

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

## FISH

RRID:SCR\_024378

Type: Tool

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### Proper Citation

FISH (RRID:SCR\_024378)

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### Resource Information

**URL:** <http://labs.bio.unc.edu/Vision/FISH/>

**Proper Citation:** FISH (RRID:SCR\_024378)

**Description:** Software tool for identifying regions of common ancestry between genome maps. Used for identification and statistical evaluation of segmental homologies in comparative maps.

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

**Defining Citation:** [PMID:12855440](#)

**Keywords:** identifying regions of common ancestry, genome maps, identification and statistical evaluation, segmental homologies in comparative maps,

**Availability:** Free, Available for download, Freely available,

**Resource Name:** FISH

**Resource ID:** SCR\_024378

**Alternate IDs:** OMICS\_11724

**Old URLs:** <https://sources.debian.org/src/unc-fish/>

**Record Creation Time:** 20230830T050217+0000

**Record Last Update:** 20260905T133030+0000

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### Ratings and Alerts

No rating or validation information has been found for FISH.

No alerts have been found for FISH.

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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 [PRECISE-TBI](#) .

Tang Z, et al. (2021) Analytical and clinical performance of chromosomal microarrays compared with FISH panel and conventional karyotyping in patients with chronic lymphocytic leukemia. Leukemia research, 108, 106616.