



Medical and Research Library News November 2026

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Training opportunities

The webinars and online classes listed here are shared solely as opportunities to learn more information of interest to public health personnel. All times listed are in Central Time.

November 5, 2026; 1–2:30 p.m. [How PubMed Works: Introduction](#). This presentation from the [Network of the National Library of Medicine](#) (NNLM) will highlight features of the National Library of Medicine's PubMed bibliographic database. Participants will learn about PubMed and the types of resources it contains, how to locate the original research behind a news article, find publications by a specific author, and search for articles on a particular subject. The session will also cover techniques for narrowing search results to a more focused set of articles and introduce the Advanced Search Builder and Search History features.

November 12, 2026; 1–2:30 p.m. [How PubMed Works: MeSH](#). This session from the [Network of the National Library of Medicine](#) (NNLM) will explore the use of Medical Subject Headings (MeSH), the controlled and hierarchically organized vocabulary produced by the National Library of Medicine. It is used for indexing, cataloging, and searching biomedical and health-related information. MeSH includes the subject headings appearing in MEDLINE/PubMed, the NLM Catalog, and other NLM databases.

November 19, 2026; 1–2:30 p.m. [How PubMed Works: Automatic Term Mapping \(ATM\)](#). This interactive webinar from the [Network of the National Library of Medicine](#) (NNLM) will provide an in-depth examination of Automatic Term Mapping (ATM), PubMed's behind-the-scenes process for interpreting your keyword search terms. This session offers a mix of live demonstrations, hands-on exercises, and practical search tips from the National Library of Medicine. Key topics include the ATM keyword translation process, leveraging the Subject, Journals, and Author Name tables, phrase searching, finding 'your' author, and strategies for refining searches when ATM doesn't deliver expected results.

November 19; 2026; 1–2:15 p.m. [Coaching Forward: From Feedback to Growth](#).

This webinar from the [Association of State and Territorial Health Officials](#) (ASTHO) will build on the fundamentals of feedback to develop leaders' coaching skills, focusing on the conversations that happen after feedback is delivered. Participants will practice shifting from advice-giving to inquiry, learn how to clarify expectations without micromanaging, and develop a follow-up strategy that reinforces growth and accountability over time.

Websites and reports on trending topics

[CDC Stacks](#) is a free digital archive of publications from the Centers for Disease Control and Prevention, including reports, guidelines, MMWR articles, and other public health documents. It serves as a central repository for CDC-authored and funded materials and is a key source of U.S. public health gray literature.

[medRxiv](#) is a free online archive and distribution server for complete but unpublished manuscripts (preprints) in the medical, clinical, and related health sciences.

[ProQuest Ebook Central](#) is a science and technology ebook collection provided through the DSHS library's TexShare affiliation. It offers more than 28,000 e-book titles on a diverse range of topics such as chemistry, physics, math, geology, geography, IT, computer science, engineering, agriculture, environmental studies, natural history, medicine, and more. Register [here](#) to create an account for access.

Journal articles of note

The articles listed here are authored by DSHS employees or are related to public health in Texas. Please email the [library](#) if you need assistance accessing the full text of these or any other articles.

Enwere M, Bryan NS, Onu A, et al. The microbiome-nitric oxide axis in cancer immunotherapy: a targeted qualitative systematic review of mechanistic and translational evidence. *Front Immunol.* 2026;17:1904698. Published 2026 Sep 24. [doi:10.3389/fimmu.2026.1904698](https://doi.org/10.3389/fimmu.2026.1904698)

Abstract

Background: Immune checkpoint inhibitors (ICIs) have transformed cancer treatment, but responses vary substantially among patients. Clinical studies have associated features of the gut microbiome with ICI outcomes, while experimental evidence suggests that microbial metabolites and nitric oxide (NO)-related pathways may influence antitumor immunity and tumor vascular biology. This qualitative systematic review evaluated the evidence supporting a proposed microbiome-NO-ICI framework.

Methods: Five databases were searched for peer-reviewed studies published between January 2000 and August 2025. Fifty-four distinct primary studies

met the eligibility criteria, comprising 21 clinical studies, 19 animal studies and 14 *in vitro* mechanistic studies. Evidence was synthesized narratively according to study type and thematic domain.

Results: Several clinical cohorts associated enrichment of *Akkermansia muciniphila*, *Faecalibacterium prausnitzii*, *Bifidobacterium* species and other short-chain fatty acid-producing taxa with favorable ICI outcomes; however, the reported microbial signatures varied across cohorts and analytical platforms. Microbial-transfer experiments and early non-randomized fecal microbiota transplantation studies provide proof-of-concept evidence that microbiome composition can influence antitumor immune responses, although the clinical intervention evidence remains preliminary. Animal and cellular studies indicate that microbial metabolites, host nitric oxide synthase pathways and reactive nitrogen signaling can affect immune-cell function, vascular regulation and tumor hypoxia. Direct clinical evidence linking microbiota-mediated nitrate reduction or dietary nitrate supplementation to improved ICI outcomes is lacking. Human dietary nitrate studies conducted outside oncology demonstrate increased circulating nitrate and nitrite and measurable vascular effects but do not establish anticancer or ICI efficacy.

