

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

glmnet

RRID:SCR_015505

Type: Tool

Proper Citation

glmnet (RRID:SCR_015505)

Resource Information

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

Proper Citation: glmnet (RRID:SCR_015505)

Description: Procedures for fitting the entire lasso or elastic-net regularization path for linear regression, logistic and multinomial regression models, Poisson regression and the Cox model. The algorithm uses cyclical coordinate descent in a path-wise fashion.

Synonyms: Lasso and Elastic-Net Regularized Generalized Linear Models

Resource Type: software toolkit, software resource

Keywords: data regression, cyclical coordinate descent, linear model

Availability: Free, Available for download

Resource Name: glmnet

Resource ID: SCR_015505

Alternate URLs: <https://www.jstatsoft.org/article/view/v033i01>

License: GNU GENERAL PUBLIC LICENSE Version 2

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260803T040656+0000

Ratings and Alerts

No rating or validation information has been found for glmnet.

No alerts have been found for glmnet.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 464 mentions in open access literature.

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

Hua S, et al. (2026) Spatiotemporal profiling of endocytic regulators in the immunosuppressive TAM microenvironment of glioma. *Brain research*, 1872, 150086.

Jiang Y, et al. (2025) An integrated analysis of scRNA-seq and RNA-seq data revealed metastasis-related regulators as prognostic indicators in lung adenocarcinoma. *Journal of thoracic disease*, 17(4), 2473.

Yan M, et al. (2025) Whole lung radiomic features are associated with overall survival in patients with locally advanced non-small cell lung cancer treated with definitive radiotherapy. *Radiation oncology (London, England)*, 20(1), 9.

Beaumont C, et al. (2025) Interspecies predictions of growth traits from quantitative transcriptome data acquired during fruit development. *Journal of experimental botany*, 76(12), 3390.

Xiang L, et al. (2025) Hub biomarkers and their clinical relevance in glycometabolic disorders: A comprehensive bioinformatics and machine learning approach. *Chinese medical journal*, 138(16), 2016.

Jiang N, et al. (2025) Machine learning and deep learning to improve overall survival prediction in cervical cancer patients. *Translational cancer research*, 14(5), 3057.

Su M, et al. (2025) Hypoxia-related signatures predicts survival, immunosuppression and PARP inhibitor resistance in HCC. *Discover oncology*, 16(1), 1116.

Zhang X, et al. (2025) A nomogram for predicting the risk of tigecycline-associated drug-induced liver injury in a Chinese population. *Scientific reports*, 15(1), 22593.

Jiang X, et al. (2025) Depletion of Effector Regulatory T Cells Associates with Major Response to Induction Dual Immune Checkpoint Blockade. *Cancer discovery*, 15(8), 1569.

Zhang L, et al. (2025) Identification of anoikis-related genes in heart failure: bioinformatics and experimental validation. *Hereditas*, 162(1), 163.

Li X, et al. (2025) Peripheral blood cytokine profiles predict the severity of SARS-CoV-2 infection: an EPIC3 study analysis. *BMC infectious diseases*, 25(1), 677.

Carneiro-Nascimento S, et al. (2025) Intravital calcium imaging of meningeal macrophages reveals niche-specific dynamics and aberrant responses to brain hyperexcitability. *bioRxiv : the preprint server for biology*.

Jin D, et al. (2025) Unveiling the prognostic and immunological role of IFI44 in glioma. *Annals of medicine*, 57(1), 2593209.

Yang Q, et al. (2025) Implication of an exosome-based gene signature for estimating clinical outcomes of triple-negative breast cancer and assisting in individualized therapy. *Scientific reports*, 15(1), 37774.

Zhao Y, et al. (2025) Identification and validation of a prognostic model for HER2-low breast cancer based on unfolded protein response-related genes. *Discover oncology*, 16(1), 1866.

Chang C, et al. (2025) Genome wide DNA methylation and transcriptome integration analysis reveals potential markers in type A aortic dissection pathogenesis. *Scientific reports*, 15(1), 42452.

Wang Y, et al. (2025) Comprehensive profiling of chemokine and NETosis-associated genes in sarcopenia: construction of a machine learning-based diagnostic nomogram. *Frontiers in medicine*, 12, 1606430.

Li X, et al. (2025) Enhancing fibroblast-epithelial cell communications: Serpine2 as a key molecule in *Fusobacterium nucleatum*-promoted colon cancer. *Frontiers in immunology*, 16, 1563922.

Jiang X, et al. (2025) Exposure accumulation drives age-dependent disease architectures and polygenic risk scores. *medRxiv : the preprint server for health sciences*.

Pappas C, et al. (2025) Identification of clinical and virological correlates associated with influenza A candidate vaccine virus (CVV) attenuation in a ferret model. *Journal of virology*, 99(10), e0102325.