Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 17, 2025

Karpas-422

RRID:CVCL_1325
Type: Cell Line

Proper Citation

(RRID:CVCL_1325)

Cell Line Information

URL: https://web.expasy.org/cellosaurus/CVCL_1325

Proper Citation: (RRID:CVCL_1325)

Sex: Female

Defining Citation: PMID:1465024, PMID:2297573, PMID:7849311, PMID:8547074, PMID:8558920, PMID:9738977, PMID:12169673, PMID:16960149, PMID:19278952, PMID:19358282, PMID:20164919, PMID:20628145, PMID:23257783, PMID:23292937, PMID:23699601, PMID:25355872, PMID:25485619, PMID:25877200, PMID:25960936, PMID:26589293, PMID:27397505, PMID:28196595, PMID:30285677, PMID:30629668, PMID:30894373, PMID:31068700, PMID:31978347, PMID:35839778

Comments: Omics: Virome analysis using RNAseq., Omics: Transcriptome analysis by RNAseq., Omics: Transcriptome analysis by microarray., Omics: SNP array analysis., Omics: Protein expression by reverse-phase protein arrays., Omics: miRNA expression profiling., Omics: H3K9ac ChIP-seq epigenome analysis., Omics: Genome sequenced., Omics: DNA methylation analysis., Omics: Deep quantitative proteome analysis., Omics: Deep exome analysis., Omics: CNV analysis., Omics: Array-based CGH., Characteristics: Quite popular cell line because of its resistance to chemotherapy., Population: Caucasian., Part of: MD Anderson Cell Lines Project., Part of: COSMIC cell lines project., Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE).

Category: Cancer cell line

Name: Karpas-422

Synonyms: KARPAS-422, Karpas 422, KARPAS 422, Karpas422, KARPAS422, K422

Cross References: BTO:BTO_0004981, CLO:CLO_0007066, EFO:EFO_0005719,

CLDB:cl2996, CLDB:cl4975, ArrayExpress:E-MTAB-783, ArrayExpress:E-MTAB-2706, ArrayExpress:E-MTAB-2770, ArrayExpress:E-MTAB-3610, BioSample:SAMN03471099, BioSample:SAMN10988506, cancercelllines:CVCL_1325, Cell_Model_Passport:SIDM01008, ChEMBL-Cells:CHEMBL3308328, ChEMBL-Targets:CHEMBL2366368, Cosmic:907274, Cosmic:1086338, Cosmic:1329088, Cosmic:1629930, Cosmic:1714156, Cosmic:1945182, Cosmic:1995467, Cosmic:2276323, Cosmic:2297003, Cosmic:2361372, Cosmic:2437320, Cosmic-CLP:907274, DepMap:ACH-000315, DSMZ:ACC-32, DSMZCellDive:ACC-32, ECACC:06101702, EGA:EGAS00001000610, EGA:EGAS00001000978, ENCODE:ENCBS171YVY, ENCODE:ENCBS301UOD, ENCODE:ENCBS530UDH, ENCODE:ENCBS850UIV, ENCODE:ENCBS869AAA, ENCODE:ENCBS870AAA, ENCODE:ENCBS992KXS, GDSC:907274, GEO:GSM115821, GEO:GSM201346, GEO:GSM380129, GEO:GSM552444, GEO:GSM907518, GEO:GSM1035313, GEO:GSM1059807, GEO:GSM1374588, GEO:GSM1669976, GEO:GSM3150249, IARC_TP53:27172, ICLC:HTL99023, LiGeA:CCLE_680, LINCS_LDP:LCL-1120, PharmacoDB:KARPAS422_730_2019, PRIDE:PXD012087, PRIDE:PXD030304, Progenetix:CVCL_1325, PubChem_Cell_line:CVCL_1325, Wikidata:Q54899500, Ximbio:152419

ID: CVCL_1325

Record Creation Time: 20250131T201119+0000

Record Last Update: 20250131T202624+0000

Ratings and Alerts

No rating or validation information has been found for Karpas-422.

Warning: Discontinued: DSMZ; ACC-32
Omics: Virome analysis using RNAseq., Omics: Transcriptome analysis by RNAseq., Omics: Transcriptome analysis by microarray., Omics: SNP array analysis., Omics: Protein expression by reverse-phase protein arrays., Omics: miRNA expression profiling., Omics: H3K9ac ChIP-seq epigenome analysis., Omics: Genome sequenced., Omics: DNA methylation analysis., Omics: Deep quantitative proteome analysis., Omics: Deep exome analysis., Omics: CNV analysis., Omics: Array-based CGH., Characteristics: Quite popular cell line because of its resistance to chemotherapy., Population: Caucasian., Part of: MD Anderson Cell Lines Project., Part of: COSMIC cell lines project., 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 11 mentions in open access literature.

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

Choi J, et al. (2024) Molecular targets of glucocorticoids that elucidate their therapeutic efficacy in aggressive lymphomas. Cancer cell, 42(5), 833.

Johnson Z, et al. (2023) IOA-244 is a Non-ATP-competitive, Highly Selective, Tolerable PI3K Delta Inhibitor That Targets Solid Tumors and Breaks Immune Tolerance. Cancer research communications, 3(4), 576.

Rodina A, et al. (2023) Systems-level analyses of protein-protein interaction network dysfunctions via epichaperomics identify cancer-specific mechanisms of stress adaptation. Nature communications, 14(1), 3742.

Donati G, et al. (2022) Targeting mitochondrial respiration and the BCL2 family in high-grade MYC-associated B-cell lymphoma. Molecular oncology, 16(5), 1132.

Wei P, et al. (2022) Mitochondrial pyruvate supports lymphoma proliferation by fueling a glutamate pyruvate transaminase 2-dependent glutaminolysis pathway. Science advances, 8(39), eabq0117.

Wenthe J, et al. (2021) Boosting CAR T-cell responses in lymphoma by simultaneous targeting of CD40/4-1BB using oncolytic viral gene therapy. Cancer immunology, immunotherapy : CII, 70(10), 2851.

Dersh D, et al. (2021) Genome-wide Screens Identify Lineage- and Tumor-Specific Genes Modulating MHC-I- and MHC-II-Restricted Immunosurveillance of Human Lymphomas. Immunity, 54(1), 116.

Yan P, et al. (2020) Molecular Stressors Engender Protein Connectivity Dysfunction through Aberrant N-Glycosylation of a Chaperone. Cell reports, 31(13), 107840.

Hsu JH, et al. (2020) EED-Targeted PROTACs Degrade EED, EZH2, and SUZ12 in the PRC2 Complex. Cell chemical biology, 27(1), 41.

Bararia D, et al. (2020) Cathepsin S Alterations Induce a Tumor-Promoting Immune Microenvironment in Follicular Lymphoma. Cell reports, 31(5), 107522.

Li M, et al. (2019) Non-oncogene Addiction to SIRT3 Plays a Critical Role in Lymphomagenesis. Cancer cell, 35(6), 916.