

Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

Metabox

RRID:SCR_024443

Type: Tool

Proper Citation

Metabox (RRID:SCR_024443)

Resource Information

URL: <https://github.com/kwanjeeraw/metabox>

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Description: Software R toolbox for thorough metabolomic data analysis, integration and interpretation. Metabox 2.0 is updated version of R package Metabox and includes several methods for data processing, statistical analysis, biomarker analysis, integrative analysis and data interpretation.

Synonyms: metabox2, Metabox 2.0, metabox

Resource Type: software resource, software toolkit

Defining Citation: [PMID:28141874](#)

Keywords: Metabolomics, metabolomic analysis, data integration, data interpretation,

Funding: NIDDK U24 DK097154

Availability: Free, Available for download, Freely available

Resource Name: Metabox

Resource ID: SCR_024443

Alternate URLs: <https://github.com/kwanjeeraw/mETABOX>,
<https://metsysbio.com/metabox/index.html>, <http://kwanjeeraw.github.io/metabox/>,
<https://github.com/kwanjeeraw/metabox2>,

License: GNU GPL v3

Record Creation Time: 20230919T050222+0000

Record Last Update: 20260805T044531+0000

Ratings and Alerts

No rating or validation information has been found for Metabox.

No alerts have been found for Metabox.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Kurilung A, et al. (2025) LC-QTOF-MSE with MS1-based precursor ion quantification and SiMD-assisted identification enhances human urine metabolite analysis. Computational and structural biotechnology journal, 27, 3079.

Wanichthanarak K, et al. (2024) Data processing solutions to render metabolomics more quantitative: case studies in food and clinical metabolomics using Metabox 2.0. GigaScience, 13.

Gao Y, et al. (2024) Development and applications of metabolic models in plant multi-omics research. Frontiers in plant science, 15, 1361183.

Banoei MM, et al. (2023) Metabolomics Analysis of Mesenchymal Stem Cell (MSC) Therapy in a Phase I Clinical Trial of Septic Shock: An Exploratory Study. Metabolites, 13(11).

Tripathi KP, et al. (2018) An integrated approach to infer cross-talks between intracellular protein transport and signaling pathways. BMC bioinformatics, 19(Suppl 2), 58.

Aggio RB, et al. (2014) Identifying and quantifying metabolites by scoring peaks of GC-MS data. BMC bioinformatics, 15(1), 374.