

Resource Summary Report

Generated by [dkNET](#) on Sep 12, 2026

ES-E14TG2a

RRID:CVCL_9108

Type: Cell Line

Proper Citation

RCB Cat# AES0135, RRID:CVCL_9108

Cell Line Information

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

Proper Citation: RCB Cat# AES0135, 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

Vendor: RCB

Catalog Number: AES0135

Hierarchy: cvcl_c320

Record Creation Time: 20220427T215835+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).

Gjonlleshaj 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.

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

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.

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

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