

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](http://FDILab.SciCrunch.org) on May 3, 2025

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

Funding:

Resource Name: National Library of Medicine

Resource ID: SCR_011446

Alternate IDs: nlx_inv_1005117

Record Creation Time: 20220129T080304+0000

Record Last Update: 20250420T014541+0000

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 381 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Mao B, et al. (2025) Congenital muscular dystrophies and myopathies: the leading cause of genetic muscular disorders in eleven Chinese families. BMC musculoskeletal disorders, 26(1), 51.

Williamson BD, et al. (2024) Predicting neutralization susceptibility to combination HIV-1 monoclonal broadly neutralizing antibody regimens. *PloS one*, 19(9), e0310042.

Shi K, et al. (2024) Predicting microbe-disease association based on graph autoencoder and inductive matrix completion with multi-similarities fusion. *Frontiers in microbiology*, 15, 1438942.

Prokazyuk A, et al. (2024) Development and validation of a machine learning-based model to assess probability of systemic inflammatory response syndrome in patients with severe multiple traumas. *BMC medical informatics and decision making*, 24(1), 235.

Digumarthi V, et al. (2024) Preoperative prediction model for risk of readmission after total joint replacement surgery: a random forest approach leveraging NLP and unfairness mitigation for improved patient care and cost-effectiveness. *Journal of orthopaedic surgery and research*, 19(1), 287.

Zingg A, et al. (2024) A pilot acceptability evaluation of MomMind: A digital health intervention for Peripartum Depression prevention and management focused on health disparities. *PLOS digital health*, 3(5), e0000508.

Brazier E, et al. (2024) Long-term HIV care outcomes under universal HIV treatment guidelines: A retrospective cohort study in 25 countries. *PLoS medicine*, 21(3), e1004367.

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.

Clark-Sevilla AO, et al. (2024) Diving into CDC pregnancy data in the United States: longitudinal study and interactive application. *JAMIA open*, 7(1), ooae024.

Qu J, et al. (2024) Three-layer heterogeneous network based on the integration of CircRNA information for MiRNA-disease association prediction. *PeerJ. Computer science*, 10, e2070.

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.

Li Z, et al. (2024) HHOMR: a hybrid high-order moment residual model for miRNA-disease association prediction. *Briefings in bioinformatics*, 25(5).

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

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

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.

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

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.

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.

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

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.