Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

BioNumbers

RRID:SCR_002782
Type: Tool

Proper Citation

BioNumbers (RRID:SCR_002782)

Resource Information

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

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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: database, data or information resource

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: Free, Freely available

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: 20260808T190354+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 53 mentions in open access literature.

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

Castellanos-Girouard X, et al. (2026) Protein-protein interactions are a major source of epistasis in genetic interaction networks. Nature communications, 17(1).

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.

Platzek A, et al. (2025) Dynamic Organellar Mapping in yeast reveals extensive protein localization changes during ER stress. Nature communications, 16(1), 10842.

Duman?i? M, et al. (2025) Microdosimetry calculations in situ for clinically relevant photon sources and their correlation with the early DNA damage response. Medical physics, 52(7), e17979.

Levak V, et al. (2025) Jasmonic acid and salicylic acid interact to determine spatial regulation of gene expression responses in potato leaf to herbivory by Colorado potato beetle and mechanical wounding. Plant & cell physiology, 66(12), 1878.

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.

Liu D, et al. (2022) Molecular bases of morphologically diffused tumors across multiple cancer types. National science review, 9(11), nwac177.

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.

Chure G, et al. (2022) Anthroponumbers.org: A quantitative database of human impacts on Planet Earth. Patterns (New York, N.Y.), 3(9), 100552.

Liu X, et al. (2022) Quantifying substantial carcinogenesis of genetic and environmental factors from measurement error in the number of stem cell divisions. BMC cancer, 22(1), 1194.

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.

Jahn M, et al. (2021) Protein allocation and utilization in the versatile chemolithoautotroph Cupriavidus necator. eLife, 10.

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

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).

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