Resource Summary Report

Generated by NIF on May 17, 2025

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

Funding:

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: 20250420T014608+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

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.

Bulashevska 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.