Resource Summary Report

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modENCODE

RRID:SCR_006206
Type: Tool

Proper Citation

modENCODE (RRID:SCR_006206)

Resource Information

URL: http://modencode.org/

Proper Citation: modENCODE (RRID:SCR_006206)

Description: A comprehensive encyclopedia of genomic functional elements in the model organisms C. elegans and D. melanogaster. modENCODE is run as a Research Network and the consortium is formed by 11 primary projects, divided between worm and fly, spanning the domains of gene structure, mRNA and ncRNA expression profiling, transcription factor binding sites, histone modifications and replacement, chromatin structure, DNA replication initiation and timing, and copy number variation. The raw and interpreted data from this project is vetted by a data coordinating center (DCC) to ensure consistency and completeness. The entire modENCODE data corpus is now available on the Amazon Web Services EC2 cloud. What this means is that virtual machines and virtual compute clusters that you run within the EC2 cloud can mount the modENCODE data set in whole or in part. Your software can run analyses against the data files directly without experiencing the long waits and logistics associated with copying the datasets over to your local hardware. You may also view the data using GBrowse, Dataset Search, or download the data via FTP, as well as download pre-release datasets.

Abbreviations: modENCODE

Synonyms: NHGRI model organism ENCyclopedia Of DNA Elements, National Human Genome Research Institute model organism ENCyclopedia Of DNA Elements, model organism ENCyclopedia Of DNA Elements

Resource Type: analysis service resource, data analysis service, data or information resource, data set, production service resource, service resource

Defining Citation: PMID:19536255

Keywords: epigenomics, epigenetics, genomics, functional element, model organism, genome, copy number variation, gene structure, genome sequence, histone modification, histone replacement, chromatin binding site, expression profiling, replication, transcription

factor binding site, transcription factor, binding site, chromatin, rna, expression profiling, regulatory network, mrna, ncrna, dna replication, genotype

Funding: NHGRI

Availability: Public, With some restrictions on its use for 9 months following publication, Acknowledgement requested

Resource Name: modENCODE

Resource ID: SCR_006206

Alternate IDs: nlx_151752

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260829T182233+0000

Ratings and Alerts

No rating or validation information has been found for modENCODE.

No alerts have been found for modENCODE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 260 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Vedelek V, et al. (2026) Machine learning analysis of Drosophila testis transcriptomic data reveals potential regulatory sequences. BioData mining, 19(1).

Tsui HN, et al. (2026) Dual genomic localizations and gene regulatory functions of MBD-2 with and without NuRD in Caenorhabditis elegans which lacks DNA methylation. Nature communications, 17(1).

Whittle CA, et al. (2026) Evidence for Non-optimal Codon Choice in Highly Transcribed Sex-Biased Genes of Drosophila melanogaster. Genome biology and evolution, 18(5).

Ostal?? CM, et al. (2025) A function of Spalt proteins in heterochromatin organization and maintenance of genomic DNA integrity. Development (Cambridge, England), 152(10).

Yheskel M, et al. (2025) Local chromatin context informs transcriptional outcomes for the histone demethylase KDM5. Epigenetics & chromatin, 18(1), 78.

Kinney B, et al. (2025) FLYWCH transcription factors act in a LIN-42/Period autoregulatory loop during gonad migration in C. elegans. bioRxiv : the preprint server for biology.

Yin J, et al. (2025) Glia-derived noncanonical fatty acid binding protein modulates brain lipid storage and clearance. Science advances, 11(31), eadv2902.

Varoqui M, et al. (2025) Temporal and spatial niche partitioning in a retrotransposon community of the Drosophila melanogaster genome. Nucleic acids research, 53(11).

Funk OH, et al. (2025) Epidermal cell fusion promotes the transition from an embryonic to a larval transcriptome in C. elegans. Development (Cambridge, England), 152(24).

Brown JC, et al. (2024) Lysine-36 of Drosophila histone H3.3 supports adult longevity. G3 (Bethesda, Md.), 14(4).

Sepulveda GP, et al. (2024) DOT1L stimulates MYC/Mondo transcription factor activity by promoting its degradation cycle on chromatin. bioRxiv : the preprint server for biology.

Li Z, et al. (2024) Exportin-5 binding precedes 5'- and 3'-end processing of tRNA precursors in Drosophila. The Journal of biological chemistry, 300(9), 107632.

Vergani-Junior CA, et al. (2024) An Intricate Network Involving the Argonaute ALG-1 Modulates Organismal Resistance to Oxidative Stress. Nature communications, 15(1), 3070.

Whittle CA, et al. (2024) Gene Protein Sequence Evolution Can Predict the Rapid Divergence of Ovariole Numbers in the Drosophila melanogaster Subgroup. Genome biology and evolution, 16(7).

Sklias A, et al. (2024) Comprehensive map of ribosomal 2'-O-methylation and C/D box snoRNAs in Drosophila melanogaster. Nucleic acids research, 52(6), 2848.

Bollepogu Raja KK, et al. (2024) Integrative genomic analyses reveal putative cell type-specific targets of the Drosophila ets transcription factor Pointed. BMC genomics, 25(1), 103.

Lv P, et al. (2024) The CoREST complex regulates multiple histone modifications temporal-specifically in clock neurons. Open biology, 14(7), 230355.

Yin J, et al. (2024) Glia-derived secretory fatty acid binding protein Obp44a regulates lipid storage and efflux in the developing Drosophila brain. bioRxiv : the preprint server for biology.

Chandrasekhara C, et al. (2023) A single N-terminal amino acid determines the distinct roles of histones H3 and H3.3 in the Drosophila male germline stem cell lineage. PLoS biology, 21(5), e3002098.

Johnson LC, et al. (2023) NHR-23 activity is necessary for C. elegans developmental progression and apical extracellular matrix structure and function. Development (Cambridge, England), 150(10).