

Resource Summary Report

Generated by [RRID](#) on Aug 31, 2026

HeLa S3

RRID:CVCL_0058

Type: Cell Line

Proper Citation

CLS Cat# 300384, RRID:CVCL_0058

Cell Line Information

URL: https://web.expasy.org/cellosaurus/CVCL_0058

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Description: Cell line HeLa S3 is a Cancer cell line with a species of origin Homo sapiens (Human)

Sex: Female

Disease: Human papillomavirus-related endocervical adenocarcinoma

Defining Citation: [PMID:566722](#), [PMID:978597](#), [PMID:1180926](#), [PMID:1522048](#), [PMID:3180844](#), [PMID:3756862](#), [PMID:3986962](#), [PMID:6256643](#), [PMID:6825208](#), [PMID:9290701](#), [PMID:10338214](#), [PMID:11416159](#), [PMID:13286432](#), [PMID:13531635](#), [PMID:14518029](#), [PMID:16589695](#), [PMID:19450234](#), [PMID:23325432](#), [PMID:23925245](#), [PMID:24185095](#), [PMID:26550473](#), [PMID:30175587](#), [PMID:30778230](#), [PMID:33205894](#)

Comments: Anecdotal: The 'S' series of HeLa clones was named after Dr. Florence Sabin., Virology: Has at least 4 five HPV18 integration sites in the genome (PubMed=26550473)., Population: African American., Part of: Naval Biosciences Laboratory (NBL) collection (transferred to ATCC in 1982)., Part of: ENCODE project common cell types; tier 2.

Category: Cancer cell line

Organism: Homo sapiens (Human)

Name: HeLa S3

Synonyms: HeLa s3, HeLa-S3, HELA-S3, HeLa/S3, HeLa.S3, HeLa S 3, HeLa S-3, HeLaS3, HeLa, S3 clone, S3-HeLa, S3 HeLa

Cross References: BTO:BTO_0000568, CLO:CLO_0003695, CLO:CLO_0003696, CLO:CLO_0003699, CLO:CLO_0050921, CLO:CLO_0050936, EFO:EFO_0002791,

