Resource Summary Report

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BioLayout Express 3D

RRID:SCR_007179
Type: Tool

Proper Citation

BioLayout Express 3D (RRID:SCR_007179)

Resource Information

URL: http://www.biolayout.org

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Description: BioLayout Express3D is a powerful new tool for the visualization and analysis of networks derived from biological systems. Network-based approaches are becoming increasing popular for the analysis of ''omics and other high dimensional data. Networks can be produced from a wide variety of biological relationships, such as interactions between individuals, disease transmission, sequence similarity, metabolic pathways, protein interactions, pathways, regulatory cascades, gene expression, etc. BioLayout Express3D has been specifically designed for visualization, clustering and analysis of large network graphs in two- and three-dimensional space derived primarily, but not exclusively, from biological data. Sponsors: This resource is supported by BBSRC (BB / F003722 / 1) and the Wellcome Trust (GR077040RP). Keywords: Biology, Tool, Software, visualization, Analysis, Network, Biological, System, Dimentional, Data, Disease, Transmission, Sequence, Metabolic, Pathway, Protein, Interaction, Gene, Expression, Clustering, Analysis,

Synonyms: BioLayout Express

Resource Type: software resource, data visualization software, data processing software, software application, data analysis software

Resource Name: BioLayout Express 3D

Resource ID: SCR_007179

Alternate IDs: nif-0000-30182

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260803T040500+0000

Ratings and Alerts

No rating or validation information has been found for BioLayout Express 3D.

No alerts have been found for BioLayout Express 3D.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 123 mentions in open access literature.

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

Hou X, et al. (2025) Gut bacteriophages induce specific-reprogramming of macrophages to generate a protective innate immunity response to lipopolysaccharide exposure. Gut microbes, 17(1), 2524540.

Whiley PJ, et al. (2025) Transcriptomic signatures of host immune responses in aphthous ulcers, the earliest lesions of Crohn's disease, suggest that bacterial uptake, rather than global dysbiosis, is the initiating factor. Immunology and cell biology, 103(5), 473.

Yang J, et al. (2025) Physiological response of safflower to water deficit and genome-wide identification of its NAC transcription factor family. Scientific reports, 15(1), 31257.

Carter-Cusack D, et al. (2025) Wild-type bone marrow cells repopulate tissue resident macrophages and reverse the impacts of homozygous CSF1R mutation. PLoS genetics, 21(1), e1011525.

Matzko RO, et al. (2024) BioNexusSentinel: a visual tool for bioregulatory network and cytohistological RNA-seq genetic expression profiling within the context of multicellular simulation research using ChatGPT-augmented software engineering. Bioinformatics advances, 4(1), vbae046.

Reimann MJ, et al. (2024) Mitral valve transcriptome analysis in thirty-four age-matched Cavalier King Charles Spaniels with or without congestive heart failure caused by myxomatous mitral valve disease. Mammalian genome : official journal of the International Mammalian Genome Society, 35(1), 77.

O'Brien CL, et al. (2024) The relationship between extreme inter-individual variation in macrophage gene expression and genetic susceptibility to inflammatory bowel disease. Human genetics, 143(3), 233.

Liu C, et al. (2024) Genome-wide identification and integrated analysis of TCP genes controlling ginsenoside biosynthesis in Panax ginseng. BMC plant biology, 24(1), 47.

Hu J, et al. (2023) Genome-wide characterization, evolutionary analysis, and expression pattern analysis of the trihelix transcription factor family and gene expression analysis under MeJA treatment in Panax ginseng. BMC plant biology, 23(1), 376.

Prabhu SR, et al. (2023) Erythrocyte miRNA-92a-3p interactions with PfEMP1 as determinants of clinical malaria. Functional & integrative genomics, 23(2), 93.

Val-Calvo J, et al. (2023) Mycobacteriales taxonomy using network analysis-aided, context-uniform phylogenomic approach for non-subjective genus demarcation. mBio, 14(5), e0220723.

Li X, et al. (2023) DNA methylome and transcriptome profiling reveal key electrophysiology and immune dysregulation in hypertrophic cardiomyopathy. Epigenetics, 18(1), 2195307.

Baßler K, et al. (2023) Identification of the novel FOXP3-dependent Treg cell transcription factor MEOX1 by high-dimensional analysis of human CD4+ T cells. Frontiers in immunology, 14, 1107397.

Silvin A, et al. (2022) Dual ontogeny of disease-associated microglia and disease inflammatory macrophages in aging and neurodegeneration. Immunity, 55(8), 1448.

Glenn KC, et al. (2022) Biochemical and clinical studies of putative allergens to assess what distinguishes them from other non-allergenic proteins in the same family. Transgenic research, 31(4-5), 507.

Nirmal AJ, et al. (2022) The Spatial Landscape of Progression and Immunoediting in Primary Melanoma at Single-Cell Resolution. Cancer discovery, 12(6), 1518.

Keshvari S, et al. (2021) CSF1R-dependent macrophages control postnatal somatic growth and organ maturation. PLoS genetics, 17(6), e1009605.

Patkar OL, et al. (2021) Analysis of homozygous and heterozygous Csf1r knockout in the rat as a model for understanding microglial function in brain development and the impacts of human CSF1R mutations. Neurobiology of disease, 151, 105268.

Donaldson DS, et al. (2021) Aging-Related Impairments to M Cells in Peyer's Patches Coincide With Disturbances to Paneth Cells. Frontiers in immunology, 12, 761949.

Gažová I, et al. (2021) CRISPR-Cas9 Editing of Human Histone Deubiquitinase Gene USP16 in Human Monocytic Leukemia Cell Line THP-1. Frontiers in cell and developmental biology, 9, 679544.