

# Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 15, 2026

## HLAforest

RRID:SCR\_012146

Type: Tool

### Proper Citation

HLAforest (RRID:SCR\_012146)

### Resource Information

**URL:** <https://code.google.com/p/hlaforest/>

**Proper Citation:** HLAforest (RRID:SCR\_012146)

**Description:** Software that predicts HLA haplotype by hierarchically weighting reads and using an iterative, greedy, top down pruning technique. HLAforest uses BioPerl to read in FASTA files. Alignments use Bow tie, although any alignment tool can be used to generate SAM alignments for use as input to HLAforest.

**Resource Type:** software resource

**Defining Citation:** [PMID:23840783](#)

**Keywords:** standalone software, perl

**Availability:** Free for academic use, Apache License

**Resource Name:** HLAforest

**Resource ID:** SCR\_012146

**Alternate IDs:** OMICS\_06170

**Record Creation Time:** 20220129T080308+0000

**Record Last Update:** 20260912T195746+0000

### Ratings and Alerts

No rating or validation information has been found for HLAforest.

No alerts have been found for HLAforest.

### 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 [SPARC SAWG](#) .

Kim D, et al. (2024) Large-scale integrative analysis of juvenile idiopathic arthritis for new insight into its pathogenesis. Arthritis research & therapy, 26(1), 47.

Yu D, et al. (2024) A rigorous benchmarking of alignment-based HLA typing algorithms for RNA-seq data. bioRxiv : the preprint server for biology.

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

Liu P, et al. (2021) Benchmarking the Human Leukocyte Antigen Typing Performance of Three Assays and Seven Next-Generation Sequencing-Based Algorithms. Frontiers in immunology, 12, 652258.

Chelysheva I, et al. (2021) RNA2HLA: HLA-based quality control of RNA-seq datasets. Briefings in bioinformatics, 22(5).

Hayashi S, et al. (2018) ALPHLARD: a Bayesian method for analyzing HLA genes from whole genome sequence data. BMC genomics, 19(1), 790.