Resource Summary Report

Generated by NIF on Apr 30, 2025

StrVCTVRE

RRID:SCR_021776
Type: Tool

Proper Citation

StrVCTVRE (RRID:SCR_021776)

Resource Information

URL: https://compbio.berkeley.edu/proj/strvctvre/

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Description: Software tool as structural variant classifier for exonic deletions and duplications. Supervised learning method to predict pathogenicity of human genome structural variants.Used to distinguish pathogenic SVs from benign SVs that overlap exons.

Synonyms: Structural Variant Classifier Trained on Variants Rare and Exonic

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

Defining Citation: DOI:10.1101/2020.05.15.097048

Keywords: structural variant classifier, exonic deletions, human genome structural variants, predict pathogenicity, pathogenic SVs, benign SVs

Funding: National Science Foundation

Resource Name: StrVCTVRE

Resource ID: SCR_021776

Alternate URLs: https://github.com/andrewSharo/StrVCTVRE

License: MIT License

Record Creation Time: 20220129T080357+0000

Record Last Update: 20250429T060117+0000

Ratings and Alerts

No rating or validation information has been found for StrVCTVRE.

No alerts have been found for StrVCTVRE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Liu Z, et al. (2023) Deep multiple-instance learning accurately predicts gene haploinsufficiency and deletion pathogenicity. bioRxiv : the preprint server for biology.

Sharo AG, et al. (2022) StrVCTVRE: A supervised learning method to predict the pathogenicity of human genome structural variants. American journal of human genetics, 109(2), 195.

Schwarz JM, et al. (2021) Novel sequencing technologies and bioinformatic tools for deciphering the non-coding genome. Medizinische Genetik : Mitteilungsblatt des Berufsverbandes Medizinische Genetik e.V, 33(2), 133.