

Resource Summary Report

Generated by [dkNET](#) on Sep 9, 2026

Howard Hughes Medical Institute

RRID:SCR_011281

Type: Tool

Proper Citation

Howard Hughes Medical Institute (RRID:SCR_011281)

Resource Information

URL: <http://www.hhmi.org/>

Proper Citation: Howard Hughes Medical Institute (RRID:SCR_011281)

Description: Nonprofit medical research organization that ranks as one of the nation's largest philanthropies for advancing biomedical research and science education in the United States. Known for its scientific research and modern architecture.

Abbreviations: HHMI

Synonyms: Howard Hughes Medical Institute

Resource Type: institution

Keywords: institution, medical, research, nonprofit, biomedical, USA

Resource Name: Howard Hughes Medical Institute

Resource ID: SCR_011281

Alternate IDs: Wikidata: Q1512226, Crossref funder ID: 100000011, ISNI: 0000 0001 2167 1581, grid.413575.1, nlx_98347

Alternate URLs: <https://ror.org/006w34k90>

Record Creation Time: 20220129T080303+0000

Record Last Update: 20260905T132700+0000

Ratings and Alerts

No rating or validation information has been found for Howard Hughes Medical Institute.

No alerts have been found for Howard Hughes Medical Institute.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 228 mentions in open access literature.

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

Pathak M, et al. (2026) Mouse germline cysts contain a fusome-like structure that mediates oocyte development. *eLife*, 14.

Stephens Z, et al. (2026) Insights into substrate binding and utilization by hyaluronan synthase. *eLife*, 14.

Dinshaw KM, et al. (2026) High-throughput characterization of *Mycobacterium tuberculosis* gene function across diverse conditions. *PLoS biology*, 24(4), e3003529.

McClave MK, et al. (2026) Isolation and characterization of broadly-neutralizing anti-HCMV-gB antibodies from human donors using a prefusion-stabilized HCMV gB variant. *PLoS pathogens*, 22(2), e1013950.

Matsen FA, et al. (2026) Separating selection from mutation in antibody language models. *eLife*, 15.

Cuentas-Condori A, et al. (2026) SynaptoTagMe, a toolkit for in vivo mapping and modulating neurotransmission at single-cell resolution. *eLife*, 14.

Zeng WW, et al. (2026) Cryo-EM structure revealed a novel F-actin binding motif in a *Legionella pneumophila* lysine fatty acyltransferase. *eLife*, 14.

Canales BI, et al. (2026) map3k1 is required for spatial restriction of progenitor differentiation in planarians. *eLife*, 14.

Atanas AA, et al. (2026) Deep neural networks to register and annotate cells in moving and deforming nervous systems. *eLife*, 14.

Lane EA, et al. (2026) Cholinergic signaling modulates intestinal pathophysiology in a *Drosophila* model of cystic fibrosis. *PLoS genetics*, 22(2), e1012048.

Kong L, et al. (2026) Unbend, correction of local beam-induced sample motion in cryo-EM images using a 3D spline model. *eLife*, 14.

Kolb I, et al. (2026) iGABASnFR2 is an improved genetically encoded protein sensor of GABA. *eLife*, 14.

Tulloch AJ, et al. (2026) Massively parallel reporter assay for mapping gene-specific regulatory regions at single-nucleotide resolution. *eLife*, 14.

Tian M, et al. (2026) Maturation of HIV-1 neutralizing antibodies in a germinal center conditional expression mouse model. *PLoS pathogens*, 22(6), e1014373.

Ralph DK, et al. (2026) Inference of germinal center evolutionary dynamics via simulation-based deep learning. *eLife*, 14.

Eroglu M, et al. (2026) A pilot study for whole proteome tagging in *Caenorhabditis elegans*. *eLife*, 15.

Ross SJ, et al. (2026) RNA Folding Energy of Long-Range Genomic Interactions Regulates Discontinuous Transcription in SARS-CoV-2. *Viruses*, 18(6).

Pournejati R, et al. (2026) Functionally coupled ion channels begin co-assembling at the start of their synthesis. *eLife*, 14.

Kito Y, et al. (2026) GMCL1 controls 53BP1 stability and modulates taxane sensitivity. *eLife*, 14.

Kikawa C, et al. (2026) High-throughput neutralization measurements correlate strongly with evolutionary success of human influenza strains. *eLife*, 14.