MCCL:MCC:0000220, CLDB:cl1616, CLDB:cl1617, CLDB:cl1619, CLDB:cl1620, CLDB:cl1621, CLDB:cl1622, 4DN:4DNSRGTEEYSL, ATCC:CCL-2.2, ATCC:CRL-7924, BCRC:60101, BioSample:SAMN03472408, BioSample:SAMN03472767, CCRID:1101HUM-PUMC000188, CCRID:1102HUM-NIFDC00009, CCRID:4201HUM-CCTCC00193, CCTCC:GDC0193, ChEMBL-Cells:CHEMBL3886002, ChEMBL-Targets:CHEMBL4296436, CLS:300384, Cosmic:846181, Cosmic:1201780, Cosmic:1324209, dbGAP:phs000665.v9.p1, DSMZ:ACC-161, DSMZCellDive:ACC-161, ECACC:87110901, ENCODE:ENCBS031GUL, ENCODE:ENCBS061SJE, ENCODE:ENCBS075PNA, ENCODE:ENCBS094KYE, ENCODE:ENCBS113ENC, ENCODE:ENCBS146YHK, ENCODE:ENCBS163VBG, ENCODE:ENCBS199XIN, ENCODE:ENCBS229UDI, ENCODE:ENCBS254ZSR, ENCODE:ENCBS292TEU, ENCODE:ENCBS352IHZ, ENCODE:ENCBS376OKH, ENCODE:ENCBS403WXR, ENCODE:ENCBS417UAY, ENCODE:ENCBS423QWP, ENCODE:ENCBS424JTA, ENCODE:ENCBS432ENC, ENCODE:ENCBS434SUM, ENCODE:ENCBS450RLH, ENCODE:ENCBS468RLW, ENCODE:ENCBS493MKF, ENCODE:ENCBS500SDW, ENCODE:ENCBS529RSF, ENCODE:ENCBS575PET, ENCODE:ENCBS577WSP, ENCODE:ENCBS580FYL, ENCODE:ENCBS585KIN, ENCODE:ENCBS598ZWC, ENCODE:ENCBS635AAA, ENCODE:ENCBS636AAA, ENCODE:ENCBS637AAA, ENCODE:ENCBS646PGB, ENCODE:ENCBS647UNF, ENCODE:ENCBS655ARO, ENCODE:ENCBS656NDW, ENCODE:ENCBS658BKJ, ENCODE:ENCBS681BHB, ENCODE:ENCBS684AAA, ENCODE:ENCBS685AAA, ENCODE:ENCBS686AAA, ENCODE:ENCBS687AAA, ENCODE:ENCBS688AAA, ENCODE:ENCBS689AAA, ENCODE:ENCBS714AAA, ENCODE:ENCBS735AAA, ENCODE:ENCBS736AAA, ENCODE:ENCBS737AAA, ENCODE:ENCBS738AAA, ENCODE:ENCBS739AAA, ENCODE:ENCBS740AAA, ENCODE:ENCBS748HNU, ENCODE:ENCBS804AAA, ENCODE:ENCBS805AAA, ENCODE:ENCBS812AOY, ENCODE:ENCBS822AAA, ENCODE:ENCBS823AAA, ENCODE:ENCBS833ISA, ENCODE:ENCBS834AAA, ENCODE:ENCBS838AAA, ENCODE:ENCBS839AAA, ENCODE:ENCBS854BZN, ENCODE:ENCBS877WSH, ENCODE:ENCBS890POO, ENCODE:ENCBS899VUW, ENCODE:ENCBS979JZP, FANTOM5_SSTAR:10815-111B5, FANTOM5_SSTAR:10816-111B6, FANTOM5_SSTAR:10817-111B7, GEO:GSM472905, GEO:GSM472916, GEO:GSM472932, GEO:GSM733669, GEO:GSM733682, GEO:GSM733684, GEO:GSM733689, GEO:GSM733696, GEO:GSM733711, GEO:GSM733734, GEO:GSM733756, GEO:GSM733785, GEO:GSM736510, GEO:GSM736564, GEO:GSM749721, GEO:GSM749729, GEO:GSM749739, GEO:GSM798322, GEO:GSM803454, GEO:GSM803455, GEO:GSM803478, GEO:GSM803533, GEO:GSM816436, GEO:GSM816633, GEO:GSM816643, GEO:GSM822273, GEO:GSM822285, GEO:GSM822286, GEO:GSM923449, GEO:GSM935272, GEO:GSM935276, GEO:GSM935290, GEO:GSM935302, GEO:GSM935317, GEO:GSM935318, GEO:GSM935320, GEO:GSM935326, GEO:GSM935328, GEO:GSM935341, GEO:GSM935342, GEO:GSM935351, GEO:GSM935362, GEO:GSM935365, GEO:GSM935366, GEO:GSM935367, GEO:GSM935369, GEO:GSM935370, GEO:GSM935383, GEO:GSM935384, GEO:GSM935395, GEO:GSM935405, GEO:GSM935408, GEO:GSM935416, GEO:GSM935432, GEO:GSM935435, GEO:GSM935436, GEO:GSM935459, GEO:GSM935476, GEO:GSM935484, GEO:GSM935486, GEO:GSM935489, GEO:GSM935498, GEO:GSM935500, GEO:GSM935508, GEO:GSM935511, GEO:GSM935552, GEO:GSM935553, GEO:GSM935554, GEO:GSM935555, GEO:GSM935560, GEO:GSM935561, GEO:GSM935570, GEO:GSM935571, GEO:GSM935578, GEO:GSM935582, GEO:GSM935606, GEO:GSM935615, GEO:GSM935625,

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ID: CVCL_0058

Vendor: CLS

Catalog Number: 300384

Hierarchy: cvcl_0030

Record Creation Time: 20220624T070759+0000

Record Last Update: 20260830T000509+0000

Ratings and Alerts

No rating or validation information has been found for HeLa S3.

