

Resource Summary Report

Generated by [dkNET](#) on Aug 7, 2026

ES-E14TG2a

RRID:CVCL_9108

Type: Cell Line

Proper Citation

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Cell Line Information

URL: https://web.expasy.org/cellosaurus/CVCL_9108

Proper Citation: RRID:CVCL_9108

Description: Cell line ES-E14TG2a is a Embryonic stem cell with a species of origin Mus musculus (Mouse)

Sex: Male

Defining Citation: [PMID:3821905](#), [PMID:25277546](#), [PMID:25894527](#)

Category: Embryonic stem cell

Organism: Mus musculus (Mouse)

Name: ES-E14TG2a

Synonyms: E14TG2a, E14Tg2a, E14tg2a, E14.Tg2a, E14 Tg2a

Cross References: CLO:CLO_0002952, EFO:EFO_0006275, ATCC:CRL-1821, BCRC:60206, CCRID:3101MOUSCSP204, ECACC:08021401, ENCODE:ENCBS340HTQ, ENCODE:ENCBS841DCQ, ENCODE:ENCBS917UCO, PRIDE:PXD000589, RCB:AES0135, SKIP:SKIP003029, TOKU-E:1158, Wikidata:Q54832450

ID: CVCL_9108

Hierarchy: cvcl_c320

Record Creation Time: 20220427T215835+0000

Record Last Update: 20260802T000223+0000

Ratings and Alerts

No rating or validation information has been found for ES-E14TG2a.

No alerts have been found for ES-E14TG2a.

Data and Source Information

Source: [Cellosaurus](#)

Usage and Citation Metrics

We found 188 mentions in open access literature.

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

Li S, et al. (2026) Microhomology-mediated end joining acts directly on replication forks to repair single-ended double-strand breaks. *Molecular cell*, 86(7), 1230.

Bonilla B, et al. (2026) esBAF and INO80C fine-tune subcompartments and differentially regulate enhancer-promoter interactions. *Genetics*, 232(4).

Xu W, et al. (2026) Single-nucleus chromatin accessibility and gene expression co-profiling by ISSAAC-seq. *Nature protocols*.

GjoniLeshaj P, et al. (2026) African pygmy mouse iPSCs as a model for in vitro embryogenesis, interspecies chimerism, and blastocyst complementation. *Cell reports methods*, 6(2), 101293.

Lu T, et al. (2026) PUMILIO proteins maintain lineage balance via post-transcriptional repression of germline fate and promotion of somatic differentiation. *Cell reports*, 45(7), 117682.

Iyer DP, et al. (2026) Putting mammalian early embryonic cells into dormancy. *Nature protocols*, 21(7), 3199.

Sankar R, et al. (2026) FACT depletion results in a temporal cascade of chromatin disruption preceding transcriptional collapse in stem cells. *bioRxiv : the preprint server for biology*.

Zhou Y, et al. (2026) Murine Embryonic Stem Cells Possess Distinct E2F Activity That Activates Tumor Suppressor Promoter Elements. *Genes to cells : devoted to molecular & cellular mechanisms*, 31(3), e70121.

Lucero K, et al. (2025) CTCF-RNA interactions orchestrate cell-specific chromatin loop organization. *bioRxiv : the preprint server for biology*.

García-Blay Ó, et al. (2025) Protocol to identify proteins as regulators of gene expression noise. *STAR protocols*, 6(2), 103763.

Cingaram PKR, et al. (2025) Enhancing transcriptome mapping with rapid PRO-seq profiling of nascent RNA. *Molecular cell*, 85(15), 2988.

Magnitov MD, et al. (2025) ZNF143 is a transcriptional regulator of nuclear-encoded mitochondrial genes that acts independently of looping and CTCF. *Molecular cell*, 85(1), 24.

Bryan E, et al. (2025) Nucleosomal asymmetry shapes histone mark binding and promotes poising at bivalent domains. *Molecular cell*, 85(3), 471.

Rabeling A, et al. (2025) Signaling Centers Drive Brachyury Dynamics and Lineage Commitment in mESC Aggregates. *FASEB bioAdvances*, 7(6), e70012.

Patty BJ, et al. (2025) Widespread impact of nucleosome remodelers on transcription at cis-regulatory elements. *Cell reports*, 44(6), 115767.

Edupuganti RR, et al. (2025) Integrator promotes the association of TFIID and RNA polymerase II to maintain pluripotency during development. *Molecular cell*, 85(15), 2937.

Tripplehorn SA, et al. (2025) A direct interaction between the Chd1 CHCT domain and Rtf1 controls Chd1 distribution and nucleosome positioning on active genes. *Nucleic acids research*, 53(16).

Wolff R, et al. (2025) Protocol for the enhanced analysis of electrophysiological data from high-density multi-electrode arrays with nicespike and spikeNburst. *STAR protocols*, 6(4), 104195.

Dingare C, et al. (2024) Mannose controls mesoderm specification and symmetry breaking in mouse gastruloids. *Developmental cell*, 59(12), 1523.

Ortabozkoyun H, et al. (2024) Members of an array of zinc-finger proteins specify distinct Hox chromatin boundaries. *Molecular cell*, 84(18), 3406.