**cwltool**

RRID:SCR_015528  
Type: Tool

**Proper Citation**

cwltool (RRID:SCR_015528)

**Resource Information**

**URL:** [https://github.com/common-workflow-language/cwltool](https://github.com/common-workflow-language/cwltool)

**Proper Citation:** cwltool (RRID:SCR_015528)

**Description:** Reference implementation of the Common Workflow Language standards. It provides complete features and tools and comprehensive validation of CWL. The reference implementation consists of two packages. The cwltool package is the primary Python module containing the reference implementation in the cwltool module and console executable by the same name. The cwlref-runner package is optional and provides an additional entry point under the alias cwl-runner, which is the implementation-agnostic name for the default CWL interpreter installed on a host.

**Synonyms:** CWLtool, Common Workflow Language Tool

**Resource Type:** software toolkit, software resource, source code

**Defining Citation:** [DOI:10.6084/m9.figshare.3115156.v2](https://doi.org/10.6084/m9.figshare.3115156.v2)

**Keywords:** language, reference implementation, python

**Availability:** Available for download

**Resource Name:** cwltool

**Resource ID:** SCR_015528

**Alternate IDs:** OMICS_28977

**Alternate URLs:** [https://sources.debian.org/src/cwltool/](https://sources.debian.org/src/cwltool/)
Record Creation Time: 20220129T080326+0000
Record Last Update: 20240705T054204+0000

Ratings and Alerts

No rating or validation information has been found for cwltool.
No alerts have been found for cwltool.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Haft DH, et al. (2024) RefSeq and the prokaryotic genome annotation pipeline in the age of metagenomes. Nucleic acids research, 52(D1), D762.


Lim HG, et al. (2021) Orchestrating an Optimized Next-Generation Sequencing-Based Cloud Workflow for Robust Viral Identification during Pandemics. Biology, 10(10).


Vera Alvarez R, et al. (2021) PM4NGS, a project management framework for next-generation sequencing data analysis. GigaScience, 10(1).


Corley M, et al. (2021) fSHAPE, fSHAPE-eCLIP, and SHAPE-eCLIP probe transcript regions that interact with specific proteins. STAR protocols, 2(3), 100762.


