

Resource Summary Report

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NIH Common Fund

RRID:SCR_012790

Type: Tool

Proper Citation

NIH Common Fund (RRID:SCR_012790)

Resource Information

URL: <http://commonfund.nih.gov/>

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Description: Supports cross-cutting, trans-NIH programs that require participation by at least two NIH Institutes or Centers (ICs) or would otherwise benefit from strategic planning and coordination. The requirements for the Common Fund encourage collaboration across the ICs while providing the NIH with flexibility to determine priorities for Common Fund support. To date, the Common Fund has been used to support a series of short term, exceptionally high impact, trans-NIH programs known collectively as the NIH Roadmap for Medical Research. The Common Fund is coordinated by the Office of Strategic Coordination, one of the six offices of the Division of Program Coordination, Planning, and Strategic Initiatives (DPCPSI) within the Office of the Director. The intent of NIH Common Fund programs is to provide a strategic and nimble approach to address key roadblocks in biomedical research that impede basic scientific discovery and its translation into improved human health. In addition, these programs capitalize on emerging opportunities to catalyze the rate of progress across multiple biomedical fields. Common Fund programs are expected to transform the way a broad spectrum of health research is conducted. Initiatives that comprise Common Fund programs are intended to be catalytic in nature by providing limited term investments in strategic areas to stimulate further research through IC-funded mechanisms.

Abbreviations: NIH Common Fund

Synonyms: NIH Roadmap for Medical Research, NIH Roadmap Initiative

Resource Type: government granting agency

Resource Name: NIH Common Fund

Resource ID: SCR_012790

Alternate IDs: nlx_146248

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260912T195753+0000

Ratings and Alerts

No rating or validation information has been found for NIH Common Fund.

No alerts have been found for NIH Common Fund.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Stephen NA, et al. (2026) Sustaining grant-funded programs: Conditions for sustaining initiatives that enhance diversity in STEMM. PloS one, 21(2), e0343368.

Liu L, et al. (2025) Identification and functional analysis of GNAI1 as a biomarker associated with immune-related genes in pediatric acute myeloid leukemia. Translational cancer research, 14(5), 2858.

Huang B, et al. (2025) Genome-wide selection inference at short tandem repeats. PLoS genetics, 21(12), e1011959.

Cai H, et al. (2025) Relationship between CTF1 gene expression and prognosis and tumor immune microenvironment in glioma. European journal of medical research, 30(1), 17.

Nesta A, et al. (2025) Alternative splicing of transposable elements in human breast cancer. Mobile DNA, 16(1), 6.

Fadeel B, et al. (2024) Editorial: Five grand challenges in toxicology. Frontiers in toxicology, 6, 1533238.

Nesta A, et al. (2024) Alternative splicing of transposable elements in human breast cancer. bioRxiv : the preprint server for biology.

Liu W, et al. (2024) Multiple omics integrative analysis identifies GARS1 as a novel prognostic and immunological biomarker: from pan-cancer to bladder cancer. Scientific reports, 14(1), 19025.

Stuifbergen AK, et al. (2024) Nurturing Longitudinal Samples 2.0. Western journal of nursing research, 46(10), 831.

Gong Y, et al. (2023) Identified RP2 as a prognostic biomarker for glioma, facilitating glioma pathogenesis mainly via regulating tumor immunity. *Aging*, 15(16), 8155.

Roy AL, et al. (2020) A Blueprint for Characterizing Senescence. *Cell*, 183(5), 1143.

Herbert E, et al. (2020) The occurrence of tarsal injuries in male mice of C57BL/6N substrains in multiple international mouse facilities. *PloS one*, 15(6), e0230162.

Vornhagen J, et al. (2019) The *Klebsiella pneumoniae* citrate synthase gene, *gltA*, influences site specific fitness during infection. *PLoS pathogens*, 15(8), e1008010.

Budd A, et al. (2015) A quick guide for building a successful bioinformatics community. *PLoS computational biology*, 11(2), e1003972.