# Resource Summary Report

Generated by Kravitz on Sep 10, 2026

## PyLOH

RRID:SCR_001511
Type: Tool

### Proper Citation

PyLOH (RRID:SCR_001511)

### Resource Information

**URL:** https://github.com/uci-cbcl/PyLOH

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**Description:** Software for deconvolving tumor purity and ploidy by integrating copy number alterations and loss of heterozygosity. The model resolves the identifiability problem by integrating two types of sequencing information - somatic copy number alterations and loss of heterozygosity - within an unified probabilistic framework.

**Resource Type:** software resource

**Defining Citation:** PMID:24695406

**Keywords:** standalone software, python, bio.tools

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

**Resource Name:** PyLOH

**Resource ID:** SCR_001511

**Alternate IDs:** OMICS_03559, biotools:pyloh

**Alternate URLs:** https://bio.tools/pyloh

**License:** GNU General Public License, v2

**Record Creation Time:** 20220129T080208+0000

**Record Last Update:** 20260905T132435+0000

### Ratings and Alerts

No rating or validation information has been found for PyLOH.

No alerts have been found for PyLOH.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 6 mentions in open access literature.

**Listed below are recent publications.** The full list is available at Kravitz .

Song Y, et al. (2025) The dual role of whole-genome duplication: biological mechanisms, functional consequences, and detection advances. Acta biochimica et biophysica Sinica, 58(2), 231.

Cheng Y, et al. (2025) Stromal architecture and fibroblast subpopulations with opposing effects on outcomes in hepatocellular carcinoma. Cell discovery, 11(1), 1.

Song Y, et al. (2025) Benchmarking Ploidy Estimation Methods for Bulk and Single-Cell Whole Genome Sequencing. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(45), e07839.

Ji D, et al. (2021) Tumor mutation burden in blood predicts benefit from neoadjuvant chemo/radiotherapy in locally advanced rectal cancer. Genomics, 113(1 Pt 2), 957.

Park S, et al. (2019) Paired whole exome and transcriptome analyses for the Immunogenomic changes during concurrent chemoradiotherapy in esophageal squamous cell carcinoma. Journal for immunotherapy of cancer, 7(1), 128.

Li Y, et al. (2015) MixClone: a mixture model for inferring tumor subclonal populations. BMC genomics, 16 Suppl 2(Suppl 2), S1.