Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 2, 2025

Hs 578T

RRID:CVCL_0332
Type: Cell Line

Proper Citation

(RRID:CVCL_0332)

Cell Line Information

URL: https://web.expasy.org/cellosaurus/CVCL_0332

Proper Citation: (RRID:CVCL_0332)

Sex: Female

Defining Citation: PMID:283258, PMID:761205, PMID:864756, PMID:1961733, PMID:3335022, PMID:7902062, PMID:10700174, PMID:10969801, PMID:15153330, PMID:15677628, PMID:15748285, PMID:16142302, PMID:16397213, PMID:16541312, PMID:16959974, PMID:17088437, PMID:17157791, PMID:17932254, PMID:18277095, PMID:18386134, PMID:18516279, PMID:19372543, PMID:19582160, PMID:19593635, PMID:20070913, PMID:20164919, PMID:21778573, PMID:22068913, PMID:22347499, PMID:22384151, PMID:22460905, PMID:22585861, PMID:22628656, PMID:23151021, PMID:23601657, PMID:23856246, PMID:23933261, PMID:24009699, PMID:24094812, PMID:24162158, PMID:24176112, PMID:24279929, PMID:24670534, PMID:25485619, PMID:25877200, PMID:25892236, PMID:25960936, PMID:26589293, PMID:27377824, PMID:27397505, PMID:27807467, PMID:28196595, PMID:28287265, PMID:28889351, PMID:29671673, PMID:30894373, PMID:30971826, PMID:31068700, PMID:31978347, PMID:35839778

Comments: Omics: Transcriptome analysis by RNAseq., Omics: Transcriptome analysis by microarray., Omics: SNP array analysis., Omics: Protein expression by reverse-phase protein arrays., Omics: N-glycan profiling., Omics: Mitochondrial genome sequenced., Omics: miRNA expression profiling., Omics: Metabolome analysis., Omics: lncRNA expression profiling., Omics: Glycoproteome analysis by proteomics., Omics: Fluorescence phenotype profiling., Omics: DNA methylation analysis., Omics: Deep quantitative proteome analysis., Omics: Deep proteome analysis., Omics: Deep exome analysis., Omics: CRISPR phenotypic screen., Omics: CNV analysis., Omics: Array-based CGH., Population: Caucasian., Part of: NCI-60 cancer cell line panel., Part of: Naval Biosciences Laboratory (NBL) collection (transferred to ATCC in 1982)., Part of: MD Anderson Cell Lines Project., Part of: KuDOS 95 cell line panel., Part of: JWGray breast cancer cell line panel., Part of:

COSMIC cell lines project., Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE)., Group: Triple negative breast cancer (TNBC) cell line.

Category: Cancer cell line

Name: Hs 578T

Synonyms: HS 578T, Hs-578T, HS-578T, Hs_578t, Hs-578-T, HS-578-T, Hs 578.T, HS578T, Hs578T, Hs578t, HS0578T, 578T, HS578, Hs578, Homo sapiens No. 578, tumor cells

