

Resource Summary Report

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

[arcasHLA](#)

RRID:SCR_022286

Type: Tool

Proper Citation

arcasHLA (RRID:SCR_022286)

Resource Information

URL: <https://github.com/RabadanLab/arcasHLA>

Proper Citation: arcasHLA (RRID:SCR_022286)

Description: Software tool for high resolution HLA typing from RNAseq. Fast and accurate in silico inference of HLA genotypes from RNA-seq.

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

Defining Citation: [PMID:31173059](#)

Keywords: in silico inference of HLA genotypes, RNA-seq data, HLA typing

Funding: DARPA ;
NCI U54CA193313;
NIGMS R01GM117591;
Phillip A. Sharp award

Availability: Free

Resource Name: arcasHLA

Resource ID: SCR_022286

License: GNU GPL v3.0

Record Creation Time: 20220512T050141+0000

Record Last Update: 20260829T182904+0000

Ratings and Alerts

No rating or validation information has been found for arcasHLA.

No alerts have been found for arcasHLA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Stephenson E, et al. (2025) Temporal multi-omics analysis of COVID-19 in end-stage kidney disease. *Cell genomics*, 5(8), 100918.

Chiaro J, et al. (2025) Proteogenomic approach to immunopeptidomics of ovarian tumors identifies shared peptide vaccine candidates. *NPJ vaccines*, 10(1), 195.

Wang W, et al. (2025) Liver transplant-facilitated CD161+V α 7.2+ MAIT cell recovery demonstrates clinical benefits in hepatic failure patients. *Nature communications*, 16(1), 4022.

Ricker CA, et al. (2024) Historical perspective and future directions: computational science in immuno-oncology. *Journal for immunotherapy of cancer*, 12(1).

Bulashevskaya A, et al. (2024) Artificial intelligence and neoantigens: paving the path for precision cancer immunotherapy. *Frontiers in immunology*, 15, 1394003.

Burnham KL, et al. (2024) eQTLs identify regulatory networks and drivers of variation in the individual response to sepsis. *Cell genomics*, 4(7), 100587.

Jarosch S, et al. (2023) Multimodal immune cell phenotyping in GI biopsies reveals microbiome-related T cell modulations in human GvHD. *Cell reports. Medicine*, 4(7), 101125.

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