

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 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: 20260725T190702+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 7 mentions in open access literature.

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

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.