Cross References: BTO:BTO_0003885, CLO:CLO_0004009, EFO:EFO_0001192, MCCL:MCC:0000228, CLDB:cl1716, CLDB:cl1717, CLDB:cl5023, ArrayExpress:E-MTAB-783, ArrayExpress:E-MTAB-2706, ArrayExpress:E-MTAB-2770, ArrayExpress:E-MTAB-3610, ArrayExpress:E-TABM-157, ArrayExpress:E-TABM-244, ATCC:CRL-7849, ATCC:HTB-126, BCRC:60120, BioGRID_ORCS_Cell_line:654, BioSample:SAMN03473213, BioSample:SAMN10987893, cancercelllines:CVCL_0332, CCRID:1101HUM-PUMC000670, CCRID:3101HUMTCHu127, CCRID:4201HUM-CCTCC00252, CCTCC:GDC0252, Cell_Model_Passport:SIDM00135, ChEMBL-Cells:CHEMBL3307672, ChEMBL-Targets:CHEMBL614645, CLS:305089, Cosmic:871142, Cosmic:875877, Cosmic:897418, Cosmic:904372, Cosmic:905957, Cosmic:921973, Cosmic:934524, Cosmic:974234, Cosmic:979715, Cosmic:997928, Cosmic:1010929, Cosmic:1017164, Cosmic:1018473, Cosmic:1027051, Cosmic:1044232, Cosmic:1046945, Cosmic:1047714, Cosmic:1092606, Cosmic:1136373, Cosmic:1175831, Cosmic:1176633, Cosmic:1218873, Cosmic:1235086, Cosmic:1287921, Cosmic:1289390, Cosmic:1305385, Cosmic:1312371, Cosmic:1430343, Cosmic:1473054, Cosmic:1518105, Cosmic:1603214, Cosmic:1609463, Cosmic:1998448, Cosmic:2009515, Cosmic:2164996, Cosmic:2301525, Cosmic:2560243, Cosmic:2668302, Cosmic-CLP:905957, DepMap:ACH-000148, DSMZ:ACC-781, DSMZCellDive:ACC-781, ECACC:86082104, EGA:EGAS00001000610, EGA:EGAS00001000978, GDSC:905957, GEO:GSM2113, GEO:GSM50182, GEO:GSM50246, GEO:GSM217581, GEO:GSM219968, GEO:GSM344346, GEO:GSM344396, GEO:GSM421868, GEO:GSM750776, GEO:GSM783962, GEO:GSM799319, GEO:GSM799382, GEO:GSM839032, GEO:GSM847392, GEO:GSM847488, GEO:GSM846359, GEO:GSM844563, GEO:GSM844564, GEO:GSM844565, GEO:GSM887098, GEO:GSM888169, GEO:GSM1008903, GEO:GSM1053700, GEO:GSM1153388, GEO:GSM1172877, GEO:GSM1181262, GEO:GSM1181319, GEO:GSM1214564, GEO:GSM1238131, GEO:GSM1374549, GEO:GSM1374550, GEO:GSM1833625, GEO:GSM1669895, GEO:GSM2124656, IARC_TP53:579, IBRC:C10150, ICLC:HTL00007, KCB:KCB 2012025YJ, KCLB:30126, LiGeA:CCLE_743, LINCS_HMS:50238, LINCS_LDP:LCL-1315, Lonza:1444, NCI-DTP:HS 578T, PharmacoDB:Hs578T_614_2019, PRIDE:PXD005292, PRIDE:PXD005942, PRIDE:PXD005946, PRIDE:PXD008222, PRIDE:PXD030304, Progenetix:CVCL_0332, PubChem_Cell_line:CVCL_0332, SKY/M-FISH/CGH:2663, SLKBase:3558, Wikidata:Q54895774

ID: CVCL_0332

Record Creation Time: 20250131T200922+0000

Record Last Update: 20250131T202342+0000

Ratings and Alerts

No rating or validation information has been found for Hs 578T.

Warning: Discontinued: ATCC; CRL-7849
Omics: Transcriptome analysis by RNAseq., Omics: Transcriptome analysis by microarray., Omics: SNP array analysis., Omics: Protein expression by reverse-phase protein arrays., Omics: N-glycan profiling., Omics: Mitochondrial genome sequenced., Omics: miRNA expression profiling., Omics: Metabolome analysis., Omics: lncRNA expression profiling., Omics: Glycoproteome analysis by proteomics., Omics: Fluorescence phenotype profiling., Omics: DNA methylation analysis., Omics: Deep quantitative proteome analysis., Omics: Deep proteome analysis., Omics: Deep exome analysis., Omics: CRISPR phenotypic screen., Omics: CNV analysis., Omics: Array-based CGH., Population: Caucasian., Part of: NCI-60 cancer cell line panel., Part of: Naval Biosciences Laboratory (NBL) collection (transferred to ATCC in 1982)., Part of: MD Anderson Cell Lines Project., Part of: KuDOS 95 cell line panel., Part of: JWGray breast cancer cell line panel., Part of: COSMIC cell lines project., Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE)., Group: Triple negative breast cancer (TNBC) cell line.

