Resource Summary Report

Generated by NIF on Aug 7, 2026

CRISP

RRID:SCR_010759
Type: Tool

Proper Citation

CRISP (RRID:SCR_010759)

Resource Information

URL: https://sites.google.com/site/vibansal/software/crisp

Proper Citation: CRISP (RRID:SCR_010759)

Description: A software program to detect SNPs and short indels from pooled sequencing data generated using next-generation sequencing instruments.

Abbreviations: CRISP

Resource Type: software resource

Resource Name: CRISP

Resource ID: SCR_010759

Alternate IDs: OMICS_00057

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260801T190416+0000

Ratings and Alerts

No rating or validation information has been found for CRISP.

No alerts have been found for CRISP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Gao Y, et al. (2026) Methodologies for Sample Multiplexing and Computational Deconvolution in Single-Cell Sequencing. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(3), e13396.

Knizia D, et al. (2025) Improving Soybean Seed Sucrose Content using TILLING by Sequencing Analyses of The Soybean Sucrose Synthase Gene Family. Frontiers in plant science, 16, 1606321.

Wang L, et al. (2025) CRISP: A causal relationships-guided deep learning framework for advanced ICU mortality prediction. BMC medical informatics and decision making, 25(1), 165.

Crona BI, et al. (2023) Four ways blue foods can help achieve food system ambitions across nations. Nature, 616(7955), 104.

Duc M, et al. (2022) Current practices of physiotherapists in Switzerland regarding fall risk-assessment for community-dwelling older adults: A national cross-sectional survey. F1000Research, 11, 513.

Lagunes-Cordoba E, et al. (2022) Evaluation of an anti-stigma intervention for Mexican psychiatric trainees. Pilot and feasibility studies, 8(1), 5.

Daru BH, et al. (2020) Endemism patterns are scale dependent. Nature communications, 11(1), 2115.

Bansal V, et al. (2016) A statistical method for the detection of variants from next-generation resequencing of DNA pools. Bioinformatics (Oxford, England), 32(20), 3213.