Resource Summary Report

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LYSIS

RRID:SCR_001385
Type: Tool

Proper Citation

LYSIS (RRID:SCR_001385)

Resource Information

URL: http://bmsr.usc.edu/software/lysis/

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Description: Interactive software of a set of modular programs (each performing a specific task) that provide an integrated computing environment for data analysis and system modeling. Unique capabilities of LYSIS include input-output nonlinear system modeling and the novel methodology of Principal Dynamic Modes (PDMs). LYSIS is currently available in two versions: one for LYSIS 7.1 Windows and one for LYSIS 7.2 Matlab. Early versions are also available for UNIX environments, distributed as source code that can be compiled for each UNIX implementation (e.g., Solaris, HPUX, Linux). Specific features of LYSIS that cannot be found in commercially available packages include the efficient kernel estimation using Laguerre expansions and the use of Principal Dynamic Modes (PDMs). These enable input-output modeling of dynamic nonlinear systems with relatively short data-records (even in the presence of considerable noise). System Requirements * Operating System ** Windows XP/Vista/7 ** Sun/Unix: Solaris 2.x

Abbreviations: LYSIS

Resource Type: software application, simulation software, software resource, data analysis software, data processing software, software toolkit, source code

Keywords: modeling, data analysis, system modeling, analysis, nonlinear, principal dynamic modes, nonlinear modeling, windows, matlab

Funding: NIBIB P41-EB001978;
NCRR P41-RR01861

Availability: Free, Freely Available

Resource Name: LYSIS

Resource ID: SCR_001385

Alternate IDs: nlx_152571

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260819T044027+0000

Ratings and Alerts

No rating or validation information has been found for LYSIS.

No alerts have been found for LYSIS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 56 mentions in open access literature.

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

Lu W, et al. (2025) Fructose 1,6-bisphosphatase 1 is a potential biomarker affecting the malignant phenotype and aerobic glycolysis in glioblastoma. PeerJ, 13, e18926.

Wysocka A, et al. (2025) High-light-inducible proteins control associations between chlorophyll synthase and the Photosystem II biogenesis factor Ycf39. Plant physiology, 198(2).

Yao B, et al. (2025) A core stemness-associated module reveals PLK1, NUF2, KIF23, CDCA8, TOP2A, CENPF, AURKA, and ASPM as key genes in rectal cancer. European journal of medical research, 31(1), 75.

Wang L, et al. (2025) Investigation of the mechanism by which FOXJ2 inhibits proliferation, metastasis and cell cycle progression of ovarian cancer cells through the PI3K/AKT signaling pathway. European journal of medical research, 30(1), 152.

Anwar SL, et al. (2020) Dynamic Changes of Circulating Mir-155 Expression and the Potential Application as a Non-Invasive Biomarker in Breast Cancer. Asian Pacific journal of cancer prevention : APJCP, 21(2), 491.

Pirro M, et al. (2019) Glycoproteomic Analysis of MGL-Binding Proteins on Acute T-Cell Leukemia Cells. Journal of proteome research, 18(3), 1125.

Papadaki M, et al. (2019) New Insights for RANKL as a Proinflammatory Modulator in Modeled Inflammatory Arthritis. Frontiers in immunology, 10, 97.

Kovacheva M, et al. (2019) Conditional Knockdown of Osteopontin Inhibits Breast Cancer Skeletal Metastasis. International journal of molecular sciences, 20(19).

Chamberlain CA, et al. (2019) Metabolomic profiling of oxalate-degrading probiotic Lactobacillus acidophilus and Lactobacillus gasseri. PloS one, 14(9), e0222393.

Alam MW, et al. (2019) Alectinib, an Anaplastic Lymphoma Kinase Inhibitor, Abolishes ALK Activity and Growth in ALK-Positive Neuroblastoma Cells. Frontiers in oncology, 9, 579.

Imperato S, et al. (2019) Automodified Poly(ADP-Ribose) Polymerase Analysisto Monitor DNA Damagein Peripheral Lymphocytes of Floriculturists Occupationally Exposed to Pesticides. Cells, 8(2).

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Tovell H, et al. (2019) Design and Characterization of SGK3-PROTAC1, an Isoform Specific SGK3 Kinase PROTAC Degrader. ACS chemical biology, 14(9), 2024.

Wang Y, et al. (2018) NS1-binding protein radiosensitizes esophageal squamous cell carcinoma by transcriptionally suppressing c-Myc. Cancer communications (London, England), 38(1), 33.

Friedensohn S, et al. (2018) Synthetic Standards Combined With Error and Bias Correction Improve the Accuracy and Quantitative Resolution of Antibody Repertoire Sequencing in Human Na??ve and Memory B Cells. Frontiers in immunology, 9, 1401.

Peng TT, et al. (2018) Cytisine-Pterocarpan-Derived Compounds: Biomimetic Synthesis and Apoptosis-Inducing Activity in Human Breast Cancer Cells. Molecules (Basel, Switzerland), 23(12).

Shekhar S, et al. (2018) Antibodies Reactive to Commensal Streptococcus mitis Show Cross-Reactivity With Virulent Streptococcus pneumoniae Serotypes. Frontiers in immunology, 9, 747.

Lapek JD, et al. (2017) Detection of dysregulated protein-association networks by high-throughput proteomics predicts cancer vulnerabilities. Nature biotechnology, 35(10), 983.

Megger DA, et al. (2017) Deciphering of the Human Interferon-Regulated Proteome by Mass Spectrometry-Based Quantitative Analysis Reveals Extent and Dynamics of Protein Induction and Repression. Frontiers in immunology, 8, 1139.