Resource Summary Report

Generated by dkNET on May 9, 2025

forestplot

RRID:SCR_023633

Type: Tool

Proper Citation

forestplot (RRID:SCR_023633)

Resource Information

URL: https://CRAN.R-project.org/package=forestplot

Proper Citation: forestplot (RRID:SCR_023633)

Description: Software R package that allows for multiple confidence intervals per row, custom fonts for each text element, custom confidence intervals, text mixed with expressions, and more. Advanced Forest Plot using 'grid' graphics. Used to extend the use of forest plots beyond meta analyses.

Resource Type: software toolkit, software resource

Keywords: multiple confidence intervals per row, custom fonts for each text element, custom confidence intervals, text mixed with expressions,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: forestplot

Resource ID: SCR_023633

License: GPL v2

Record Creation Time: 20230601T050210+0000

Record Last Update: 20250508T070131+0000

Ratings and Alerts

No rating or validation information has been found for forestplot.

No alerts have been found for forestplot.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. Clinical and translational medicine, 15(1), e70094.

Bentley AR, et al. (2024) Lipidomics profiling and circulating triglyceride concentrations in sub-Saharan African individuals. Scientific reports, 14(1), 20834.

Zhen L, et al. (2024) Activated hedgehog gene pattern correlates with dismal clinical outcome and tumor microenvironment heterogeneity in hepatocellular carcinoma. Heliyon, 10(5), e26989.

Liu W, et al. (2024) SnapHiC-G: identifying long-range enhancer-promoter interactions from single-cell Hi-C data via a global background model. Briefings in bioinformatics, 25(5).

Lu Z, et al. (2024) High expression of CCNB2 is an independent predictive poor prognostic biomarker and correlates with immune infiltrates in breast carcinoma. Heliyon, 10(10), e31586.

Wang D, et al. (2024) Race as a prognostic factor of breast mucinous carcinoma. Journal of cancer research and clinical oncology, 151(1), 25.

Martinez-Carrasco A, et al. (2023) Genetic meta-analysis of levodopa induced dyskinesia in Parkinson's disease. NPJ Parkinson's disease, 9(1), 128.

Gallagher RI, et al. (2023) Protein signaling and drug target activation signatures to guide therapy prioritization: Therapeutic resistance and sensitivity in the I-SPY 2 Trial. Cell reports. Medicine, 4(12), 101312.