

Resource Summary Report

Generated by ASWG on Aug 26, 2026

psych

RRID:SCR_021744

Type: Tool

Proper Citation

psych (RRID:SCR_021744)

Resource Information

URL: <https://cran.r-project.org/package=psych>

Proper Citation: psych (RRID:SCR_021744)

Description: Software R package for multivariate analysis and scale construction using factor analysis, principal component analysis, cluster analysis and reliability analysis. Procedures for Psychological, Psychometric, and Personality Research. Used for personality, psychometric theory and experimental psychology.

Resource Type: software resource, software toolkit

Keywords: Psychological research procedure, Psychometric research procedure, Personality research procedure, factor analysis, principal component analysis, cluster analysis, reliability analysis

Availability: Free, Available for download, Freely available

Resource Name: psych

Resource ID: SCR_021744

Alternate URLs: <https://personality-project.org/r/psych/>, <https://sources.debian.org/src/r-cran-psych/>

License: GPL v3

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260821T194204+0000

Ratings and Alerts

No rating or validation information has been found for psych.

No alerts have been found for psych.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 82 mentions in open access literature.

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

Li N, et al. (2026) Exploration of m7G-related immune genes and construction of a prognostic risk model in gastric cancer. Scientific reports, 16(1).

Yang H, et al. (2026) Decoding the role of polyamine metabolism in lung adenocarcinoma prognosis: A triangulated approach combining transcriptome, single-cell and Mendelian randomization analyses. Oncology letters, 32(1), 310.

Lin B, et al. (2026) Transcriptome and experimental validation identify prognostic genes associated with lipotoxicity in thyroid carcinoma. BMC cancer, 26(1).

Zhu X, et al. (2026) Comparative genomics of light harvesting chlorophyll a/b binding protein (LHC) family in green jujube (Ziziphus mauritiana) reveal the effect of domestication based on haplotype-resolved genome. BMC plant biology, 26(1).

Shang C, et al. (2026) Integrated Single-Cell and Bulk RNA Sequencing Identifies Macrophage Heterogeneity and Mitophagy-Related Biomarkers in Idiopathic Pulmonary Fibrosis. International journal of molecular sciences, 27(10).

Li J, et al. (2026) Mining Potential Therapeutic Targets for T Cell Exhaustion in Osteoarthritis by Integrating Mendelian Randomization and Single-Cell Sequencing. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(2), e71483.

Geng M, et al. (2026) ZSL Orchestrates Synaptonemal Complex Assembly as a Central Region Scaffold to Ensure Synapsis Fidelity and Crossover Control in Polyploid Meiosis. Advanced science (Weinheim, Baden-Wurtemberg, Germany), 13(27), e21496.

Hu X, et al. (2026) A benchmarking of genomic selection models for predicting grain-yield related traits using haplotype-based and genome-wide association study-based markers in rice. The plant genome, 19(2), e70226.

Zhang T, et al. (2026) Identification and validation of paraptosis-related prognostic biomarkers in lung adenocarcinoma: An observational study based on transcriptomics and clinical outcomes. Medicine, 105(8), e47724.

Liu X, et al. (2026) Probing uric acid-related prognostic genes and their molecular mechanisms in prostate cancer based on transcriptomic data. Discover oncology, 17(1).

Su YT, et al. (2026) Integrative analysis of fitness and metabolic effects of a large multidrug-resistant plasmid in *Salmonella* across diverse serovars. *Microbial genomics*, 12(5).

Xiao WW, et al. (2026) Integrated Bioinformatic and Experimental Identification of DHCR24 and NRG1 as Key Cellular Aging Genes in Diabetic Cardiomyopathy. *Diabetes, metabolic syndrome and obesity : targets and therapy*, 19, 578414.

Si X, et al. (2026) Investigating the molecular mechanisms of glutamine metabolism and mitochondria-related biomarkers in Alzheimer's disease through transcriptomics and experimental validation. *European journal of medical research*, 31(1), 274.

Su Q, et al. (2026) Integrated bulk RNA-seq and scRNA-seq identification of a novel "PET-SPI1-MYL9" transcriptional axis in lung adenocarcinoma driven by polyethylene terephthalate exposure. *Translational cancer research*, 15(3), 173.

Tang D, et al. (2026) Construction and validation of risk prediction model for glioblastoma associated with cancer stem cells and disulfidptosis. *Translational cancer research*, 15(3), 157.

Wang X, et al. (2026) Combining single cell and bulk transcriptomics with Mendelian randomization identifies gut microbiota related prognostic genes and mechanisms in thyroid cancer. *Discover oncology*, 17(1).

Christian P, et al. (2026) Dissociation between implicit and explicit gaze perception and their metacognitive representations scales with the degree of autistic traits. *iScience*, 29(5), 115602.

He H, et al. (2026) Multicentre development and two-stage validation of a patient-reported outcome measure for chronic obstructive pulmonary disease. *iScience*, 29(4), 115391.

Hall BL, et al. (2026) Changes in interlimb coordination induced by within-stride changes in treadmill speed. *Journal of neurophysiology*, 136(1), 48.

Xiao Z, et al. (2025) Inflammatory Biomarkers in Coronary Artery Disease: Insights From Mendelian Randomization and Transcriptomics. *Journal of inflammation research*, 18, 3177.