Resource Summary Report

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National Library of Medicine

RRID:SCR_011446
Type: Tool

Proper Citation

National Library of Medicine (RRID:SCR_011446)

Resource Information

URL: http://www.nlm.nih.gov/

Proper Citation: National Library of Medicine (RRID:SCR_011446)

Description: NLM collects, organizes, and makes available biomedical science information to scientists, health professionals, and the public. The Library's Web-based databases, including PubMed/Medline and MedlinePlus, are used extensively around the world. NLM conducts and supports research in biomedical communications; creates information resources for molecular biology, biotechnology, toxicology, and environmental health; and provides grant and contract support for training, medical library resources, and biomedical informatics and communications research. Celebrating its 175th anniversary in 2011, the National Library of Medicine (NLM), in Bethesda, Maryland, is a part of the National Institutes of Health, U.S. Department of Health and Human Services (HHS). Since its founding in 1836 as the library of the U.S. Army Surgeon General, NLM has played a pivotal role in translating biomedical research into practice. It is the world's largest biomedical library and the developer of electronic information services that deliver trillions of bytes of data to millions of users every day. Scientists, health professionals, and the public in the United States and around the globe search the Library's online information resources more than 1 billion times each year. The Library is open to all and has many services and resources for scientists, health professionals, historians, and the general public. NLM has over 17 million books, journals, manuscripts, audiovisuals, and other forms of medical information on its shelves, making it the largest health-science library in the world. In today's increasingly digital world, NLM carries out its mission of enabling biomedical research, supporting health care and public health, and promoting healthy behavior by: * Acquiring, organizing, and preserving the world's scholarly biomedical literature; * Providing access to biomedical and health information across the country in partnership with the 5,800-member National Network of Libraries of Medicine (NN/LM); * Serving as a leading global resource for building, curating and providing sophisticated access to molecular biology and genomic information, including those from the Human Genome Project and NIH Common Fund; * Creating high-quality

information services relevant to toxicology and environmental health, health services research, and public health; * Conducting research and development on biomedical communications systems, methods, technologies, and networks and information dissemination and utilization among health professionals, patients, and the general public; * Funding advanced biomedical informatics research and serving as the primary supporter of pre- and post-doctoral research training in biomedical informatics at 18 U.S. universities.

Abbreviations: NLM

Synonyms: U.S. National Library of Medicine

Resource Type: government granting agency

Resource Name: National Library of Medicine

Resource ID: SCR_011446

Alternate IDs: nlx_inv_1005117

Ratings and Alerts

No rating or validation information has been found for National Library of Medicine.

No alerts have been found for National Library of Medicine.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 368 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Li G, et al. (2024) Node-adaptive graph Transformer with structural encoding for accurate and robust lncRNA-disease association prediction. BMC genomics, 25(1), 73.

Xuan P, et al. (2024) Complementary feature learning across multiple heterogeneous networks and multimodal attribute learning for predicting disease-related miRNAs. iScience, 27(2), 108639.

Meng X, et al. (2023) ETGPDA: identification of piRNA-disease associations based on embedding transformation graph convolutional network. BMC genomics, 24(1), 279.

Scholz S, et al. (2023) Listen to the patients! Identifying CML patients' needs analyzing patient-generated content with AI-driven methodologies. Frontiers in digital health, 5,

1243215.

Salyha N, et al. (2023) Hypoxia modeling techniques: A review. Heliyon, 9(2), e13238.

Sandhu HS, et al. (2023) Outpatient medications associated with protection from COVID-19 hospitalization. PloS one, 18(3), e0282961.

Chung HC, et al. (2023) Responsiveness to endurance training can be partly explained by the number of favorable single nucleotide polymorphisms an individual possesses. PloS one, 18(7), e0288996.

Barrott L, et al. (2023) Nurse and pharmacist systemic anti-cancer therapy review clinics and their impact on patient experience and care: A systematic review. Journal of advanced nursing, 79(2), 442.

Nakashima Y, et al. (2022) Induced hepatic stem cells are suitable for human hepatocyte production. iScience, 25(10), 105052.

Zhao Y, et al. (2022) Is coronavirus-related research becoming more interdisciplinary? A perspective of co-occurrence analysis and diversity measure of scientific articles. Technological forecasting and social change, 175, 121344.

Zhang W, et al. (2022) iSnoDi-LSGT: identifying snoRNA-disease associations based on local similarity constraints and global topological constraints. RNA (New York, N.Y.), 28(12), 1558.

Nedoshivin A, et al. (2022) Efficacy and Safety of Ivabradine in Combination with Beta-Blockers in Patients with Stable Angina Pectoris: A Systematic Review and Meta-analysis. Advances in therapy, 39(9), 4189.

Shyamala N, et al. (2022) In silico identification of single nucleotide variations at CpG sites regulating CpG island existence and size. Scientific reports, 12(1), 3574.

Lastra-Díaz JJ, et al. (2022) HESML: a real-time semantic measures library for the biomedical domain with a reproducible survey. BMC bioinformatics, 23(1), 23.

Jiang H, et al. (2022) An effective drug-disease associations prediction model based on graphic representation learning over multi-biomolecular network. BMC bioinformatics, 23(1), 9.

Padariya M, et al. (2022) The Elephant Evolved p53 Isoforms that Escape MDM2-Mediated Repression and Cancer. Molecular biology and evolution, 39(7).

Wang Y, et al. (2021) ICLRBBN: a tool for accurate prediction of potential lncRNA disease associations. Molecular therapy. Nucleic acids, 23, 501.

Brown J, et al. (2021) Interspecies chimeric conditions affect the developmental rate of human pluripotent stem cells. PLoS computational biology, 17(3), e1008778.

Nie R, et al. (2021) Efficient framework for predicting MiRNA-disease associations based on improved hybrid collaborative filtering. BMC medical informatics and decision making, 21(Suppl 1), 254.

Javed M, et al. (2021) Exploring the Potential of Interferon Gamma Gene as Major Immune Responder for Bovine Tuberculosis in River Buffalo. BioMed research international, 2021, 5532864.