

Resource Summary Report

Generated by SPARC SAWG on Aug 21, 2026

proMODMatcher

RRID:SCR_017219

Type: Tool

Proper Citation

proMODMatcher (RRID:SCR_017219)

Resource Information

URL: <http://research.mssm.edu/integrative-network-biology/Software.html>

Proper Citation: proMODMatcher (RRID:SCR_017219)

Description: Software tool as probabilistic multi omics data matching procedure to curate data, identify and correct data annotation and errors in large databases. Used to check potential labeling errors in profiles where number of cis relationships is small, such as miRNA and RPPA profiles.

Synonyms: probabilisticMulti Omics DataMatcher

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

Keywords: probabilistic, matching, curate, omic, data, identify, correct, error, large, database, analysis, sample, label, bio.tools

Funding: NHGRI U01 HG008451;
NIAID U19 AI118610;
NIA R01 AG046170

Resource Name: proMODMatcher

Resource ID: SCR_017219

Alternate IDs: biotools:modmatcher

Alternate URLs: <https://bio.tools/modmatcher>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260821T194107+0000

Ratings and Alerts

No rating or validation information has been found for proMODMatcher.

No alerts have been found for proMODMatcher.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Lee E, et al. (2019) A probabilistic multi-omics data matching method for detecting sample errors in integrative analysis. GigaScience, 8(7).