

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 30, 2026

LOHHLA

RRID:SCR_023690

Type: Tool

Proper Citation

LOHHLA (RRID:SCR_023690)

Resource Information

URL: <https://github.com/mskcc/lohhlA>

Proper Citation: LOHHLA (RRID:SCR_023690)

Description: Software tool to evaluate HLA loss using next-generation sequencing data. Computational tool to determine HLA allele-specific copy number from sequencing data.

Synonyms: Loss Of Heterozygosity in Human Leukocyte Antigen

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

Defining Citation: [PMID:29107330](#)

Keywords: evaluate HLA loss, Human Leukocyte Antigen loss, next-generation sequencing data, determine HLA allele-specific copy number, sequencing data,

Funding: Cancer Research UK ;
University College London Hospitals Biomedical Research Centre ;
European Union Seventh Framework Programme ;
UK Medical Research Council ;
Wellcome Trust ;
Rosetrees Trust ;
NovoNordisk Foundation ;
Prostate Cancer Foundation ;
Breast Cancer Research Foundation ;
European Research Council ;
Marie Curie Network PloidyNet

Availability: Restricted

Resource Name: LOHHLA

Resource ID: SCR_023690

Record Creation Time: 20230616T050221+0000

Record Last Update: 20260729T044559+0000

Ratings and Alerts

No rating or validation information has been found for LOHHLA.

No alerts have been found for LOHHLA.

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 [PRECISE-TBI](#) .

Sears T, et al. (2024) Integrated germline and somatic features reveal divergent immune pathways driving ICB response. bioRxiv : the preprint server for biology.

Ingels J, et al. (2024) Neoantigen-targeted dendritic cell vaccination in lung cancer patients induces long-lived T??cells exhibiting the full differentiation spectrum. Cell reports. Medicine, 5(5), 101516.

Sears TJ, et al. (2024) Integrated Germline and Somatic Features Reveal Divergent Immune Pathways Driving Response to Immune Checkpoint Blockade. Cancer immunology research, 12(12), 1780.

Wang S, et al. (2023) SpecHLA enables full-resolution HLA typing from sequencing data. Cell reports methods, 3(9), 100589.

Ying L, et al. (2023) Immune-active tumor-adjacent tissues are associated with favorable prognosis in stage I lung squamous cell carcinoma. iScience, 26(9), 107732.

Thummalapalli R, et al. (2023) Clinical and Molecular Features of Long-term Response to Immune Checkpoint Inhibitors in Patients with Advanced Non-Small Cell Lung Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(21), 4408.