

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 3, 2026

[refgenie](#)

RRID:SCR_017574

Type: Tool

Proper Citation

refgenie (RRID:SCR_017574)

Resource Information

URL: <http://refgenie.databio.org>

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Description: Software tool to organize, retrieve, and share genome analysis resources. Reference genome assembly asset manager. In addition to genome indexes, can manage any files related to reference genomes, including sequences and annotation files. Includes command line interface and server application that provides RESTful API, so it is useful for both tool development and analysis.

Synonyms: reference genome manager

Resource Type: software application, software resource, service resource, data management software

Defining Citation: [DOI:10.1101/698704](https://doi.org/10.1101/698704)

Keywords: Organize, retrieve, share, genome, analysis, reference, assembly, asset, manager, sequence, annotation, file, command, line, interface, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: refgenie

Resource ID: SCR_017574

Alternate IDs: biotools:Refgenie

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

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260803T040751+0000

Ratings and Alerts

No rating or validation information has been found for refgenie.

No alerts have been found for refgenie.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Zacharias NM, et al. (2025) Differential Efficacy of Bevacizumab and Erlotinib in Preclinical Models of Renal Medullary Carcinoma and Fumarate Hydratase-Deficient Renal Cell Carcinoma. Molecular cancer therapeutics.

Stolarczyk M, et al. (2021) Identity and compatibility of reference genome resources. NAR genomics and bioinformatics, 3(2), lqab036.

M??lder F, et al. (2021) Sustainable data analysis with Snakemake. F1000Research, 10, 33.

Smith JP, et al. (2021) PEPPRO: quality control and processing of nascent RNA profiling data. Genome biology, 22(1), 155.

Smith JP, et al. (2021) PEPATAC: an optimized pipeline for ATAC-seq data analysis with serial alignments. NAR genomics and bioinformatics, 3(4), lqab101.

Stolarczyk M, et al. (2020) Refgenie: a reference genome resource manager. GigaScience, 9(2).