

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

NIA Mouse cDNA Project Home Page

RRID:SCR_001472

Type: Tool

Proper Citation

NIA Mouse cDNA Project Home Page (RRID:SCR_001472)

Resource Information

URL: <http://lgsun.grc.nia.nih.gov/cDNA/cDNA.html>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23, 2022. Project portal housing NIA Mouse EST Project, NIA Mouse cDNA Clone Sets, a NIA Mouse Gene Index, NIA Mouse cDNA Database, and NIA Mouse Microarrays. Characteristics of NIA 15K Mouse cDNA Clone Set * ~15,000 unique cDNA clones were rearranged among 52,374 ESTs from pre- and periimplantation embryos, E12.5 female gonad/mesonephros, and newborn ovary. * Up to 50% are derived from novel genes. * ~1.5 kb average insert size. * Clones were sequenced from 5' and 3' termini to obtain longer reads and verify sequence. Sequence information is available at this Web Site. Clone names are from H3001A01 to H3159G07. * Handling of NIA 15k cDNA Clone Set (June 3, 2000) Characteristics of NIA mouse 7.4K cDNA Clone Set * ~7407 cDNA clones with no redundancy within the set or with NIA Mouse 15K. * ~1.5 kb average insert size for short insert clones and ~2.5-3.0 kb average insert size for long-insert enriched clones. * Clones were sequenced from 5' and 3' termini to obtain longer reads and verify sequence. Sequence information is available at this Web Site. Clone names are from H4001A01 to H4079G07. * Handling of NIA mouse 7.4k cDNA Clone Set (similar to handling of NIA mouse 15K, to be updated) Individual Clones are available from ATCC and MRC geneservice, UK. To obtain Clone, search the database using either the rearranged clone name or GenBank accession number at the Key Word Search page. Follow the link to the sequence information page for the rearranged clone to obtain source clone ATCC number. Clicking the ATCC number will bring up the ATCC ordering page for the source clone. There is essentially no overlap between the two clone sets (7.4K and 15K) said Minoru S.H. Ko, M.D., Ph.D., head of the Developmental Genomics and Aging Section in the NIA's Laboratory of Genetics. In addition, all cDNA clones in the NIA 7.4K set were purified by single colony isolation and sequence-verified, and more than half were prepared by a new procedure that yields long full-length cDNAs (average size 3-4 kb). The NIA Mouse 15k and 7.4k Clone Set Data and Published Microarray Data are available for download. NIA Mouse Microarrays *Microarray Data Download * 60-mer Oligo Array Platform ** (A) NIA 22k Oligo Microarray Gene List (21939 gene features) (

Carter et al 2003) ** (B) Agilent Mouse Development Oligo Microarray Gene List ** (Subset of Microarray (A): 20,280 gene features) * Data Analysis Tools

Abbreviations: niaEST

Synonyms: NIA Mouse cDNA Project, Mouse cDNA Project

Resource Type: biomaterial supply resource, material resource

Defining Citation: [PMID:14744099](#)

Keywords: embryonic, expression, fetal, gene, cdna, cell, clone set, human disease, microarray, mouse, mouse model, newborn, stem cell, tissue, clone

Related Condition: Aging

Funding: NIA 1ZIAAG000656-11

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: NIA Mouse cDNA Project Home Page

Resource ID: SCR_001472

Alternate IDs: nif-0000-09471

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260905T133224+0000

Ratings and Alerts

No rating or validation information has been found for NIA Mouse cDNA Project Home Page.

No alerts have been found for NIA Mouse cDNA Project Home Page.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Tagliaferri D, et al. (2016) Retinoic Acid Specifically Enhances Embryonic Stem Cell Metastate Marked by Zscan4. PloS one, 11(2), e0147683.

- Schlüter A, et al. (2012) Functional genomic analysis unravels a metabolic-inflammatory interplay in adrenoleukodystrophy. *Human molecular genetics*, 21(5), 1062.
- Ellis J, et al. (2010) Microarray analyses of mouse responses to infection by *Neospora caninum* identifies disease associated cellular pathways in the host response. *Molecular and biochemical parasitology*, 174(2), 117.
- Bueno MJ, et al. (2008) Genetic and epigenetic silencing of microRNA-203 enhances ABL1 and BCR-ABL1 oncogene expression. *Cancer cell*, 13(6), 496.
- Masui S, et al. (2008) Rex1/Zfp42 is dispensable for pluripotency in mouse ES cells. *BMC developmental biology*, 8, 45.
- Ghate A, et al. (2007) Identification of novel striatal genes by expression profiling in adult mouse brain. *Neuroscience*, 146(3), 1182.
- Müller-Brüsselbach S, et al. (2007) Deregulation of tumor angiogenesis and blockade of tumor growth in PPARbeta-deficient mice. *The EMBO journal*, 26(15), 3686.
- Kobayashi S, et al. (2006) Comparison of gene expression in male and female mouse blastocysts revealed imprinting of the X-linked gene, *Rhox5/Pem*, at preimplantation stages. *Current biology : CB*, 16(2), 166.
- Cox B, et al. (2005) Integrating gene and protein expression data: pattern analysis and profile mining. *Methods (San Diego, Calif.)*, 35(3), 303.
- Hamatani T, et al. (2004) Dynamics of global gene expression changes during mouse preimplantation development. *Developmental cell*, 6(1), 117.
- Collado-Vides J, et al. (2003) With the finished human genome in hand, what next? *Genome biology*, 4(7), 328.
- Tsai J, et al. (2001) RESOURCERER: a database for annotating and linking microarray resources within and across species. *Genome biology*, 2(11), SOFTWARE0002.