

Resource Summary Report

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SV-plaudit

RRID:SCR_016285

Type: Tool

Proper Citation

SV-plaudit (RRID:SCR_016285)

Resource Information

URL: <https://github.com/jbelyeu/SV-plaudit>

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Description: Software for rapidly curating structural variant (SVs) predictions. SV-plaudit provides a pipeline for creating image views of genomic intervals, automatically storing them in the cloud, deploying a website to view/score them, and retrieving scores for analysis.

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

Keywords: genomics, structural, variants, visualization, manual, curation, prediction, image, alignment

Funding: NCI U24 CA209999;
NHGRI K99 HG009532;
NHGRI R01 HG006693;
NIGMS R01 GM124355

Availability: Free, Available for download

Resource Name: SV-plaudit

Resource ID: SCR_016285

License: MIT License

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260829T182510+0000

Ratings and Alerts

No rating or validation information has been found for SV-plaudit.

No alerts have been found for SV-plaudit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Bertolotti AC, et al. (2020) The structural variation landscape in 492 Atlantic salmon genomes. Nature communications, 11(1), 5176.

Belyeu JR, et al. (2018) SV-plaudit: A cloud-based framework for manually curating thousands of structural variants. GigaScience, 7(7).