

# Resource Summary Report

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## WA01

RRID:CVCL\_9771

Type: Cell Line

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### Proper Citation

(WiCell Cat# wa01-cgmp-material, RRID:CVCL\_9771)

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### Cell Line Information

**URL:** [https://web.expasy.org/cellosaurus/CVCL\\_9771](https://web.expasy.org/cellosaurus/CVCL_9771)

**Proper Citation:** (WiCell Cat# wa01-cgmp-material, RRID:CVCL\_9771)

**Sex:** Male

**Defining Citation:** [PMID:9804556](#), [PMID:14745950](#), [PMID:16388305](#), [PMID:16919167](#), [PMID:17287758](#), [PMID:17570852](#), [PMID:17572666](#), [PMID:18713948](#), [PMID:20428235](#), [PMID:20641038](#), [PMID:20736931](#), [PMID:21295703](#), [PMID:21714037](#), [PMID:21983960](#), [PMID:22514597](#), [PMID:22802639](#), [PMID:23117585](#), [PMID:23325432](#), [PMID:24259714](#), [PMID:24374290](#), [PMID:27476965](#), [PMID:28445466](#), [PMID:29034888](#), [PMID:29034901](#), [PMID:30388422](#)

**Comments:** Anecdotal: WA01, WA07, WA09, WA13 and WA14 were the first human embryonic stem cells to be established., Omics: Transcriptome analysis by serial analysis of gene expression (SAGE)., Omics: Transcriptome analysis by RNAseq., Omics: Transcriptome analysis by microarray., Omics: SNP array analysis., Omics: H4K20me1 ChIP-seq epigenome analysis., Omics: H3K9me3 ChIP-seq epigenome analysis., Omics: H3K9ac ChIP-seq epigenome analysis., Omics: H3K4me3 ChIP-seq epigenome analysis., Omics: H3K4me2 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: DNA methylation analysis., Omics: Deep proteome analysis., Omics: Deep phosphoproteome analysis., Omics: Deep exome analysis., Omics: Array-based CGH., From: University of Wisconsin; Madison; USA., Part of: NHBLI Progenitor Cell Biology Consortium (PCBC) collection., Part of: ENCODE project common cell types; tier 1.

**Category:** Embryonic stem cell

**Name:** WA01

**Synonyms:** WA 01, WA-01, WA1, H1, H1-hESC, ESC H1, GE01, WAe001-A, WICELLE001-A, WA01-PCBC, PCBC02hse2011100705, SC11-014

