

Resource Summary Report

Generated by SPARC SAWG on Aug 12, 2026

InCroMAP

RRID:SCR_012964

Type: Tool

Proper Citation

InCroMAP (RRID:SCR_012964)

Resource Information

URL: <http://www.ra.cs.uni-tuebingen.de/software/InCroMAP/>

Proper Citation: InCroMAP (RRID:SCR_012964)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 5, 2023. Integrated analysis of cross-platform microarray and pathway data.

Abbreviations: InCroMAP

Resource Type: software resource

Defining Citation: [PMID:23257199](#)

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: InCroMAP

Resource ID: SCR_012964

Alternate IDs: OMICS_00855

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260808T185949+0000

Ratings and Alerts

No rating or validation information has been found for InCroMAP.

No alerts have been found for InCroMAP.

Data and Source Information

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Maghsoudi Z, et al. (2022) A comprehensive survey of the approaches for pathway analysis using multi-omics data integration. *Briefings in bioinformatics*, 23(6).

Günes Günsel G, et al. (2022) The arginine methyltransferase PRMT7 promotes extravasation of monocytes resulting in tissue injury in COPD. *Nature communications*, 13(1), 1303.

Hoene M, et al. (2021) Exercise prevents fatty liver by modifying the compensatory response of mitochondrial metabolism to excess substrate availability. *Molecular metabolism*, 54, 101359.

Tebani A, et al. (2018) Advances in metabolome information retrieval: turning chemistry into biology. Part II: biological information recovery. *Journal of inherited metabolic disease*, 41(3), 393.

Ratray NJW, et al. (2018) Beyond genomics: understanding exposotypes through metabolomics. *Human genomics*, 12(1), 4.

Wen Y, et al. (2018) Integrating genome-wide DNA methylation and mRNA expression profiles identified different molecular features between Kashin-Beck disease and primary osteoarthritis. *Arthritis research & therapy*, 20(1), 41.

He A, et al. (2018) Use of integrative epigenetic and mRNA expression analyses to identify significantly changed genes and functional pathways in osteoarthritic cartilage. *Bone & joint research*, 7(5), 343.

Eskandari E, et al. (2018) An integrated study on TFs and miRNAs in colorectal cancer metastasis and evaluation of three co-regulated candidate genes as prognostic markers. *Gene*, 679, 150.

Berggren E, et al. (2017) Ab initio chemical safety assessment: A workflow based on exposure considerations and non-animal methods. *Computational toxicology (Amsterdam, Netherlands)*, 4, 31.

El Taghdouini A, et al. (2015) In vitro reversion of activated primary human hepatic stellate cells. *Fibrogenesis & tissue repair*, 8, 14.

Schild M, et al. (2015) Basal and exercise induced label-free quantitative protein profiling of m. vastus lateralis in trained and untrained individuals. *Journal of proteomics*, 122, 119.