

Resource Summary Report

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ES-E14

RRID:CVCL_C320

Type: Cell Line

Proper Citation

(RRID:CVCL_C320)

Cell Line Information

URL: https://web.expasy.org/cellosaurus/CVCL_C320

Proper Citation: (RRID:CVCL_C320)

Description: Cell line ES-E14 is a Embryonic stem cell with a species of origin Mus musculus (Mouse)

Sex: Male

Defining Citation: [PMID:3821905](#), [PMID:19581487](#), [PMID:23850244](#), [PMID:25004115](#), [PMID:26484140](#)

Comments: Breed/subspecies: 129P2/Ola., Omics: Transcriptome analysis by microarray., Omics: H3K9me3 ChIP-seq epigenome analysis., Omics: H3K9me2 ChIP-seq epigenome analysis., Omics: H3K9ac ChIP-seq epigenome analysis., Omics: H3K4me3 ChIP-seq epigenome analysis., Omics: H3K4me1 ChIP-seq epigenome analysis., Omics: H3K36me3 ChIP-seq epigenome analysis., Omics: H3K27me3 ChIP-seq epigenome analysis., Omics: H3K27ac ChIP-seq epigenome analysis., Omics: Genome sequenced., Omics: DNA methylation analysis., Part of: ENCODE project mouse cell lines.

Category: Embryonic stem cell

Name: ES-E14

Synonyms: E14, E-14, ES (E14)

Cross References: BTO:BTO:0005136, EFO:EFO_0007075, 4DN:4DNSRR6CIPYP, BioSamples:SAMEA2155660, ENCODE:ENCBS033ENC, ENCODE:ENCBS042ENC, ENCODE:ENCBS043ENC, ENCODE:ENCBS054SMP, ENCODE:ENCBS324NLT, GEO:GSE53149, GEO:GSM344759, GEO:GSM344760, GEO:GSM397410,

GEO:GSM397411, GEO:GSM413111, GEO:GSM413112, GEO:GSM413113, GEO:GSM413117, GEO:GSM413118, GEO:GSM413119, GEO:GSM413123, GEO:GSM413124, GEO:GSM413125, GEO:GSM413129, GEO:GSM413130, GEO:GSM413131, GEO:GSM413135, GEO:GSM413136, GEO:GSM413137, GEO:GSM413141, GEO:GSM413142, GEO:GSM413143, GEO:GSM413147, GEO:GSM413148, GEO:GSM413149, GEO:GSM413153, GEO:GSM413154, GEO:GSM413155, GEO:GSM1000121, GEO:GSM1000123, GEO:GSM1000124, GEO:GSM1000125, GEO:GSM1000126, GEO:GSM1003750, GEO:GSM1003751, GEO:GSM1003756, GEO:GSM1003799, GEO:GSM1003807, GEO:GSM1003809, GEO:GSM1003810, GEO:GSM1014154, Wikidata:Q54832448

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Ratings and Alerts

No rating or validation information has been found for ES-E14.

No alerts have been found for ES-E14.

Data and Source Information

Source: [Cellosaurus](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Sun Z, et al. (2023) Chromatin regulation of transcriptional enhancers and cell fate by the Sotos syndrome gene NSD1. *Molecular cell*, 83(14), 2398.

Vainorius G, et al. (2023) Ascl1 and Ngn2 convert mouse embryonic stem cells to neurons via functionally distinct paths. *Nature communications*, 14(1), 5341.

Flury V, et al. (2023) Recycling of modified H2A-H2B provides short-term memory of chromatin states. *Cell*, 186(5), 1050.

Carraro M, et al. (2023) DAXX adds a de novo H3.3K9me3 deposition pathway to the histone chaperone network. *Molecular cell*, 83(7), 1075.

Xu X, et al. (2022) Mcm2 promotes stem cell differentiation via its ability to bind H3-H4. *eLife*, 11.

Liang X, et al. (2022) E-cadherin mediates apical membrane initiation site localisation during de?novo polarisation of epithelial cavities. The EMBO journal, 41(24), e111021.

Gopalan S, et al. (2022) Multi-CUT&Tag to simultaneously profile multiple chromatin factors. STAR protocols, 3(1), 101100.

Abe K, et al. (2022) Distinct patterns of RNA polymerase II and transcriptional elongation characterize mammalian genome activation. Cell reports, 41(13), 111865.

Pernaute B, et al. (2022) DRP1 levels determine the apoptotic threshold during embryonic differentiation through a mitophagy-dependent mechanism. Developmental cell, 57(11), 1316.

Tavares M, et al. (2022) JAZF1-SUZ12 dysregulates PRC2 function and gene expression during cell differentiation. Cell reports, 39(9), 110889.

Li R, et al. (2021) CUT&Tag-BS for simultaneous profiling of histone modification and DNA methylation with high efficiency and low cost. Cell reports methods, 1(8).

Li R, et al. (2021) A simple and robust method for simultaneous dual-omics profiling with limited numbers of cells. Cell reports methods, 1(3).

Houlard M, et al. (2021) MCPH1 inhibits Condensin II during interphase by regulating its SMC2-Kleisin interface. eLife, 10.

Petryk N, et al. (2021) Genome-wide and sister chromatid-resolved profiling of protein occupancy in replicated chromatin with ChOR-seq and SCAR-seq. Nature protocols, 16(9), 4446.

Lima A, et al. (2021) Cell competition acts as a purifying selection to eliminate cells with mitochondrial defects during early mouse development. Nature metabolism, 3(8), 1091.

Skalska L, et al. (2021) Nascent RNA antagonizes the interaction of a set of regulatory proteins with chromatin. Molecular cell, 81(14), 2944.

Alda-Catalinas C, et al. (2021) Pooled CRISPR-activation screening coupled with single-cell RNA-seq in mouse embryonic stem cells. STAR protocols, 2(2), 100426.

Li R, et al. (2021) Low-input ATAC&mRNA-seq protocol for simultaneous profiling of chromatin accessibility and gene expression. STAR protocols, 2(3), 100764.

Li Z, et al. (2021) Efficient and strand-specific profiling of replicating chromatin with enrichment and sequencing of protein-associated nascent DNA in mammalian cells. Nature protocols, 16(5), 2698.

Gopalan S, et al. (2021) Simultaneous profiling of multiple chromatin proteins in the same cells. Molecular cell, 81(22), 4736.