**Cross References:** BTO:BTO\_0006060, CLO:CLO\_0037281, EFO:EFO\_0003042, 4DN:4DNSRHNAF6M6, 4DN:4DNSRV3SKQ8M, BioSample:SAMN03471895, BioSamples:SAMEA7768168, CCRID:3101HUMSCSP301, CCRID:3101HUMSCSP306, ENCODE:ENCBS001VRA, ENCODE:ENCBS011NFB, ENCODE:ENCBS019EUF, ENCODE:ENCBS040WGM, ENCODE:ENCBS051SJH, ENCODE:ENCBS055BDT, ENCODE:ENCBS055DBZ, ENCODE:ENCBS060CKC, ENCODE:ENCBS060MZO, ENCODE:ENCBS081AUS, ENCODE:ENCBS083WOY, ENCODE:ENCBS086PQW, ENCODE:ENCBS103ZIA, ENCODE:ENCBS111ENC, ENCODE:ENCBS131GSD, ENCODE:ENCBS153GON, ENCODE:ENCBS182IPV, ENCODE:ENCBS215WGD, ENCODE:ENCBS244HDB, ENCODE:ENCBS253TYD, ENCODE:ENCBS262EHC, ENCODE:ENCBS270AGK, ENCODE:ENCBS282MUP, ENCODE:ENCBS284CPV, ENCODE:ENCBS285QSX, ENCODE:ENCBS299BNQ, ENCODE:ENCBS299NOL, ENCODE:ENCBS307HNW, ENCODE:ENCBS309DZE, ENCODE:ENCBS345JIP, ENCODE:ENCBS364BFI, ENCODE:ENCBS368BPP, ENCODE:ENCBS371MFZ, ENCODE:ENCBS380OBH, ENCODE:ENCBS409PYK, ENCODE:ENCBS428NIG, ENCODE:ENCBS440MTS, ENCODE:ENCBS479XUT, ENCODE:ENCBS484NGW, ENCODE:ENCBS497CZZ, ENCODE:ENCBS513BIK, ENCODE:ENCBS534NMZ, ENCODE:ENCBS540UTP, ENCODE:ENCBS559QNR, ENCODE:ENCBS568FYY, ENCODE:ENCBS570AYT, ENCODE:ENCBS582QGL, ENCODE:ENCBS614LXI, ENCODE:ENCBS626BQK, ENCODE:ENCBS649THQ, ENCODE:ENCBS661AAA, ENCODE:ENCBS665AAA, ENCODE:ENCBS668AAA, ENCODE:ENCBS670AAA, ENCODE:ENCBS704NOS, ENCODE:ENCBS706WYC, ENCODE:ENCBS708BLT, ENCODE:ENCBS711AAA, ENCODE:ENCBS716AAA, ENCODE:ENCBS716FMR, ENCODE:ENCBS717WTB, ENCODE:ENCBS718AAA, ENCODE:ENCBS720AAA, ENCODE:ENCBS731AAA, ENCODE:ENCBS732AAA, ENCODE:ENCBS733AAA, ENCODE:ENCBS734AAA, ENCODE:ENCBS739PSV, ENCODE:ENCBS740OND, ENCODE:ENCBS780AAA, ENCODE:ENCBS780WAB, ENCODE:ENCBS797AAA, ENCODE:ENCBS802AAA, ENCODE:ENCBS803AAA, ENCODE:ENCBS819TBN, ENCODE:ENCBS820AAA, ENCODE:ENCBS847AAA, ENCODE:ENCBS849HZG, ENCODE:ENCBS854AAA, ENCODE:ENCBS855AAA, ENCODE:ENCBS874KZJ, ENCODE:ENCBS899KQD, ENCODE:ENCBS899NYB, ENCODE:ENCBS929BKG, ENCODE:ENCBS945MCY, ENCODE:ENCBS951DDF, ENCODE:ENCBS952IPA, ENCODE:ENCBS977TKX, ENCODE:ENCBS982HXP, ENCODE:ENCBS984IPH, GEO:GSM288339, GEO:GSM347921, GEO:GSM383873, GEO:GSM383874, GEO:GSM384095, GEO:GSM384096, GEO:GSM409307, GEO:GSM409308, GEO:GSM409312, GEO:GSM410807, GEO:GSM410808, GEO:GSM428286, GEO:GSM428289, GEO:GSM428291, GEO:GSM428295, GEO:GSM428296, GEO:GSM429321, GEO:GSM429322, GEO:GSM429323, GEO:GSM432392, GEO:GSM432685, GEO:GSM432686, GEO:GSM433167, GEO:GSM433170, GEO:GSM433171, GEO:GSM433174, GEO:GSM433176, GEO:GSM433177, GEO:GSM433179, GEO:GSM434762, GEO:GSM434776, GEO:GSM434785,

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IGRhCellID:H1%20p61, NIHhESC:NIHhESC-10-0043, PRIDE:PXD003903,  
SKIP:SKIP001933, WiCell:wa01, WiCell:wa01-cgmp-material, WiCell:wa01-matched-  
research-bank, WiCell:wa01-pcbc, Wikidata:Q54993510

**ID:** CVCL\_9771

**Vendor:** WiCell

**Catalog Number:** wa01-cgmp-material

**Record Creation Time:** 20250131T203102+0000

**Record Last Update:** 20250131T205131+0000

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Ratings and Alerts

No rating or validation information has been found for WA01.

