

Resource Summary Report

Generated by RRID on Aug 7, 2026

YAML

RRID:SCR_021710

Type: Tool

Proper Citation

YAML (RRID:SCR_021710)

Resource Information

URL: <https://yaml.org>

Proper Citation: YAML (RRID:SCR_021710)

Description: YAML is a human friendly data serialization language for all programming languages. Unicode based data serialization language designed around common native data types of agile programming languages. Useful for programming needs ranging from configuration files to Internet messaging to object persistence to data auditing.

Synonyms: YAML 1.2

Resource Type: software resource

Keywords: Data serialization language, common native data types, agile programming languages, configuration files, Internet messaging, object persistence, data auditing

Availability: Free, Freely available

Resource Name: YAML

Resource ID: SCR_021710

Alternate URLs: <https://yaml.org/spec/1.2.1/>

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260801T190723+0000

Ratings and Alerts

No rating or validation information has been found for YAML.

No alerts have been found for YAML.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Arweiler J, et al. (2026) Batch Distillation Data for Developing Machine Learning Anomaly Detection Methods. Scientific data, 13(1).

Demšar J, et al. (2026) QuNex recipes: Executable, human-readable workflows for reproducible neuroimaging research. Imaging neuroscience (Cambridge, Mass.), 4.

Yedurkar DP, et al. (2025) SPA-IoT with MCSV-CNN: a novel IoT-enabled method for robust pre-ictal seizure prediction. BMC medical informatics and decision making, 25(1), 354.

Bueckle A, et al. (2025) Construction, Deployment, and Usage of the Human Reference Atlas Knowledge Graph for Linked Open Data. bioRxiv : the preprint server for biology.

Boerman JP, et al. (2025) Data processing techniques to improve data integration from dairy farms. JDS communications, 6(3), 339.

Linssen C, et al. (2025) NESTML: a generic modeling language and code generation tool for the simulation of spiking neural networks with advanced plasticity rules. Frontiers in neuroinformatics, 19, 1544143.

Demšar J, et al. (2025) QuNex Recipes: Executable, Human-Readable Workflows for Reproducible Neuroimaging Research. bioRxiv : the preprint server for biology.

Bueckle A, et al. (2025) Construction, Deployment, and Usage of the Human Reference Atlas Knowledge Graph. Scientific data, 12(1), 1100.

Polyanskiy MN, et al. (2024) Refractiveindex.info database of optical constants. Scientific data, 11(1), 94.

Cougnaud L, et al. (2024) Interactive medical and safety monitoring in clinical trials with clinDataReview: a validated and open-source reporting tool. Frontiers in medicine, 11, 1356323.

Uzuner H, et al. (2024) Orthanq: transparent and uncertainty-aware haplotype quantification with application in HLA-typing. BMC bioinformatics, 25(1), 240.

Owen RL, et al. (2023) A standard descriptor for fixed-target serial crystallography. Acta crystallographica. Section D, Structural biology, 79(Pt 8), 668.

Oliveira L, et al. (2023) CusProSe: a customizable protein annotation software with an application to the prediction of fungal secondary metabolism genes. Scientific reports,

13(1), 1417.

García S, et al. (2023) Software variability in service robotics. *Empirical software engineering*, 28(2), 24.

van der Putten BCL, et al. (2022) Software testing in microbial bioinformatics: a call to action. *Microbial genomics*, 8(3).

van der Velde KJ, et al. (2022) FAIR Genomes metadata schema promoting Next Generation Sequencing data reuse in Dutch healthcare and research. *Scientific data*, 9(1), 169.

Matentzoglou N, et al. (2022) Ontology Development Kit: a toolkit for building, maintaining and standardizing biomedical ontologies. *Database : the journal of biological databases and curation*, 2022.

Barho F, et al. (2022) Qudi-HiM: an open-source acquisition software package for highly multiplexed sequential and combinatorial optical imaging. *Open research Europe*, 2, 46.

Foley P, et al. (2022) OpenFL: the open federated learning library. *Physics in medicine and biology*, 67(21).

Parkhurst JM, et al. (2021) Parakeet: a digital twin software pipeline to assess the impact of experimental parameters on tomographic reconstructions for cryo-electron tomography. *Open biology*, 11(10), 210160.