Resource Summary Report

Generated by dkNET on Apr 16, 2025

HLA-VBSeq

RRID:SCR_022284
Type: Tool

Proper Citation

HLA-VBSeq (RRID:SCR_022284)

Resource Information

URL: http://nagasakilab.csml.org/hla/

Proper Citation: HLA-VBSeq (RRID:SCR_022284)

Description: Software for accurate HLA typing at full resolution from whole genome sequencing data. Used to estimate the most likely HLA types from high throughput sequencing data.

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

Defining Citation: PMID:25708870

Keywords: HLA types estimation, sequencing data, whole genome sequencing data, high throughput sequencing data

Funding: MEXT Tohoku Medical Megabank Project

Availability: Free, Freely available

Resource Name: HLA-VBSeq

Resource ID: SCR_022284

License URLs: http://nagasakilab.csml.org/hla/

Record Creation Time: 20220512T050141+0000

Record Last Update: 20250416T063927+0000

Ratings and Alerts

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

No alerts have been found for HLA-VBSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

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

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

Frangione E, et al. (2022) Genome Reporting for Healthy Populations-Pipeline for Genomic Screening from the GENCOV COVID-19 Study. Current protocols, 2(10), e534.