

Resource Summary Report

Generated by [dkNET](#) on Aug 17, 2026

HLAminer

RRID:SCR_022282

Type: Tool

Proper Citation

HLAminer (RRID:SCR_022282)

Resource Information

URL: <https://www.bcgsc.ca/resources/software/hlaminer>

Proper Citation: HLAminer (RRID:SCR_022282)

Description: Software for HLA predictions from next generation shotgun sequence read data and supports direct read alignment and targeted de novo assembly of sequence reads. Used for identifying HLA alleles directly from shotgun sequence datasets. Supports predictions from variety of DNA sequencing technologies including those from Illumina, MGI, PacBio and Oxford Nanopore.

Resource Type: software application, simulation software, software resource

Defining Citation: [PMID:23228053](#)

Keywords: identifying HLA alleles, shotgun sequence datasets, next generation shotgun sequence read data, direct read alignment, targeted de novo assembly, sequence reads

Funding: Canadian Institutes of Health Research

Availability: Free, Freely available

Resource Name: HLAminer

Resource ID: SCR_022282

Alternate URLs: <https://github.com/bcgsc/HLAminer>

License URLs: <https://github.com/bcgsc/HLAminer/blob/master/LICENSE>

Record Creation Time: 20220512T050141+0000

Record Last Update: 20260815T182722+0000

Ratings and Alerts

No rating or validation information has been found for HLAminer.

No alerts have been found for HLAminer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Warren RL, et al. (2025) Streaming Long-Read Sequence Alignments for HLA Predictions Using HLAminer. Current protocols, 5(3), e70124.

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