

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

MoSDi

RRID:SCR_003037

Type: Tool

Proper Citation

MoSDi (RRID:SCR_003037)

Resource Information

URL: <https://code.google.com/p/mosdi/>

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Description: Sequence analysis toolkit that contains a lot of sequence analysis algorithms, including methods for 1) motif statistics, e.g. compute the exact occurrence count distribution of a motif, 2) exact motif discovery: extraction of motifs with provably optimal p-value, 3) analysis of pattern matching algorithms: compute (for given algorithm and pattern) the exact distribution of the number of character accesses caused by searching a random text, 4) statistics of fragment masses resulting from proteolytic cleavage of proteins, 5) computing the expected read length of sequencing reads for a given dispensation order (for 454 or IonTorrent) and 6) analysing sensitivity of spaced alignment seeds.

Synonyms: Motif Statistics and Discovery, Motif Statistics and Discovery - Sequence analysis toolkit for bioinformatics

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

Defining Citation: [PMID:19478010](#)

Keywords: standalone software, unix/linux, motif

Availability: Free, Freely available

Resource Name: MoSDi

Resource ID: SCR_003037

Alternate IDs: OMICS_06271

Alternate URLs: <https://bio.tools/mosdi>

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260912T195550+0000

Ratings and Alerts

No rating or validation information has been found for MoSDi.

No alerts have been found for MoSDi.

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 [kravitz2](#) .

Berulava T, et al. (2015) N6-adenosine methylation in MiRNAs. PloS one, 10(2), e0118438.

Hamed M, et al. (2015) Integrative network-based approach identifies key genetic elements in breast invasive carcinoma. BMC genomics, 16 Suppl 5(Suppl 5), S2.