Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 17, 2025

SHREC

RRID:SCR_013009
Type: Tool

Proper Citation

SHREC (RRID:SCR_013009)

Resource Information

URL: http://sourceforge.net/projects/shrec-ec/

Proper Citation: SHREC (RRID:SCR_013009)

Description: A bioinformatics tool for error correction of HTS read data.

Abbreviations: SHREC

Resource Type: software resource

Funding:

Resource Name: SHREC

Resource ID: SCR_013009

Alternate IDs: OMICS_01110

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250410T070324+0000

Ratings and Alerts

No rating or validation information has been found for SHREC.

No alerts have been found for SHREC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Scott OB, et al. (2022) Classification of Protein-Binding Sites Using a Spherical Convolutional Neural Network. Journal of chemical information and modeling, 62(22), 5383.

Li R, et al. (2020) Few-shot learning for classification of novel macromolecular structures in cryo-electron tomograms. PLoS computational biology, 16(11), e1008227.

Ghiandoni GM, et al. (2020) Enhancing reaction-based de novo design using a multi-label reaction class recommender. Journal of computer-aided molecular design, 34(7), 783.

Qin X, et al. (2020) Simultaneous tracking of two motor domains reveals near simultaneous steps and stutter steps of myosin 10 on actin filament bundles. Biochemical and biophysical research communications.

Kong J, et al. (2019) GAAP: A Genome Assembly + Annotation Pipeline. BioMed research international, 2019, 4767354.

Chen X, et al. (2019) MFA-Net: Motion Feature Augmented Network for Dynamic Hand Gesture Recognition from Skeletal Data. Sensors (Basel, Switzerland), 19(2).

Bai J, et al. (2019) Deep Common Semantic Space Embedding for Sketch-Based 3D Model Retrieval. Entropy (Basel, Switzerland), 21(4).

Laehnemann D, et al. (2016) Denoising DNA deep sequencing data-high-throughput sequencing errors and their correction. Briefings in bioinformatics, 17(1), 154.

Magidson V, et al. (2016) Unattached kinetochores rather than intrakinetochore tension arrest mitosis in taxol-treated cells. The Journal of cell biology, 212(3), 307.

Iwaki M, et al. (2016) A programmable DNA origami nanospring that reveals force-induced adjacent binding of myosin VI heads. Nature communications, 7, 13715.

El-Metwally S, et al. (2013) Next-generation sequence assembly: four stages of data processing and computational challenges. PLoS computational biology, 9(12), e1003345.