

Resource Summary Report

Generated by SPARC SAWG on Sep 12, 2026

FISH

RRID:SCR_024378

Type: Tool

Proper Citation

FISH (RRID:SCR_024378)

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: 20260912T200046+0000

Ratings and Alerts

No rating or validation information has been found for FISH.

No alerts have been found for FISH.

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](#) .

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.