

Resource Summary Report

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cowplot

RRID:SCR_018081

Type: Tool

Proper Citation

cowplot (RRID:SCR_018081)

Resource Information

URL: <https://cran.r-project.org/web/packages/cowplot/index.html>

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Description: Software R package as streamlined plot theme and plot annotations for ggplot2. Provides various features that help with creating publication quality figures with ggplot2, such as set of themes, functions to align plots and arrange them into complex compound figures, and functions that make it easy to annotate plots and or mix plots with images.

Synonyms: R package cowplot

Resource Type: software application, data visualization software, data processing software, software resource

Keywords: Plot, annotation, publication figure, image

Availability: Free, Available for download, Freely available

Resource Name: cowplot

Resource ID: SCR_018081

Alternate URLs: <https://wilkelab.org/cowplot/>

License: GPL-2

Record Creation Time: 20220129T080338+0000

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Ratings and Alerts

No rating or validation information has been found for cowplot.

No alerts have been found for cowplot.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 56 mentions in open access literature.

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

Allen AM, et al. (2026) Differential neuronal survival defines a novel axis of sexual dimorphism in the Drosophila brain. *Cell genomics*, 101125.

Meghdadi B, et al. (2026) Digital twins for in vivo metabolic flux estimations in patients with brain cancer. *Cell metabolism*, 38(1), 228.

Xie A, et al. (2025) Utilizing Untargeted Lipidomics Technology to Elucidate Differences in Lipid Compositions Among Sensitive Dry, Sensitive Oily and Healthy Skin Types. *Metabolites*, 15(5).

Berger AH, et al. (2025) High-resolution transcriptional impact of AIRE: effects of pathogenic variants p.Arg257Ter, p.Cys311Tyr, and polygenic risk variant p.Arg471Cys. *Frontiers in immunology*, 16, 1572789.

Ali M, et al. (2025) Temporal transcriptomic changes in the THY-Tau22 mouse model of tauopathy display cell type- and sex-specific differences. *Acta neuropathologica communications*, 13(1), 93.

Davar D, et al. (2025) Combined Targeting of PD-1 and TIM-3 in Patients with Locally Advanced or Metastatic Non-Small Cell Lung Cancer: AMBER Part 2B. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(16), 3443.

Burchert HH, et al. (2025) Oxygen dissociation curve inflection point during incremental exercise: a trigger for the Bohr effect. *Pflugers Archiv : European journal of physiology*, 477(8), 1075.

Fuhrmann E, et al. (2025) Extended poly(A) tails are a shared feature of herpesvirus mRNAs. *bioRxiv : the preprint server for biology*.

Mauer Sutovska H, et al. (2025) Dark-phase melatonin administration does not reduce blood pressure but induces changes in parameters related to the control of the cardiovascular system in spontaneously hypertensive rats. *Hypertension research : official journal of the Japanese Society of Hypertension*, 48(8), 2218.

Grice GL, et al. (2025) Lipoyl deglutarylation by ABHD11 regulates mitochondrial and T cell metabolism. *Nature chemical biology*, 21(12), 1915.

Davar D, et al. (2025) Combined Targeting of PD-1 and TIM-3 in Patients with Locally Advanced or Metastatic Melanoma: AMBER Cohorts 1c, 1e, and 2A. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 31(16), 3433.

Bui HV, et al. (2025) White and brown adipose tissue share a convergent fibro-adipogenic progenitor population. *EMBO reports*, 26(22), 5612.

Allen AM, et al. (2025) A high-resolution atlas of the brain predicts lineage and birth order underlying neuronal identity. *Cell genomics*, 101103.

Peskett TR, et al. (2025) A network of P-body and Whi3 condensates adjusts cell fate decisions to cellular context. *Molecular cell*, 85(19), 3661.

Okoye GD, et al. (2025) Single-cell map of innate-like lymphocyte response to *Francisella tularensis* infection reveals interleukin-17-dependent protection by MAIT cells. *iScience*, 28(3), 111810.

Paloviita P, et al. (2025) Integrated transcriptomic analysis reveals metabolic remodeling and gene expression networks related to human 8-cell-stage embryo-like cells. *Cell reports*, 45(1), 116748.

Pierotti S, et al. (2024) FlexLMM: a Nextflow linear mixed model framework for GWAS. *Bioinformatics (Oxford, England)*, 41(1).

Banerjee S, et al. (2024) YY1 knockout in pro-B cells impairs lineage commitment, enabling unusual hematopoietic lineage plasticity. *Genes & development*, 38(17-20), 887.

Ali M, et al. (2024) Single cell transcriptome analysis of the THY-Tau22 mouse model of Alzheimer's disease reveals sex-dependent dysregulations. *Cell death discovery*, 10(1), 119.

Zeglinski K, et al. (2024) An optimized protocol for quality control of gene therapy vectors using nanopore direct RNA sequencing. *Genome research*, 34(11), 1966.