# Resource Summary Report

Generated by RRID on Apr 11, 2025

## BioCarta Pathways

RRID:SCR_006917
Type: Tool

## Proper Citation

BioCarta Pathways (RRID:SCR_006917)

## Resource Information

**URL:** http://www.biocarta.com/

**Proper Citation:** BioCarta Pathways (RRID:SCR_006917)

**Description:** BioCarta Pathways allows users to observe how genes interact in dynamic graphical models. Online maps available within this resource depict molecular relationships from areas of active research. In an open source approach, this community-fed forum constantly integrates emerging proteomic information from the scientific community. It also catalogs and summarizes important resources providing information for over 120,000 genes from multiple species. Find both classical pathways as well as current suggestions for new pathways.

**Synonyms:** BioCarta Pathways

**Resource Type:** data or information resource, database

**Keywords:** graphical model, molecular interaction, molecular relationship, pathway, proteomics, bio.tools, FASEB list

**Funding:**

**Resource Name:** BioCarta Pathways

**Resource ID:** SCR_006917

**Alternate IDs:** nif-0000-02604, biotools:biocarta

**Alternate URLs:** https://bio.tools/biocarta

**Old URLs:** http://www.biocarta.com/genes/allPathways.asp

**Record Creation Time:** 20220129T080238+0000

**Record Last Update:** 20250410T065501+0000

## Ratings and Alerts

No rating or validation information has been found for BioCarta Pathways.

No alerts have been found for BioCarta Pathways.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 1095 mentions in open access literature.

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

Corinaldesi C, et al. (2025) Single-cell transcriptomics of pediatric Burkitt lymphoma reveals intra-tumor heterogeneity and markers of therapy resistance. Leukemia, 39(1), 189.

Li X, et al. (2025) Genetic Nurture Effects on Type 2 Diabetes Among Chinese Han Adults: A Family-Based Design. Biomedicines, 13(1).

Zhou N, et al. (2025) Proteomic patterns associated with ketamine response in major depressive disorders. Cell biology and toxicology, 41(1), 26.

Hua M, et al. (2025) Multiomic machine learning on lactylation for molecular typing and prognosis of lung adenocarcinoma. Scientific reports, 15(1), 3075.

Wang X, et al. (2025) IDH-mutant glioma risk stratification via whole slide images: Identifying pathological feature associations. iScience, 28(1), 111605.

Florio A, et al. (2024) Monolayer culture alters EGFR inhibitor response through abrogation of microRNA-mediated feedback regulation. Scientific reports, 14(1), 7303.

Jaksik R, et al. (2024) Multiomics-Based Feature Extraction and Selection for the Prediction of Lung Cancer Survival. International journal of molecular sciences, 25(7).

Tseropoulos G, et al. (2024) Immobilized NRG1 Accelerates Neural Crest like Cell Differentiation Toward Functional Schwann Cells Through Sustained Erk1/2 Activation and YAP/TAZ Nuclear Translocation. Advanced science (Weinheim, Baden-Wurttemberg,

Germany), 11(33), e2402607.

Duan W, et al. (2024) Radiomic profiling for insular diffuse glioma stratification with distinct biologic pathway activities. Cancer science, 115(4), 1261.

Kim D, et al. (2024) Large-scale integrative analysis of juvenile idiopathic arthritis for new insight into its pathogenesis. Arthritis research & therapy, 26(1), 47.

Reid SE, et al. (2024) Cancer-associated fibroblasts rewire the estrogen receptor response in luminal breast cancer, enabling estrogen independence. Oncogene, 43(15), 1113.

Ismaeel A, et al. (2024) Coordinated Regulation of Myonuclear DNA Methylation, mRNA, and miRNA Levels Associates With the Metabolic Response to Rapid Synergist Ablation-Induced Skeletal Muscle Hypertrophy in Female Mice. Function (Oxford, England), 5(1), zqad062.

Xu C, et al. (2024) Discovery and validation of a 10-gene predictive signature for response to adjuvant chemotherapy in stage II and III colon cancer. Cell reports. Medicine, 5(8), 101661.

Wang S, et al. (2024) Construct prognostic models of multiple myeloma with pathway information incorporated. PLoS computational biology, 20(9), e1012444.

Khan ST, et al. (2024) Single-Cell Meta-Analysis Uncovers the Pancreatic Endothelial Cell Transcriptomic Signature and Reveals a Key Role for NKX2-3 in PLVAP Expression. Arteriosclerosis, thrombosis, and vascular biology, 44(12), 2596.

Noonepalle SKR, et al. (2024) Cell therapy using ex vivo reprogrammed macrophages enhances antitumor immune responses in melanoma. Journal of experimental & clinical cancer research : CR, 43(1), 263.

Kerr CM, et al. (2024) Decellularized heart extracellular matrix alleviates activation of hiPSC-derived cardiac fibroblasts. Bioactive materials, 31, 463.

Gézsi A, et al. (2024) GNN4DM: a graph neural network-based method to identify overlapping functional disease modules. Bioinformatics (Oxford, England), 40(10).

de Vries LE, et al. (2024) Gene-expression profiling of individuals resilient to Alzheimer's disease reveals higher expression of genes related to metallothionein and mitochondrial processes and no changes in the unfolded protein response. Acta neuropathologica communications, 12(1), 68.

Xiao H, et al. (2024) Genetic analyses of 104 phenotypes in 20,900 Chinese pregnant women reveal pregnancy-specific discoveries. Cell genomics, 4(10), 100633.