

Resource Summary Report

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EXCAVATOR-tool

RRID:SCR_012766

Type: Tool

Proper Citation

EXCAVATOR-tool (RRID:SCR_012766)

Resource Information

URL: <http://sourceforge.net/projects/excavatortool/>

Proper Citation: EXCAVATOR-tool (RRID:SCR_012766)

Description: A software package for the detection of copy number variants (CNVs) from whole-exome sequencing data.

Abbreviations: EXCAVATOR-tool

Synonyms: EXCAVATOR-tool: Tool for detecting CNVs from whole-exome sequencing data

Resource Type: software resource

Resource Name: EXCAVATOR-tool

Resource ID: SCR_012766

Alternate IDs: OMICS_00332

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260815T182449+0000

Ratings and Alerts

No rating or validation information has been found for EXCAVATOR-tool.

No alerts have been found for EXCAVATOR-tool.

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 [NIF](#) .

Xu Y, et al. (2023) Prevalence and clinico-genomic characteristics of patients with TRK fusion cancer in China. NPJ precision oncology, 7(1), 75.

Tong Z, et al. (2021) Clonal Evolution Dynamics in Primary and Metastatic Lesions of Pancreatic Neuroendocrine Neoplasms. Frontiers in medicine, 8, 620988.

Sakimura S, et al. (2021) Impaired tumor immune response in metastatic tumors is a selective pressure for neutral evolution in CRC cases. PLoS genetics, 17(1), e1009113.

Wise-Oringer BK, et al. (2019) Familial X-Linked Acrogigantism: Postnatal Outcomes and Tumor Pathology in a Prenatally Diagnosed Infant and His Mother. The Journal of clinical endocrinology and metabolism, 104(10), 4667.

Saito T, et al. (2018) A temporal shift of the evolutionary principle shaping intratumor heterogeneity in colorectal cancer. Nature communications, 9(1), 2884.

Reddy A, et al. (2017) Genetic and Functional Drivers of Diffuse Large B-Cell Lymphoma. Cell, 171(2), 481.

Magi A, et al. (2013) EXCAVATOR: detecting copy number variants from whole-exome sequencing data. Genome biology, 14(10), R120.