summary Report

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IOBR

RRID:SCR_025619

Type: Tool

Proper Citation

IOBR (RRID:SCR_025619)

Resource Information

URL: <https://github.com/IOBR/IOBR>

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Description: Software R package to perform comprehensive analysis of tumor microenvironment and signatures for immuno-oncology. Used for comprehensively interpreting multi-omics data.

Synonyms: Immuno-Oncology Biological Research

Resource Type: software application, software resource, data processing software, data analysis software

Defining Citation: [PMID:34276676](#)

Keywords: interpreting multi-omics data, perform comprehensive analysis,

Funding: National Natural Science Foundation of China ;
Guangzhou Planned Project of Science and Technology

Availability: Free, Available for download, Freely available,

Resource Name: IOBR

Resource ID: SCR_025619

License: GNU GPL v3

Record Creation Time: 20240815T053252+0000

Record Last Update: 20260820T055048+0000

Ratings and Alerts

No rating or validation information has been found for IOBR.

No alerts have been found for IOBR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Altendorf L, et al. (2026) Molecular changes during AT/RT progression associated with epithelial-mesenchymal transition and extracellular matrix changes. *Acta neuropathologica*, 152(1).

Shu Y, et al. (2026) Integrated network pharmacology and comprehensive bioinformatics analysis to identify the mechanisms and molecular targets of ketamine in ischemic stroke-depression comorbidity. *PloS one*, 21(3), e0343918.

Lin T, et al. (2026) Post-translational modification signature shapes the tumor immune microenvironment and predicts clinical outcomes in melanoma. *Discover oncology*, 17(1).

Li H, et al. (2026) Helicobacter pylori-linked gene CFAP73 rewires epithelial programs and shapes the gastric cancer microenvironment. *Discover oncology*, 17(1).

Li X, et al. (2026) A P4HA2 hypoxia signature derived from single cell atlas stratifies conserved subtypes with prognostic significance in cervical squamous cell carcinoma. *BMC cancer*, 26(1), 257.

Zhang L, et al. (2026) Retinoic Acid Reprograms Mast Cells Toward a Proinflammatory State to Enhance Antitumor Immunity. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(6), e09340.

Zhang J, et al. (2026) CD47 as a prognostic biomarker and potential immunotherapy target in penile squamous cell carcinoma. *Scientific reports*, 16(1).

Fang C, et al. (2025) Transcriptomic and morphologic vascular aberrations underlying FCDIIb etiology. *Nature communications*, 16(1), 3320.

Yang T, et al. (2025) ZNF143 as a diagnostic biomarker: Insights from gene expression and immune cell infiltration in COPD and asthma. *Medicine*, 104(43), e45317.

Yu Q, et al. (2025) Knockdown TNF family prognosis index crucial gene PDE4B promoted PANoptosis of ovarian carcinoma cell:Based in vitro and in vivo experiments. *Translational oncology*, 56, 102333.

Liu L, et al. (2025) Revealing the role of cancer-associated fibroblast senescence in prognosis and immune landscape in pancreatic cancer. *iScience*, 28(1), 111612.

Hua M, et al. (2025) Multiomic machine learning on lactylation for molecular typing and prognosis of lung adenocarcinoma. *Scientific reports*, 15(1), 3075.

Ke J, et al. (2025) Single-cell and bulk transcriptome analyses revealed the role of macrophage cholesterol metabolism in atherosclerosis. *Lipids in health and disease*, 25(1), 3.

Huang W, et al. (2025) Identification of molecular subtypes and a prognostic signature based on machine learning and purine metabolism-related genes in breast cancer. *Medicine*, 104(21), e42288.

Zhong Y, et al. (2025) Identification of SETD4 as an Onco-Immunological Biomarker Encompassing the Tumor Microenvironment, Prognoses, and Therapeutic Responses in Various Human Cancers. *Immunity, inflammation and disease*, 13(1), e70126.

Li X, et al. (2025) Mapping glioma progression: single-cell RNA sequencing illuminates cell-cell interactions and immune response variability. *Discover oncology*, 16(1), 302.

Huang R, et al. (2025) Integrated mendelian randomization and bioinformatics approach unveiling the immunological and prognostic significance of FBXO2 in breast cancer. *Discover oncology*, 16(1), 2187.

Zhao L, et al. (2025) ASAH1-mediated sphingolipid metabolic reprogramming in venetoclax resistance of AML: beyond the monocytic phenotypes. *BMC cancer*, 26(1), 36.

Qiao S, et al. (2025) Targeting SQLE-mediated cholesterol metabolism to enhance CD8+ T cell activation and immunotherapy efficacy in hepatocellular carcinoma. *Journal for immunotherapy of cancer*, 13(9).

Van Laethem JL, et al. (2025) CD40 agonist mitazalimab with mFOLFIRINOX in untreated metastatic pancreatic cancer: Biomarkers associated with outcomes from OPTIMIZE-1. *Cell reports. Medicine*, 6(10), 102407.