# Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

## Polysolver

RRID:SCR_022278
Type: Tool

### Proper Citation

Polysolver (RRID:SCR_022278)

### Resource Information

**URL:** https://software.broadinstitute.org/cancer/cga/polysolver

**Proper Citation:** Polysolver (RRID:SCR_022278)

**Description:** Software tool for HLA typing based on whole exome sequencing data and infers alleles for three major MHC class I genes. Enables accurate inference of germline alleles of class I HLA-A, B and C genes and subsequent detection of mutations in these genes using inferred alleles as reference.

**Synonyms:** POLYmorphic loci reSOLVER, POLYSOLVER

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

**Defining Citation:** PMID:26372948

**Keywords:** HLA typing, whole exome sequencing data, accurate inference of germline alleles, high precision HLA-typing, alleles of class I HLA-A, B and C genes, detection of mutations, inferred alleles

**Funding:** AACR ;
Blavatnik Family Foundation ;
NCI 1R01CA155010;
NHLBI 1RO1HL103532

**Availability:** Free, Available for download, Freely available

**Resource Name:** Polysolver

**Resource ID:** SCR_022278

**Record Creation Time:** 20220512T050141+0000

**Record Last Update:** 20260905T133012+0000

## Ratings and Alerts

No rating or validation information has been found for Polysolver.

No alerts have been found for Polysolver.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 33 mentions in open access literature.

**Listed below are recent publications.** The full list is available at PRECISE-TBI .


Xu J, et al. (2026) deltaHED predicts survival and immune evasion in PD-1 blockade therapy: A multi-cohort study across three cancer types. Clinical and translational medicine, 16(2), e70595.

Culliford R, et al. (2026) Contrasting Features of Papillary and Chromophobe Renal Cell Carcinoma Revealed by Whole-Genome Sequencing. Molecular cancer research : MCR, 24(5), 327.

Zeng Q, et al. (2026) Intratumoral Tertiary Lymphoid Structures Characterized by a B Cell-Related Signature Elicit Antitumor Effect through HAPLN3 in Hepatocellular Carcinoma. Cancer immunology research, 14(5), 771.

Padul VG, et al. (2025) Assessment of Functional Status of Human Leukocyte Antigen Class I Genes in Cancer Tissues in the Context of Personalized Neoantigen Peptide Vaccine Immunotherapy. JCO clinical cancer informatics, 9, e2400174.

Kayhanian H, et al. (2024) Homopolymer switches mediate adaptive mutability in mismatch repair-deficient colorectal cancer. Nature genetics, 56(7), 1420.

Zhang H, et al. (2024) Genomic profiling and associated B cell lineages delineate the efficacy of neoadjuvant anti-PD-1-based therapy in oesophageal squamous cell carcinoma. EBioMedicine, 100, 104971.

Sun Y, et al. (2024) Integrated multi-omics profiling to dissect the spatiotemporal evolution of metastatic hepatocellular carcinoma. Cancer cell, 42(1), 135.

Lee Y, et al. (2023) Characterization of the genomic alterations in poorly differentiated thyroid cancer. Scientific reports, 13(1), 19154.

Filip I, et al. (2023) Pervasiveness of HLA allele-specific expression loss across tumor types. Genome medicine, 15(1), 8.

Thummalapalli R, et al. (2023) Clinical and Molecular Features of Long-term Response to Immune Checkpoint Inhibitors in Patients with Advanced Non-Small Cell Lung Cancer.

Clinical cancer research : an official journal of the American Association for Cancer Research, 29(21), 4408.

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

Yin J, et al. (2023) Neoadjuvant adebrelimab in locally advanced resectable esophageal squamous cell carcinoma: a phase 1b trial. Nature medicine, 29(8), 2068.

Spain L, et al. (2023) Late-Stage Metastatic Melanoma Emerges through a Diversity of Evolutionary Pathways. Cancer discovery, 13(6), 1364.

Semaan A, et al. (2023) Integrated Molecular Characterization of Intraductal Papillary Mucinous Neoplasms: An NCI Cancer Moonshot Precancer Atlas Pilot Project. Cancer research communications, 3(10), 2062.

Zhang X, et al. (2022) Single-cell sequencing reveals CD133+CD44--originating evolution and novel stemness related variants in human colorectal cancer. EBioMedicine, 82, 104125.

Vázquez-García I, et al. (2022) Ovarian cancer mutational processes drive site-specific immune evasion. Nature, 612(7941), 778.

Sammut SJ, et al. (2022) Multi-omic machine learning predictor of breast cancer therapy response. Nature, 601(7894), 623.

Gatenbee CD, et al. (2022) Immunosuppressive niche engineering at the onset of human colorectal cancer. Nature communications, 13(1), 1798.

Nguyen PHD, et al. (2021) Intratumoural immune heterogeneity as a hallmark of tumour evolution and progression in hepatocellular carcinoma. Nature communications, 12(1), 227.

Claeys A, et al. (2021) Low immunogenicity of common cancer hot spot mutations resulting in false immunogenic selection signals. PLoS genetics, 17(2), e1009368.