

# Resource Summary Report

Generated by [kravitz2](#) on Sep 23, 2026

## proMODMatcher

RRID:SCR\_017219

Type: Tool

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### Proper Citation

proMODMatcher (RRID:SCR\_017219)

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### 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:** 20260919T195336+0000

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### Ratings and Alerts

No rating or validation information has been found for proMODMatcher.

No alerts have been found for proMODMatcher.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

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