Resource Summary Report

Generated by SPARC SAWG on Aug 30, 2026

HLA-LA

RRID:SCR_022283
Type: Tool

Proper Citation

HLA-LA (RRID:SCR_022283)

Resource Information

URL: https://github.com/DiltheyLab/HLA-LA

Proper Citation: HLA-LA (RRID:SCR_022283)

Description: Software implements new graph alignment model for human leukocyte antigen, based on projection of linear alignments onto variation graph. Enables accurate HLA type inference from whole genome and whole exome Illumina data; from long-read Oxford Nanopore and Pacific Biosciences data and from genome assemblies.

Synonyms: HLA*LA

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

Defining Citation: PMID:30942877

Keywords: HLA type inference, human leukocyte antigen, linear alignments onto variation graph projection,

Funding: Agence Nationale de la Recherche ;
European Union ;
Intramural Research Program of the National Human Genome Research Institute ;
J??rgen Manchot Foundation ;
Korea Health Industry Development Institute ;
Wellcome Trust Fellowship

Availability: Free, Available for download, Freely available

Resource Name: HLA-LA

Resource ID: SCR_022283

License: GNU GPL v3.0

Record Creation Time: 20220512T050141+0000

Record Last Update: 20260829T182756+0000

Ratings and Alerts

No rating or validation information has been found for HLA-LA.

No alerts have been found for HLA-LA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Kinnersley B, et al. (2025) Genomic landscape of diffuse glioma revealed by whole genome sequencing. Nature communications, 16(1), 4233.

Liu Y, et al. (2025) Uncovering genetic diversity and admixture of British Africans with HLA alleles inferred from whole genome sequencing. European journal of human genetics : EJHG, 33(8), 1057.

Willoughby D, et al. (2025) Exome sequencing shows same pattern of clonal tumor mutational burden, intratumor heterogenicity and clonal neoantigen between autologous tumor and Vigil product. Scientific reports, 15(1), 8637.

Xu ZM, et al. (2024) Joint host-pathogen genomic analysis identifies hepatitis B virus mutations associated with human NTCP and HLA class I variation. American journal of human genetics, 111(6), 1018.

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