

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

Resource Name: SHREC

Resource ID: SCR_013009

Alternate IDs: OMICS_01110

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260905T132731+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 14 mentions in open access literature.

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

Zhang D, et al. (2026) Geometric moment-based spectral descriptors for robust non-rigid 3D shape analysis. *Scientific reports*, 16(1), 5687.

Pungitore SA, et al. (2025) SHREC: A Framework for Advancing Next-Generation Computational Phenotyping with Large Language Models. *ArXiv*.

Chaillet ML, et al. (2025) pytom-match-pick: A tophat-transform constraint for automated classification in template matching. *Journal of structural biology*: X, 11, 100125.

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*.

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

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

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.