Resource Summary Report

Generated by RRID 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: data analysis service, service resource, production 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: 20260801T191028+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 RRID .

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

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.

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).

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.

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.