

Resource Summary Report

Generated by [NIF](#) on Sep 11, 2026

[signalalign](#)

RRID:SCR_024339

Type: Tool

Proper Citation

signalalign (RRID:SCR_024339)

Resource Information

URL: <https://github.com/ArtRand/signalAlign>

Proper Citation: signalalign (RRID:SCR_024339)

Description: Software tool to align ionic current from MinION to reference sequence using trainable hidden Markov model. HMM-HDP models for MinION signal alignments,

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

Keywords: Oxford Nanopore Technologies, MinION sequences DNA, align ionic current, reference sequence, trainable hidden Markov model, HMM-HDP models, MinION signal alignments,

Availability: Free, Available for download, Freely available,

Resource Name: signalalign

Resource ID: SCR_024339

Old URLs: <https://sources.debian.org/src/signalalign/>

License: MIT license

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260905T133030+0000

Ratings and Alerts

No rating or validation information has been found for signalalign.

No alerts have been found for signalalign.

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](#) .

Yue X, et al. (2022) Simultaneous profiling of histone modifications and DNA methylation via nanopore sequencing. Nature communications, 13(1), 7939.

Bailey AD, et al. (2022) Concerted modification of nucleotides at functional centers of the ribosome revealed by single-molecule RNA modification profiling. eLife, 11.