No alerts have been found for WA01.

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## Data and Source Information

**Source:** [Cellosaurus](#)

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## Usage and Citation Metrics

We found 194 mentions in open access literature.

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

Moss KR, et al. (2024) hESC- and hiPSC-derived Schwann cells are molecularly comparable and functionally equivalent. *iScience*, 27(6), 109855.

Luongo R, et al. (2024) Protocol for generating human cortical organoids enriched in outer radial glia by guided differentiation. *STAR protocols*, 5(3), 103280.

Dhaliwal NK, et al. (2024) Protocol for the efficient and inducible generation of CRISPR-Cas9-edited human cortical neurons from the iCas9-iNgn2 hPSCs. *STAR protocols*, 5(4), 103352.

Guerra San Juan I, et al. (2024) KIF5A regulates axonal repair and time-dependent axonal transport of SFPQ granules and mitochondria in human motor neurons. *bioRxiv : the preprint server for biology*.

Dhaliwal NK, et al. (2024) Synergistic hyperactivation of both mTORC1 and mTORC2 underlies the neural abnormalities of PTEN-deficient human neurons and cortical organoids. *Cell reports*, 43(5), 114173.

Shen J, et al. (2024) Activating innate immune responses repolarizes hPSC-derived CAR macrophages to improve anti-tumor activity. *Cell stem cell*, 31(7), 1003.

Logsdon DM, et al. (2024) Transcriptome comparisons of trophoblasts from regenerative cell models with peri-implantation human embryos. *Biology of reproduction*.

Walsh RM, et al. (2024) Generation of human cerebral organoids with a structured outer subventricular zone. *Cell reports*, 43(4), 114031.

Janssens DH, et al. (2024) Scalable single-cell profiling of chromatin modifications with sciCUT&Tag. *Nature protocols*, 19(1), 83.

Qu N, et al. (2024) Human Pluripotent Stem Cell Derived Organoids Reveal a Role for WNT Signaling in Dorsal-Ventral Patterning of the Hindgut. *bioRxiv : the preprint server for biology*.

Guerra San Juan I, et al. (2024) KIF5A regulates axonal repair and time-dependent axonal transport of SFPQ granules and mitochondria in human motor neurons. *Neurobiology of disease*, 204, 106759.

Brenes AJ, et al. (2024) Proteomic and functional comparison between human induced and embryonic stem cells. *eLife*, 13.

Sun P, et al. (2024) Generation of self-renewing neuromesodermal progenitors with neuronal and skeletal muscle bipotential from human embryonic stem cells. *Cell reports methods*, 4(11), 100897.

Negueruela J, et al. (2024) Protocol for CRISPR-Cas12a genome editing of protein tyrosine phosphatases in human pluripotent stem cells and functional  $\gamma$ -like cell generation. *STAR protocols*, 5(3), 103297.

Funa NS, et al. (2024) TGF- $\beta$  modulates cell fate in human ES cell-derived foregut endoderm by inhibiting Wnt and BMP signaling. *Stem cell reports*, 19(7), 973.

Liu Y, et al. (2024) A human pluripotent stem cell-based somitogenesis model using microfluidics. *Cell stem cell*, 31(8), 1113.

Peng CS, et al. (2024) Nanometer-resolution tracking of single cargo reveals dynein motor mechanisms. *Nature chemical biology*.

Gong H, et al. (2023) MINE is a method for detecting spatial density of regulatory chromatin interactions based on a multi-modal network. *Cell reports methods*, 3(1), 100386.

Shi Y, et al. (2023) Characterization of genome-wide STR variation in 6487 human genomes. *Nature communications*, 14(1), 2092.

Yang R, et al. (2023) Epiphany: predicting Hi-C contact maps from 1D epigenomic signals. *Genome biology*, 24(1), 134.