

Resource Summary Report

Generated by PRECISE-TBI on Aug 2, 2026

CRAVAT

RRID:SCR_012776

Type: Tool

Proper Citation

CRAVAT (RRID:SCR_012776)

Resource Information

URL: <http://www.cravat.us/>

Proper Citation: CRAVAT (RRID:SCR_012776)

Description: A web-based application designed with an easy-to-use interface to facilitate the high-throughput assessment and prioritization of genes and missense alterations important for cancer tumorigenesis.

Abbreviations: CRAVAT

Synonyms: cancer-related analysis of variants toolkit

Resource Type: production service resource, data analysis service, service resource, analysis service resource

Related Condition: Cancer

Funding: NCI CA 152432;
NSF DBI 0845275;
NCI 1U01CA180956-01

Resource Name: CRAVAT

Resource ID: SCR_012776

Alternate IDs: OMICS_00147

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260803T040602+0000

Ratings and Alerts

No rating or validation information has been found for CRAVAT.

No alerts have been found for CRAVAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Krull JE, et al. (2024) Follicular lymphoma B cells exhibit heterogeneous transcriptional states with associated somatic alterations and tumor microenvironments. *Cell reports. Medicine*, 5(3), 101443.

Wang L, et al. (2024) CDMPred: a tool for predicting cancer driver missense mutations with high-quality passenger mutations. *PeerJ*, 12, e17991.

Koh HYK, et al. (2024) Machine learning optimized DriverDetect software for high precision prediction of deleterious mutations in human cancers. *Scientific reports*, 14(1), 22618.

Boyd S, et al. (2024) NGS of brush cytology samples improves the detection of high-grade dysplasia and cholangiocarcinoma in patients with primary sclerosing cholangitis: A retrospective and prospective study. *Hepatology communications*, 8(4).

Eng ZH, et al. (2023) Changes in antioxidant status and DNA repair capacity are corroborated with molecular alterations in malignant thyroid tissue of patients with papillary thyroid cancer. *Frontiers in molecular biosciences*, 10, 1237548.

Madsen AT, et al. (2023) In Silico Examination of Single Nucleotide Missense Mutations in NHLH2, a Gene Linked to Infertility and Obesity. *International journal of molecular sciences*, 24(4).

Sicotte H, et al. (2022) Molecular Profile Changes in Patients with Castrate-Resistant Prostate Cancer Pre- and Post-Abiraterone/Prednisone Treatment. *Molecular cancer research : MCR*, 20(12), 1739.

Tang J, et al. (2021) Single-cell exome sequencing reveals multiple subclones in metastatic colorectal carcinoma. *Genome medicine*, 13(1), 148.

Raimondi D, et al. (2021) Current cancer driver variant predictors learn to recognize driver genes instead of functional variants. *BMC biology*, 19(1), 3.

Milanese JS, et al. (2021) eTumorMetastasis: A Network-based Algorithm Predicts Clinical Outcomes Using Whole-exome Sequencing Data of Cancer Patients. *Genomics, proteomics & bioinformatics*, 19(6), 973.

- Chen H, et al. (2020) Comprehensive assessment of computational algorithms in predicting cancer driver mutations. *Genome biology*, 21(1), 43.
- Lyu J, et al. (2020) DORGE: Discovery of Oncogenes and tumor suppressor genes using Genetic and Epigenetic features. *Science advances*, 6(46).
- Jin H, et al. (2020) Identification of potential causal variants for premature ovarian failure by whole exome sequencing. *BMC medical genomics*, 13(1), 159.
- Karczmarski J, et al. (2019) Mutation Profiling of Premalignant Colorectal Neoplasia. *Gastroenterology research and practice*, 2019, 2542640.
- La Ferla M, et al. (2019) ANKRD44 Gene Silencing: A Putative Role in Trastuzumab Resistance in Her2-Like Breast Cancer. *Frontiers in oncology*, 9, 547.
- Li D, et al. (2018) Transcription Factor and lncRNA Regulatory Networks Identify Key Elements in Lung Adenocarcinoma. *Genes*, 9(1).
- Singh AA, et al. (2018) Multi-omics profiling reveals a distinctive epigenome signature for high-risk acute promyelocytic leukemia. *Oncotarget*, 9(39), 25647.
- Wang B, et al. (2018) NIPS, a 3D network-integrated predictor of deleterious protein SAPs, and its application in cancer prognosis. *Scientific reports*, 8(1), 6021.
- Pannuti A, et al. (2018) Novel putative drivers revealed by targeted exome sequencing of advanced solid tumors. *PloS one*, 13(3), e0194790.
- Castellana S, et al. (2017) High-confidence assessment of functional impact of human mitochondrial non-synonymous genome variations by APOGEE. *PLoS computational biology*, 13(6), e1005628.