

Resource Summary Report

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METAFflux

RRID:SCR_028022

Type: Tool

Proper Citation

METAFflux (RRID:SCR_028022)

Resource Information

URL: <https://github.com/KChen-lab/METAFflux?tab=readme-ov-file>

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Description: Software tool that predicts cancer metabolic fluxes from bulk RNA-seq and scRNA-seq data to address these analytic gaps. Used for characterizing metabolic circuits and output non-degenerative fluxes using cancer gene expression data.

Resource Type: software application, software resource, source code

Defining Citation: [PMID:37573313](#)

Keywords: predict cancer metabolic fluxes, RNA-seq data, scRNA-seq data, characterizing metabolic circuits, non-degenerative fluxes, cancer gene expression data,

Funding: Chan Zuckerberg Initiative ;
MD Anderson Moonshot programs ;
NCI P30 CA016672;
NCI U01CA247760;
Silicon Valley Community Foundation

Availability: Free, Available for download, Freely available

Resource Name: METAFflux

Resource ID: SCR_028022

License: MIT license

Record Creation Time: 20260225T055938+0000

Record Last Update: 20260904T001222+0000

Ratings and Alerts

No rating or validation information has been found for METAFIux.

No alerts have been found for METAFIux.

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 [NIF](#) .

Hamid S, et al. (2025) Human papilloma virus infection drives unique metabolic and immune profiles in head and neck and cervical cancers: implications for targeted therapies and prognostic markers. *Discover oncology*, 16(1), 676.

Latendresse M, et al. (2018) Evaluation of reaction gap-filling accuracy by randomization. *BMC bioinformatics*, 19(1), 53.

Karp PD, et al. (2018) How accurate is automated gap filling of metabolic models? *BMC systems biology*, 12(1), 73.

Weaver DS, et al. (2014) A genome-scale metabolic flux model of *Escherichia coli* K-12 derived from the EcoCyc database. *BMC systems biology*, 8, 79.

Latendresse M, et al. (2014) Efficiently gap-filling reaction networks. *BMC bioinformatics*, 15, 225.

Latendresse M, et al. (2012) Construction and completion of flux balance models from pathway databases. *Bioinformatics (Oxford, England)*, 28(3), 388.