

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[seq2HLA](#)

RRID:SCR_001199

Type: Tool

Proper Citation

seq2HLA (RRID:SCR_001199)

Resource Information

URL: <http://tron-mainz.de/tron-facilities/computational-medicine/seq2hla/>

Proper Citation: seq2HLA (RRID:SCR_001199)

Description: Software for obtaining an individual's HLA class I and II type and expression using standard NGS (Next-generation sequencing) RNA-Seq data. It comprises mapping RNA-Seq reads against a reference database of HLA alleles, determining and reporting HLA type, confidence score and locus-specific expression level.

Abbreviations: seq2HLA

Synonyms: seq2HLA - HLA typing from RNA-Seq sequence reads

Resource Type: software resource

Defining Citation: [PMID:23259685](#)

Keywords: illumina, next-generation sequencing, rna-seq, hla, hla allele, hla typing

Funding: BMBF

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: seq2HLA

Resource ID: SCR_001199

Alternate IDs: OMICS_02152

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260801T190125+0000

Ratings and Alerts

No rating or validation information has been found for seq2HLA.

No alerts have been found for seq2HLA.

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 [RRID](#) .

Zhang S, et al. (2025) Immunosequencing identifies signatures of T cell responses for early detection of nasopharyngeal carcinoma. Cancer cell, 43(8), 1423.

Hosomichi K, et al. (2015) The impact of next-generation sequencing technologies on HLA research. Journal of human genetics, 60(11), 665.