Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

Ximmer

RRID:SCR_016427
Type: Tool

Proper Citation

Ximmer (RRID:SCR_016427)

Resource Information

URL: http://ssadedin.github.io/ximmer/

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Description: Software to help users of targeted high throughput genomic sequencing data to accurately detect copy number variants (CNVs). Framework for running and evaluating other copy number detection tools.Used for evaluating and improving performance of CNV detection in exome and targeted sequencing data.

Resource Type: data processing software, data analysis software, data visualization software, simulation software, software resource, software application

Defining Citation: DOI:10.1101/260927

Keywords: cnv, copy, number, variant, exome, targeted, sequencing, data, next, generation, genomic

Funding: National Human Genome Research Institute ;
National Eye Institute ;
National Heart Lung and Blood Institute ;
Australian National Health and Medical Research Council ;
Victorian State Government

Availability: Open source, Free, Available for download, Freely available

Resource Name: Ximmer

Resource ID: SCR_016427

Alternate URLs: https://omictools.com/ximmer-tool, http://ximmer.org

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260731T043009+0000

Ratings and Alerts

No rating or validation information has been found for Ximmer.

No alerts have been found for Ximmer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Rudaka I, et al. (2023) Genetic Basis of Early Onset Atrial Fibrillation in Patients without Risk Factors. Journal of cardiovascular development and disease, 10(3).

Sreenivasan R, et al. (2022) Whole exome sequencing reveals copy number variants in individuals with disorders of sex development. Molecular and cellular endocrinology, 546, 111570.

Frazier AE, et al. (2021) Fatal perinatal mitochondrial cardiac failure caused by recurrent de novo duplications in the ATAD3 locus. Med (New York, N.Y.), 2(1), 49.

Sadedin SP, et al. (2018) Ximmer: a system for improving accuracy and consistency of CNV calling from exome data. GigaScience, 7(10).