Resource Summary Report

Generated by NIF on Apr 22, 2025

BioNumbers

RRID:SCR_002782
Type: Tool

Proper Citation

BioNumbers (RRID:SCR_002782)

Resource Information

URL: http://bionumbers.hms.harvard.edu/

Proper Citation: BioNumbers (RRID:SCR_002782)

Description: Database of key numbers in molecular and cell biology--the quantitative properties of biological systems of interest to computational, systems and molecular cell biologists. Contents of the database range from cell sizes to metabolite concentrations, from reaction rates to generation times, from genome sizes to the number of mitochondria in a cell. Along with the numbers, you'll find the relevant references to the original literature, useful comments, and related numbers. While always of importance to biologists, having numbers in hand is becoming increasingly critical for experimenting, modeling, and analyzing biological systems. BioNumbers was motivated by an appreciation of how long it can take to find even the simplest number in the vast biological literature. All numbers are taken directly from a literature source and that reference is provided with the number. BioNumbers is designed to be highly searchable and queries can be performed by keywords or browsed by menus. BioNumbers is a collaborative community platform where registered users can add content and make comments on existing data. All new entries and commentary are curated to maintain high quality.

Abbreviations: BioNumbers

Synonyms: BioNumbers: The Database of Useful Biological Numbers

Resource Type: data or information resource, database

Defining Citation: PMID:19854939

Keywords: biological, biological system, bionumber, molecular biology, number, photosynthesis, quantitative, sporulation, quantitative analysis, bio.tools, FASEB list

Funding: Harvard University; Massachusetts; USA ;
Weizmann Institute of Science; Rehovot; Israel

Availability: Acknowledgement requested, The community can contribute to this resource

Resource Name: BioNumbers

Resource ID: SCR_002782

Alternate IDs: nif-0000-24396, biotools:bionumbers

Alternate URLs: https://bio.tools/bionumbers

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250422T055042+0000

Ratings and Alerts

No rating or validation information has been found for BioNumbers.

No alerts have been found for BioNumbers.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 45 mentions in open access literature.

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

Hari K, et al. (2025) Low dimensionality of phenotypic space as an emergent property of coordinated teams in biological regulatory networks. iScience, 28(2), 111730.

Rayl ML, et al. (2024) Agonists of the Nuclear Receptor PPAR? Can Produce Biased Signaling. Molecular pharmacology, 106(6), 309.

Carlson HK, et al. (2023) Geochemical constraints on bacteriophage infectivity in terrestrial environments. ISME communications, 3(1), 78.

Culhane KJ, et al. (2022) Kinetic model of GPCR-G protein interactions reveals allokairic

modulation of signaling. Nature communications, 13(1), 1202.

Rashid M, et al. (2022) Network topology metrics explaining enrichment of hybrid epithelial/mesenchymal phenotypes in metastasis. PLoS computational biology, 18(11), e1010687.

Jeanclos E, et al. (2022) Glycolytic flux control by drugging phosphoglycolate phosphatase. Nature communications, 13(1), 6845.

Reyes BC, et al. (2022) A numerical approach for detecting switch-like bistability in mass action chemical reaction networks with conservation laws. BMC bioinformatics, 23(1), 1.

Wang CY, et al. (2021) Metabolome and proteome analyses reveal transcriptional misregulation in glycolysis of engineered E. coli. Nature communications, 12(1), 4929.

Xu P, et al. (2021) Dynamics of microbial competition, commensalism, and cooperation and its implications for coculture and microbiome engineering. Biotechnology and bioengineering, 118(1), 199.

Catozzi S, et al. (2021) Predicted 'wiring landscape' of Ras-effector interactions in 29 human tissues. NPJ systems biology and applications, 7(1), 10.

Steinberg G, et al. (2020) A lipophilic cation protects crops against fungal pathogens by multiple modes of action. Nature communications, 11(1), 1608.

Pasani S, et al. (2020) Hybrid E/M Phenotype(s) and Stemness: A Mechanistic Connection Embedded in Network Topology. Journal of clinical medicine, 10(1).

Horvath N, et al. (2020) Toward a genome scale sequence specific dynamic model of cell-free protein synthesis in Escherichia coli. Metabolic engineering communications, 10, e00113.

Begg BE, et al. (2020) Concentration-dependent splicing is enabled by Rbfox motifs of intermediate affinity. Nature structural & molecular biology, 27(10), 901.

Xu P, et al. (2020) Branch point control at malonyl-CoA node: A computational framework to uncover the design principles of an ideal genetic-metabolic switch. Metabolic engineering communications, 10, e00127.

Zeng W, et al. (2020) Application of an antibody chip for screening differentially expressed proteins during peach ripening and identification of a metabolon in the SAM cycle to generate a peach ethylene biosynthesis model. Horticulture research, 7, 31.

Salvy P, et al. (2020) The ETFL formulation allows multi-omics integration in thermodynamics-compliant metabolism and expression models. Nature communications, 11(1), 30.

Carlson HK, et al. (2020) Selective carbon sources influence the end products of microbial nitrate respiration. The ISME journal, 14(8), 2034.

Ibrahim AFM, et al. (2020) Antibody RING-Mediated Destruction of Endogenous Proteins. Molecular cell, 79(1), 155.

Mikolajewicz N, et al. (2019) Meta-Analytic Methodology for Basic Research: A Practical Guide. Frontiers in physiology, 10, 203.