Conclusion: The microbiome-NO-ICI axis should be regarded as a testable integrative model linking microbial ecology, immune regulation and tumor vascular biology. Current evidence supports biological plausibility but is insufficient to establish NO- or microbiome-directed interventions as effective adjuncts to ICI therapy. Prospective mechanistic studies and biomarker-driven clinical trials are required before therapeutic translation.

Martinez-Lopez YE, Black BW, Lee J, et al. Frailty as a framework to understand tuberculosis severity, recovery and sequelae. *J Infect Dis*. Published online August 14, 2026. [doi:10.1093/infdis/jiag415](https://doi.org/10.1093/infdis/jiag415)

Abstract

Tuberculosis (TB) causes profound systemic illness, and many survivors experience long-term sequelae associated with disability and premature mortality. Current TB severity indicators capture isolated aspects of disease and may not reflect the integrated physiological impact of infection on the host. Frailty, a multidimensional syndrome characterized by reduced physiological reserve and increased vulnerability to stressors, predicts adverse outcomes and guides clinical management in geriatrics. We propose frailty as an integrative framework for understanding the systemic effects of TB across the life course, encompassing disease severity, recovery, and long-term sequelae. We discuss biological mechanisms through which *Mycobacterium tuberculosis* infection may erode physiological reserve and promote frailty, including inflammation and metabolic and endocrine dysregulation. We further consider how frailty assessment could improve risk stratification and guide individualized supportive care to mitigate post-TB sequelae. Unlike aging-related frailty, TB-associated frailty may provide a

unique opportunity to study mechanisms of resilience and recovery following severe infection.

Schraw JM, Mims KC, Stephens SB, et al. Association between nonsyndromic congenital heart disease and childhood cancer in a population-based, retrospective cohort of 11 million children. *J Am Heart Assoc*.

2026;15(18):e050164. [doi:10.1161/JAHA.125.050164](https://doi.org/10.1161/JAHA.125.050164)

Abstract

Background: Epidemiologic studies have demonstrated associations between congenital heart disease (CHD) and childhood cancer. However, these assessments have not fully accounted for the pathogenetic and clinical heterogeneity of CHD, limiting their capacity to inform pathogenetic studies and the clinical management of children with CHD.

Methods: To achieve a more detailed understanding of cancer risk in children with nonsyndromic CHD, we evaluated 60 cardiac lesions in 7 categories in a cohort of 11 million children from Massachusetts, North Carolina, Oklahoma, and Texas. We used Cox proportional hazards regression to estimate the hazard ratios (HRs) and 95% CIs of cancer in children with each lesion relative to children without congenital anomalies when there were ≥ 3 co-occurring cases.

Results: We identified 74,755 children with CHD and observed increased hazards for several malignancies. Notable associations included aortic arch obstruction-lymphoma (HR, 12.7 [95% CI, 4.9-31.0]); single-ventricle disease-lymphoma (HR, 9.7 [95% CI, 3.8-24.4]); complex atrioventricular septal defect-leukemia (HR, 8.05 [95% CI, 2.8-23.0]); ventricular septal defect-hepatoblastoma (HR, 11.2 [95% CI, 5.9-21.1]); and conotruncal defects-neuroblastoma (HR, 6.4 [95% CI, 1.9-22.2]). The cumulative incidence of cancer was $<1\%$ for all CHD groups evaluated.

Conclusions: Cancer incidence in children with nonsyndromic CHD was generally low. However, we identified >5 -fold increases in the hazard of hepatoblastoma, neuroblastoma, leukemia, and lymphoma in children with certain lesions. Our findings may assist in generating hypotheses about the causes of cancer in children with CHD.

Smith HS, Stein S, Henry MW, et al. Decision analysis to inform screening of the young: an interactive newborn screening model. *Pediatrics*.

2026;158(Suppl 2):e2026077357G. [doi:10.1542/peds.2026-077357G](https://doi.org/10.1542/peds.2026-077357G)

Abstract

Decision analytic models that project the outcomes of population-based newborn screening compared with clinical identification can inform newborn screening policymaking. A flexible decision analytic model that could be adapted for the many and growing number of conditions being considered for newborn screening would help expedite decision making while reducing the time and resources required to develop new condition-specific models. To address this need, we developed Decision Analysis to Inform Screening of

the Young (DAISY), an interactive and adaptable generic newborn screening model that incorporates user-supplied inputs. To illustrate the use of this tool, we present a model of newborn screening for metachromatic leukodystrophy (MLD). DAISY projects that newborn screening would identify a greater number of MLD cases and improve survival outcomes over a 5-year time horizon compared with clinical identification. In a US birth cohort of 3.6 million newborns, we project that 36 infants with early-onset MLD cases would be identified per year through newborn screening, each of whom would be treatment eligible. In contrast, in the absence of screening, only 11.5 infants with early-onset MLD cases would be identified, 10 of whom would be treatment eligible. The number of children surviving without motor impairment approximately 5 years after symptom onset is projected to be 32.8 with newborn screening and 9.1 in the absence of screening. DAISY can be used to evaluate other newborn screening candidate conditions through specification of input parameters such as population size, clinical validity of the screening algorithm, and treatment effectiveness.

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