

Resource Summary Report

Generated by [ASWG](#) on Aug 3, 2026

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,

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: 20260803T040850+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

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Xie H, et al. (2026) B2M regulates ELANE in pyroptosis to affect pancreatic cancer progression. *Translational oncology*, 63, 102613.

You P, et al. (2025) Knockdown of RFC4 inhibits cell proliferation of oral squamous cell carcinoma in vitro and in vivo. *FEBS open bio*, 15(2), 346.

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.

Liu J, et al. (2025) Identification and validation of T cell senescence-related prognostic genes in gastric carcinoma and investigation of their potential regulatory mechanisms. *Discover oncology*, 16(1), 986.

Pang KL, et al. (2025) Deciphering a proliferation-essential gene signature based on CRISPR-Cas9 screening to predict prognosis and characterize the immune microenvironment in HNSCC. *BMC cancer*, 25(1), 756.

Yao XR, et al. (2025) C16orf74 is a novel prognostic biomarker and associates with immune infiltration in head and neck squamous cell carcinoma. *PloS one*, 20(5), e0322701.

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.

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

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.

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).

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

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.

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