

Resource Summary Report

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CSHL - Hannon Lab

RRID:SCR_005982

Type: Tool

Proper Citation

CSHL - Hannon Lab (RRID:SCR_005982)

Resource Information

URL: <http://hannonlab.cshl.edu/index.html>

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Description: The Hannon laboratory comprises a broad spectrum of programs in small RNA biology, mammalian genetics and genomics. We study RNAi and related pathways in a wide variety of organisms to extract common themes that define both the mechanisms by which small RNAs act and the biological processes which they impact. Currently, we focus on microRNAs, endogenous siRNAs and piRNAs and their roles in gene regulation, cancer biology, stem cell biology and in defense of the genome against transposons. In collaboration with Steve Elledge (Harvard) and Scott Lowe (CSHL), we develop genome-wide shRNA tools for RNAi-based genetics in mammalian cells, and we are now producing similar collections of artificial microRNAs for Arabidopsis with Detlef Weigel (MPI), Dick McCombie (CSHL) and Rob Martienssen (CSHL) as part of the 2010 project (see 2010.cshl.edu). Our genomic efforts include the application of RNAi-based genetic screens to cancer biology and stem cells. We also make heavy use of next generation sequencing methodologies for probing small RNA populations, in part as a member of the ENCODE consortium (with Tom Gingeras, CSHL). Finally, we develop (with Dick McCombie) and apply focal re-sequencing methods for identifying disease relevant mutations, for probing the epigenetic landscape and for the study of human evolution.

Abbreviations: Hannon Lab

Synonyms: Cold Spring Harbor Laboratory - Hannon Lab

Resource Type: data or information resource, laboratory portal, organization portal, portal

Keywords: rnai, rna, mammal, genetics, genomics, microRNA, siRNA, piRNA, gene regulation, cancer biology, stem cell biology, defense, genome, transposon, cancer, stem cell

Resource Name: CSHL - Hannon Lab

Resource ID: SCR_005982

Alternate IDs: nlx_151354

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260905T132545+0000

Ratings and Alerts

No rating or validation information has been found for CSHL - Hannon Lab.

No alerts have been found for CSHL - Hannon Lab.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 70 mentions in open access literature.

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

Chen W, et al. (2025) OCT4 translationally promotes AKT signaling as an RNA-binding protein in stressed pluripotent stem cells. Stem cell research & therapy, 16(1), 84.

Hoang CV, et al. (2025) Two virulent bacteriophages targeting carbapenem-resistant Raoultella planticola. Frontiers in microbiology, 16, 1726803.

Cole L, et al. (2024) Land use effects on soil microbiome composition and traits with consequences for soil carbon cycling. ISME communications, 4(1), ycae116.

Okada N, et al. (2024) Intron retention as an excellent marker for diagnosing depression and for discovering new potential pathways for drug intervention. Frontiers in psychiatry, 15, 1450708.

Giroud M, et al. (2023) The obesity-linked human lncRNA AATBC stimulates mitochondrial function in adipocytes. EMBO reports, 24(10), e57600.

Zhi J, et al. (2023) A multi-omic resource of wheat seed tissues for nutrient deposition and improvement for human health. Scientific data, 10(1), 269.

Cao K, et al. (2023) Integrated workflow for discovery of microprotein-coding small open reading frames. STAR protocols, 4(4), 102649.

Thieffry A, et al. (2022) PAMP-triggered genetic reprogramming involves widespread alternative transcription initiation and an immediate transcription factor wave. The Plant cell, 34(7), 2615.

Aiello U, et al. (2022) Sen1 is a key regulator of transcription-driven conflicts. *Molecular cell*, 82(16), 2952.

Boeckman J, et al. (2022) Sheep in wolves' clothing: Temperate T7-like bacteriophages and the origins of the Autographiviridae. *Virology*, 568, 86.

Sun Z, et al. (2022) tRNA-derived fragments from wheat are potentially involved in susceptibility to *Fusarium* head blight. *BMC plant biology*, 22(1), 3.

Hisaoka M, et al. (2022) Preferential translation of p53 target genes. *RNA biology*, 19(1), 437.

Klunder L, et al. (2022) Quantification of marine benthic communities with metabarcoding. *Molecular ecology resources*, 22(3), 1043.

Zein HS, et al. (2022) Clr-f expression regulates kidney immune and metabolic homeostasis. *Scientific reports*, 12(1), 4834.

Stengel KR, et al. (2021) Definition of a small core transcriptional circuit regulated by AML1-ETO. *Molecular cell*, 81(3), 530.

Ereful NC, et al. (2021) Unraveling regulatory divergence, heterotic malleability, and allelic imbalance switching in rice due to drought stress. *Scientific reports*, 11(1), 13489.

Jones B, et al. (2021) Beyond Taxonomic Identification: Integration of Ecological Responses to a Soil Bacterial 16S rRNA Gene Database. *Frontiers in microbiology*, 12, 682886.

Layden HM, et al. (2021) A protocol for rapid degradation of endogenous transcription factors in mammalian cells and identification of direct regulatory targets. *STAR protocols*, 2(2), 100530.

Xie Y, et al. (2021) Differential Bacteriophage Efficacy in Controlling *Salmonella* in Cattle Hide and Soil Models. *Frontiers in microbiology*, 12, 657524.

Guadagnin E, et al. (2021) Transcriptome analysis of collagen VI-related muscular dystrophy muscle biopsies. *Annals of clinical and translational neurology*, 8(11), 2184.