Resource Summary Report

Generated by RRID on Sep 8, 2026

SK-MEL-19

RRID:CVCL_6025
Type: Cell Line

Proper Citation

RRID:CVCL_6025

Cell Line Information

URL: https://web.expasy.org/cellosaurus/CVCL_6025

Proper Citation: RRID:CVCL_6025

Description: Cell line SK-MEL-19 is a Cancer cell line with a species of origin Homo sapiens (Human)

Sex: Male

Disease: Cutaneous melanoma

Defining Citation: PMID:833871, PMID:978138, PMID:1067619, PMID:2499655, PMID:2784858, PMID:2983346, PMID:3518877, PMID:6582512, PMID:6864164, PMID:6933476, PMID:7017212, PMID:7175440, PMID:9598804, PMID:17260012, PMID:18505964, PMID:21343389, PMID:21725359, PMID:24576830

Comments: Characteristics: Pigmented., Population: Caucasian., From: Memorial Sloan Kettering Cancer Center; New York; USA., Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE).

Category: Cancer cell line

Organism: Homo sapiens (Human)

Name: SK-MEL-19

Synonyms: SK-Mel-19, SKMEL-19, SkMEL-19, SK-MEL19, SK-Mel19, Sk Mel19, SKMEL19, AL-Mel

Cross References: cancercelllines:CVCL_6025, Cell_Model_Passport:SIDM01423, ChEMBL-Cells:CHEMBL3307448, ChEMBL-Targets:CHEMBL614915, Cosmic:685202, Cosmic:721841, Cosmic:886830, Cosmic:923385, Cosmic:933126, Cosmic:1047686, Cosmic:1060427, Cosmic:1122255, Cosmic:1669136, DepMap:ACH-002005, GEO:GSM156032, GEO:GSM555122, GEO:GSM555175, GEO:GSM784508,

IARC_TP53:26112, Lonza:1332, Progenetix:CVCL_6025, PubChem_Cell_line:CVCL_6025, Wikidata:Q54953894

ID: CVCL_6025

Record Creation Time: 20220427T221545+0000

Record Last Update: 20260905T182401+0000

Ratings and Alerts

No rating or validation information has been found for SK-MEL-19.

No alerts have been found for SK-MEL-19.

Data and Source Information

Source: Cellosaurus

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID .

Arroyo Villora S, et al. (2026) A Bioinformatics and Wet-Lab-Based Pipeline Identifies CLDN10 and GJB2 as Epigenetically Silenced Tumor Suppressor Genes in Cutaneous Melanoma. International journal of molecular sciences, 27(5).

Deutschmeyer VE, et al. (2025) SIAH3 is frequently epigenetically silenced in cancer and regulates mitochondrial metabolism. International journal of cancer, 156(2), 353.

Degefu YN, et al. (2025) Cell state plasticity emerging from co-regulated, competitive, and configurable interactions within the AP-1 network. bioRxiv : the preprint server for biology.

Gadal S, et al. (2025) Tumorigenesis Driven by BRAFV600E Requires Secondary Mutations That Overcome Its Feedback Inhibition of RAC1 and Migration. Cancer research, 85(9), 1611.

Foda BM, et al. (2024) Inhibition of the Rho/MRTF pathway improves the response of BRAF-resistant melanoma to PD1/PDL1 blockade. International journal of cancer, 155(7), 1303.

Arroyo Villora S, et al. (2024) Biomarker RIPK3 Is Silenced by Hypermethylation in Melanoma and Epigenetic Editing Reestablishes Its Tumor Suppressor Function. Genes, 15(2).

Comandante-Lou N, et al. (2022) AP-1 transcription factor network explains diverse patterns of cellular plasticity in melanoma cells. Cell reports, 40(5), 111147.

Pudelko K, et al. (2022) Increased Microtubule Growth Triggered by Microvesicle-mediated Paracrine Signaling is Required for Melanoma Cancer Cell Invasion. Cancer research communications, 2(5), 366.

Nguyen TT, et al. (2021) Mutations in the IFN??-JAK-STAT Pathway Causing Resistance to Immune Checkpoint Inhibitors in Melanoma Increase Sensitivity to Oncolytic Virus Treatment. Clinical cancer research : an official journal of the American Association for Cancer Research, 27(12), 3432.

Pinto LC, et al. (2021) Anticancer potential of limonoids from Swietenia macrophylla: Genotoxic, antiproliferative and proapoptotic effects towards human colorectal cancer. Life sciences, 285, 119949.

Geng J, et al. (2018) Empty conformers of HLA-B preferentially bind CD8 and regulate CD8+ T cell function. eLife, 7.