Data and Source Information

Source: Cellosaurus

Usage and Citation Metrics

We found 1303 mentions in open access literature.

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

Lerévérend C, et al. (2025) Enhanced expression of galectin-9 in triple negative breast cancer cells following radiotherapy: Implications for targeted therapy. International journal of cancer, 156(1), 229.

Graham K, et al. (2024) Discovery of YAP1/TAZ pathway inhibitors through phenotypic screening with potent anti-tumor activity via blockade of Rho-GTPase signaling. Cell chemical biology, 31(7), 1247.

Yen HR, et al. (2024) Targeting chondroitin sulfate suppresses macropinocytosis of breast cancer cells by modulating syndecan-1 expression. Molecular oncology, 18(10), 2569.

Shen Y, et al. (2024) Coptisine exerts anti-tumour effects in triple-negative breast cancer by

targeting mitochondrial complex I. British journal of pharmacology, 181(21), 4262.

Kunkel MW, et al. (2024) HTS384 NCI60: The Next Phase of the NCI60 Screen. Cancer research, 84(15), 2403.

Cetin M, et al. (2024) A highly potent bi-thiazole inhibitor of LOX rewires collagen architecture and enhances chemoresponse in triple-negative breast cancer. Cell chemical biology.

Marks MP, et al. (2024) Role of hydroxymethylglutharyl-coenzyme A reductase in the induction of stem-like states in breast cancer. Journal of cancer research and clinical oncology, 150(2), 106.

Zheng SM, et al. (2024) MILIP Binding to tRNAs Promotes Protein Synthesis to Drive Triple-Negative Breast Cancer. Cancer research, 84(9), 1460.

Ni Q, et al. (2024) Cytoskeletal activation of NHE1 regulates mechanosensitive cell volume adaptation and proliferation. Cell reports, 43(12), 114992.

Manouchehri JM, et al. (2024) The role of heparan sulfate in enhancing the chemotherapeutic response in triple-negative breast cancer. Breast cancer research : BCR, 26(1), 153.

Huang YM, et al. (2024) Exploring the multifaceted impact of lanthanides on physiological pathways in human breast cancer cells. Toxicology, 502, 153731.

Chen X, et al. (2024) Adipocytes promote metastasis of breast cancer by attenuating the FOXO1 effects and regulating copper homeostasis. Cancer cell international, 24(1), 284.

Lai YS, et al. (2024) Store-operated calcium entry inhibits primary ciliogenesis via the activation of Aurora A. The FEBS journal, 291(5), 1027.

Waas M, et al. (2024) Droplet-based proteomics reveals CD36 as a marker for progenitors in mammary basal epithelium. Cell reports methods, 4(4), 100741.

Giannakakis A, et al. (2024) KDM7A-DT induces genotoxic stress, tumorigenesis, and progression of p53 missense mutation-associated invasive breast cancer. Frontiers in oncology, 14, 1227151.

Bjørnstad OV, et al. (2024) Global and single-cell proteomics view of the co-evolution between neural progenitors and breast cancer cells in a co-culture model. EBioMedicine, 108, 105325.

Takaki EO, et al. (2024) A PDE3A-SLFN12 Molecular Glue Exhibits Significant Antitumor Activity in TKI-Resistant Gastrointestinal Stromal Tumors. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(16), 3603.

He J, et al. (2023) NCAPD2 promotes breast cancer progression through E2F1 transcriptional regulation of CDK1. Cancer science, 114(3), 896.

Almaraz Postigo S, et al. (2023) Neuregulin modulates hormone receptor levels in breast cancer through concerted action on multiple signaling pathways. Clinical science (London, England : 1979), 137(1), 1.

Muley H, et al. (2023) Cpt1c Downregulation Causes Plasma Membrane Remodelling and Anthracycline Resistance in Breast Cancer. International journal of molecular sciences, 24(2).