

Resource Summary Report

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Docker Desktop

RRID:SCR_016445

Type: Tool

Proper Citation

Docker Desktop (RRID:SCR_016445)

Resource Information

URL: <https://www.docker.com/products/docker-desktop>

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Description: Software development environment that helps users build containerized software using Docker and Kubernetes softwares. It is executable on desktop and cloud, and allows access to a vast library of community containerized content in Docker Hub.

Abbreviations: DD

Synonyms: Docker, DockerDesktop

Resource Type: software application, software development environment, software development tool, software resource

Keywords: software, container, build, code, coding, containerize, develop, development, environment, application

Availability: Free, Commercially available, Requires account to download, Available for download

Resource Name: Docker Desktop

Resource ID: SCR_016445

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260821T194105+0000

Ratings and Alerts

No rating or validation information has been found for Docker Desktop.

No alerts have been found for Docker Desktop.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

David MA, et al. (2026) Demystifying machine learning approaches in digital bone imaging using microCT and HRpQCT. Bone reports, 29, 101911.

Tang J, et al. (2026) Protocol for AI-powered classification of IDH-mutant astrocytoma using GUIDE. STAR protocols, 7(2), 104512.

Bangert K, et al. (2026) Modular Open-Source Stirred Tank Reactor (MOSTR), an Internet of Things (IoT) system for engineering education. HardwareX, 26, e00776.

Rutz A, et al. (2026) MultiMS2: A curated multi-modal, multi-energy spectral library for metabolomics. GigaScience, 15.

Nathan N, et al. (2026) Tumor-draining lymph nodes in ovarian cancer lack germinal centers but harbor tumor-reactive memory B cells clonally linked to intra-tumoral B cells. Immunity, 59(6), 1743.

Bowman DE, et al. (2025) Protocol for predicting single- and multiple-dose-dependent gene expression using deep generative learning. STAR protocols, 6(3), 103932.

Ospina OE, et al. (2025) spatialGE Is a User-Friendly Web Application That Facilitates Spatial Transcriptomics Data Analysis. Cancer research, 85(5), 848.

Grewal JK, et al. (2025) Protocol for obtaining cancer type and subtype predictions using subSCOPE. STAR protocols, 6(2), 103705.

Jayasinghe RG, et al. (2025) Single-cell transcriptomic profiling reveals diversity in human iNKT cells across hematologic tissues. Cell reports, 44(5), 115587.

Holsten L, et al. (2024) hCoCena: A toolbox for network-based co-expression analysis and horizontal integration of transcriptomic datasets. STAR protocols, 5(1), 102922.

Cotugno G, et al. (2024) A containerised approach for multiform robotic applications. Frontiers in robotics and AI, 11, 1358978.

Aoki H, et al. (2024) CD8+ T cell memory induced by successive SARS-CoV-2 mRNA vaccinations is characterized by shifts in clonal dominance. Cell reports, 43(3), 113887.

Bokor BJ, et al. (2023) Network-centric analysis of co-fractionated protein complex profiles using SECAT. STAR protocols, 4(2), 102293.

Galeano Niño JL, et al. (2023) INVADeseq to identify cell-adherent or invasive bacteria and the associated host transcriptome at single-cell-level resolution. *Nature protocols*, 18(11), 3355.

Wirth JS, et al. (2023) Automating microbial taxonomy workflows with PHANTASM: phylogenomic analyses for the taxonomy and systematics of microbes. *Nucleic acids research*, 51(7), 3067.

Aschenbrenner AC, et al. (2023) huva: A human variation analysis framework to predict gene perturbation from population-scale multi-omics data. *STAR protocols*, 4(2), 102193.

Fairbrother-Browne A, et al. (2023) ensemblQueryR: fast, flexible and high-throughput querying of Ensembl LD API endpoints in R. *GigaByte (Hong Kong, China)*, 2023, 1.

Chaerony Siffa I, et al. (2022) Adamant: a JSON schema-based metadata editor for research data management workflows. *F1000Research*, 11, 475.

Bonaguro L, et al. (2022) Human variation in population-wide gene expression data predicts gene perturbation phenotype. *iScience*, 25(11), 105328.

Cheng Z, et al. (2021) Identifying tumorigenic non-coding mutations through altered cis-regulation. *STAR protocols*, 2(4), 100934.