

# Resource Summary Report

Generated by [dkNET](#) on Aug 7, 2026

## PyLOH

RRID:SCR\_001511

Type: Tool

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### Proper Citation

PyLOH (RRID:SCR\_001511)

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### Resource Information

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

**Proper Citation:** PyLOH (RRID:SCR\_001511)

**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:** 20260801T190142+0000

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### Ratings and Alerts

No rating or validation information has been found for PyLOH.

No alerts have been found for PyLOH.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.