

Resource Summary Report

Generated by [kravitz2](#) on Aug 3, 2026

MANOR

RRID:SCR_001305

Type: Tool

Proper Citation

MANOR (RRID:SCR_001305)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/MANOR.html>

Proper Citation: MANOR (RRID:SCR_001305)

Description: Software package for importation, normalization, visualization, and quality control functions to correct identified sources of variability in array-CGH (Comparative genomic hybridization) experiments.

Abbreviations: MANOR

Synonyms: CGH Micro-Array NORmalization

Resource Type: software resource

Keywords: copy number variation, data import, microarray, preprocessing, quality control, two channel, comparative genomic hybridization

Availability: Free, Available for download, Freely available

Resource Name: MANOR

Resource ID: SCR_001305

Alternate IDs: OMICS_02028

License: GNU General Public License, v3

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260801T190127+0000

Ratings and Alerts

No rating or validation information has been found for MANOR.

No alerts have been found for MANOR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Sisák A, et al. (2025) The Association Between Psychosocial Stress and Perinatal Maternal Depressive Symptoms: A Case-Control Study in a Regional Medical Center in Hungary. *Journal of personalized medicine*, 15(7).

Jung HS, et al. (2024) Coumarin derivatives ameliorate the intestinal inflammation and pathogenic gut microbiome changes in the model of infectious colitis through antibacterial activity. *Frontiers in cellular and infection microbiology*, 14, 1362773.

Chanda D, et al. (2024) Meta-analysis reveals obesity associated gut microbial alteration patterns and reproducible contributors of functional shift. *Gut microbes*, 16(1), 2304900.

Ye X, et al. (2024) Leveraging baseline transcriptional features and information from single-cell data to power the prediction of influenza vaccine response. *Frontiers in cellular and infection microbiology*, 14, 1243586.

Wang L, et al. (2024) Cyber warfare: a study of Zelenskyy's social media political performance strategies and effects. *Frontiers in psychology*, 15, 1478639.

Douglas GM, et al. (2022) Integrating phylogenetic and functional data in microbiome studies. *Bioinformatics (Oxford, England)*, 38(22), 5055.

Xu D, et al. (2021) The bacterial community and metabolome dynamics and their interactions modulate fermentation process of whole crop corn silage prepared with or without inoculants. *Microbial biotechnology*, 14(2), 561.

Rapp JZ, et al. (2021) Divergent Genomic Adaptations in the Microbiomes of Arctic Subzero Sea-Ice and Cryopeg Brines. *Frontiers in microbiology*, 12, 701186.

Eidlin Levy H, et al. (2021) Numbers (but not words) make math anxious individuals sweat: Physiological evidence. *Biological psychology*, 165, 108187.

Liu J, et al. (2021) A high-risk retinoblastoma subtype with stemness features, dedifferentiated cone states and neuronal/ganglion cell gene expression. *Nature communications*, 12(1), 5578.

Arslan Aydin Ü, et al. (2021) Speech Driven Gaze in a Face-to-Face Interaction. *Frontiers in neurorobotics*, 15, 598895.

McGivern C, et al. (2021) Alcohol attention bias in 14-16 year old adolescents: an eye tracking study. *Psychopharmacology*, 238(3), 655.

Yuen NH, et al. (2021) Driving With Distraction: Measuring Brain Activity and Oculomotor Behavior Using fMRI and Eye-Tracking. *Frontiers in human neuroscience*, 15, 659040.

Yin X, et al. (2020) A Comparative Evaluation of Tools to Predict Metabolite Profiles From Microbiome Sequencing Data. *Frontiers in microbiology*, 11, 595910.

Bolton KL, et al. (2010) Common variants at 19p13 are associated with susceptibility to ovarian cancer. *Nature genetics*, 42(10), 880.

van Hijum SA, et al. (2008) Supervised Lowess normalization of comparative genome hybridization data--application to lactococcal strain comparisons. *BMC bioinformatics*, 9, 93.