Warning: Discontinued: ATCC; CRL-7924

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Data and Source Information

Source: [Cellosaurus](#)

Usage and Citation Metrics

We found 1315 mentions in open access literature.

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

Hotta T, et al. (2026) Accessibility of the unstructured γ -tubulin C-terminal tail is controlled by microtubule lattice conformation. eLife, 14.

Li Y, et al. (2026) Genetically encoded lockdown of SERCA in the endoplasmic reticulum membrane arrests Ca²⁺ signaling through proximity-covalent crosslinking. FEBS letters.

Malfatti MC, et al. (2026) The cooperative regulation of miR-221 by APE1 and AUF1 impacts p27Kip1 defining a miR signature relevant for cervical cancer. *FEBS open bio*, 16(6), 1222.

Lin SL, et al. (2026) Coiled-coil centrosomal proteins facilitate tubulin concentration via polyKR motifs. *The FEBS journal*.

Harmanda B, et al. (2026) Spatial control of Keratin 8 phosphorylation by Aurora B facilitates cytokinesis in cancer cells of epithelial origin. *The FEBS journal*, 293(14), 4149.

Fu B, et al. (2026) The molecular asynchrony of single cells. *bioRxiv : the preprint server for biology*.

Rosencrans WM, et al. (2025) Putative PINK1/Parkin activators lower the threshold for mitophagy by sensitizing cells to mitochondrial stress. *Science advances*, 11(35), eady0240.

Fantin RF, et al. (2025) Human monoclonal antibodies targeting A35 protect from death caused by mpox. *Cell*.

Li Q, et al. (2025) SUV39H1-dependent methyl-degron is a critical regulator of skeletal homeostasis. *Cell reports*, 44(7), 115910.

Hotta T, et al. (2025) Accessibility of the unstructured γ -tubulin C-terminal tail is controlled by microtubule lattice conformation. *bioRxiv : the preprint server for biology*.

Yi E, et al. (2025) Selective Depletion of Cancer Cells with Extrachromosomal DNA via Lentiviral Infection. *Cancer research communications*, 5(8), 1458.

Bäumlin E, et al. (2025) The impact of Coronavirus Nsp1 on host mRNA degradation is independent of its role in translation inhibition. *Cell reports*, 44(4), 115488.

Adriaenssens E, et al. (2025) Reconstitution of BNIP3/NIX-mitophagy initiation reveals hierarchical flexibility of the autophagy machinery. *Nature cell biology*, 27(8), 1272.

Hashizume T, et al. (2025) Biology-aware machine learning for culture medium optimization. *New biotechnology*, 89, 141.

Oflaz FE, et al. (2025) Annexin A5 controls VDAC1-dependent mitochondrial Ca²⁺ homeostasis and determines cellular susceptibility to apoptosis. *The EMBO journal*, 44(12), 3413.

Jenkins TW, et al. (2025) Highly specific Immunoproteasome inhibitor M3258 induces proteotoxic stress and apoptosis in KMT2A::AFF1 driven acute lymphoblastic leukemia. *Scientific reports*, 15(1), 17284.

Tang L, et al. (2025) Joint analysis of chromatin accessibility and gene expression in the same single cells reveals cancer-specific regulatory programs. *Cell systems*, 16(5), 101266.

Bruno F, et al. (2024) Collisions of RNA polymerases behind the replication fork promote alternative RNA splicing in newly replicated chromatin. *Molecular cell*, 84(2), 221.

McShane E, et al. (2024) A kinetic dichotomy between mitochondrial and nuclear gene expression processes. *Molecular cell*.

Wahl N, et al. (2024) SATB2 organizes the 3D genome architecture of cognition in cortical neurons. *Molecular cell*, 84(4), 621.