

Resource Summary Report

Generated by [ASWG](#) on Aug 31, 2026

PyLOH

RRID:SCR_001511

Type: Tool

Proper Citation

PyLOH (RRID:SCR_001511)

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: 20260829T182055+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 [ASWG](#) .

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.