# **Resource Summary Report**

Generated by RRID on Apr 28, 2025

# **MoDIL**

RRID:SCR\_010764

Type: Tool

## **Proper Citation**

MoDIL (RRID:SCR\_010764)

#### **Resource Information**

URL: http://compbio.cs.toronto.edu/modil/

**Proper Citation:** MoDIL (RRID:SCR\_010764)

**Description:** Software for a novel method for finding medium sized indels from high

throughput sequencing datasets.

Abbreviations: MoDIL

Synonyms: MoDIL: Detecting INDEL Variation with Clone-end Sequencing

Resource Type: software resource

Keywords: bio.tools

**Funding:** 

Resource Name: MoDIL

Resource ID: SCR\_010764

Alternate IDs: OMICS\_00066, biotools:modil

Alternate URLs: https://bio.tools/modil

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20250420T014508+0000

### Ratings and Alerts

No rating or validation information has been found for MoDIL.

No alerts have been found for MoDIL.

### **Data and Source Information**

Source: SciCrunch Registry

# **Usage and Citation Metrics**

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at RRID.

Russell CW, et al. (2019) Comprehensive Identification of Fim-Mediated Inversions in Uropathogenic Escherichia coli with Structural Variation Detection Using Relative Entropy. mSphere, 4(2).

Xia LC, et al. (2016) A genome-wide approach for detecting novel insertion-deletion variants of mid-range size. Nucleic acids research, 44(15), e126.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database: the journal of biological databases and curation, 2015.

Keane TM, et al. (2014) Identification of structural variation in mouse genomes. Frontiers in genetics, 5, 192.