SK-BR-3
RRID:CVCL_0033
Type: Cell Line

Proper Citation

(RRID:CVCL_0033)

Cell Line Information

**URL:** [https://web.expasy.org/cellosaurus/CVCL_0033](https://web.expasy.org/cellosaurus/CVCL_0033)

**Proper Citation:** (RRID:CVCL_0033)

**Description:** Cell line SK-BR-3 is a Cancer cell line with a species of origin Homo sapiens

**Sex:** Female

**Disease:** Breast adenocarcinoma


**Category:** Cancer cell line

**Organism:** Homo sapiens

**Name:** SK-BR-3

**Synonyms:** SK-Br-3, Sk-Br-3, SK BR 03, SKBR-3, SKBR3, SK-BR3, SKBr3, SkBr3, SKBR3

Ratings and Alerts

No rating or validation information has been found for SK-BR-3.

Warning: Discontinued: TKG; TKG 0592
37.4 hours (PubMed=24389870); ~30 hours (CLS); ~2-3 days (DSMZ); 56.19 hours (GrayJW panel), Population: Caucasian, From: Memorial Sloan Kettering Cancer Center; New York; USA, Part of: MD Anderson Cell Lines Project, Part of: KuDOS 95 cell line panel, Part of: ICBP43 breast cancer cell line panel, Part of: GrayJW breast cancer cell line panel, Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE). Warning: Discontinued: RCB; RCB2132
Derived from metastatic site: Pleural effusion, Misspelling: SKBR3B; In PubMed=26378940, Anecdotal: Used in a study utilising the fruit fly's olfactory system to detect cancer cells (PubMed=24389870), Omics: Transcriptome analysis, Omics: SNP array analysis, Omics: Protein expression by reverse-phase protein arrays, Omics: N-glycan profiling, Omics: miRNA expression profiling, Omics: H4K8ac ChIP-seq epigenome analysis, Omics: H3K9me3 ChIP-seq epigenome analysis, Omics: H3K9ac ChIP-seq epigenome analysis, Omics: H3K79me2 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: H3K23ac ChIP-seq epigenome analysis, Omics: H3K4me3 ChIP-seq epigenome analysis, Omics: H3K27me3 ChIP-seq epigenome analysis, Omics: H3K27ac ChIP-seq epigenome analysis, Omics: H2BK120ub ChIP-seq epigenome analysis, Omics: Glycoproteome analysis by proteomics, Omics: Genome sequenced, Omics: Exosome proteome analysis, Omics: Deep RNAseq analysis, Omics: Deep quantitative proteome analysis, Omics: Deep proteome analysis, Omics: Deep exome analysis, Omics: Deep antibody staining analysis, Omics: CNV analysis, Omics: Array-based CGH, Microsatellite instability: Stable (MSS) (PubMed=23671654), Doubling time: 37.4 hours (PubMed=24389870); ~30 hours (CLS); ~2-3 days (DSMZ); 56.19 hours (GrayJW panel), Population: Caucasian, From: Memorial Sloan Kettering Cancer Center; New York; USA, Part of: MD Anderson Cell Lines Project, Part of: KuDOS 95 cell line panel, Part of: ICBP43 breast cancer cell line panel, Part of: GrayJW breast cancer cell line panel, Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE).

Data and Source Information

Source: Cellosaurus

Usage and Citation Metrics

We found 98 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Scott DC, et al. (2023) E3 ligase autoinhibition by C-degron mimicry maintains C-degron
substrate fidelity. Molecular cell, 83(5), 770.


Blasquez L, et al. (2023) Ebseilen oxide and derivatives are new allosteric HER2 inhibitors for HER2-positive cancers. Molecular oncology.


Raghavakaimal A, et al. (2022) CCR5 activation and endocytosis in circulating tumor-derived cells isolated from the blood of breast cancer patients provide information about clinical outcome. Breast cancer research: BCR, 24(1), 35.


Su W, et al. (2022) ARAF protein kinase activates RAS by antagonizing its binding to RASGAP NF1. Molecular cell, 82(13), 2443.
