

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 22, 2025

Hep-G2

RRID:CVCL_0027

Type: Cell Line

Proper Citation

(RRID:CVCL_0027)

Cell Line Information

URL: https://web.expasy.org/cellosaurus/CVCL_0027

Proper Citation: (RRID:CVCL_0027)

Sex: Male

Defining Citation: [PMID:233137](#), [PMID:2439335](#), [PMID:6248960](#), [PMID:6288577](#), [PMID:7972006](#), [PMID:8050184](#), [PMID:8224613](#), [PMID:8384076](#), [PMID:8389256](#), [PMID:8835345](#), [PMID:9178645](#), [PMID:9359923](#), [PMID:11050057](#), [PMID:11416159](#), [PMID:11981770](#), [PMID:12029633](#), [PMID:12068308](#), [PMID:14980111](#), [PMID:15767549](#), [PMID:16181800](#), [PMID:16935386](#), [PMID:17254797](#), [PMID:19215227](#), [PMID:19751877](#), [PMID:20069059](#), [PMID:20215515](#), [PMID:20228232](#), [PMID:20937217](#), [PMID:21269460](#), [PMID:22278370](#), [PMID:22460905](#), [PMID:23325432](#), [PMID:23505090](#), [PMID:23887712](#), [PMID:24116068](#), [PMID:24618588](#), [PMID:25485619](#), [PMID:25574106](#), [PMID:25877200](#), [PMID:25960936](#), [PMID:26160117](#), [PMID:26589293](#), [PMID:26825538](#), [PMID:27027780](#), [PMID:27329724](#), [PMID:27470094](#), [PMID:28196595](#), [PMID:29610054](#), [PMID:29660373](#), [PMID:30629668](#), [PMID:30864654](#), [PMID:30894373](#), [PMID:31063779](#), [PMID:31068700](#), [PMID:31378681](#), [PMID:31395879](#), [PMID:31561354](#), [PMID:31978347](#), [PMID:32471280](#), [PMID:32899426](#), [PMID:34320349](#)

Comments: Omics: Virome analysis using proteomics., Omics: Transcriptome analysis by RNAseq., Omics: Transcriptome analysis by microarray., Omics: SNP array analysis., Omics: Secretome proteome analysis., Omics: Protein expression by reverse-phase protein arrays., Omics: miRNA expression profiling., Omics: Metabolome analysis., Omics: Genome sequenced., Omics: DNA methylation analysis., Omics: Deep quantitative proteome analysis., Omics: Deep proteome analysis., Omics: Deep phosphoproteome analysis., Omics: Deep exome analysis., Omics: Deep antibody staining analysis., Omics: H4K20me1 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: 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: CTCF ChIP-seq epigenome analysis., Population: Caucasian., Part of: TCGA-110-CL cell line panel., Part of: MD Anderson Cell Lines Project., Part of: Liver Cancer Model Repository (LIMORE)., Part of: JFCR45 cancer cell line panel., Part of: ENCODE project common cell types; tier 1., Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE)., Problematic cell line: Misclassified. Originally thought to be a hepatocellular carcinoma cell line but shown to be from an hepatoblastoma (PubMed=19751877)..., Group: Patented cell line.

Category: Cancer cell line

Name: Hep-G2

Synonyms: HEP-G2, Hep G2, HEP G2, HepG2, HEPG2

Cross References: BTO:BTO_0000599, CLO:CLO_0003704, CLO:CLO_0003713, CLO:CLO_0050856, CLO:CLO_0050858, EFO:EFO_0001187, MCCL:MCC:0000222, CLDB:cl1635, CLDB:cl1636, CLDB:cl1637, CLDB:cl1638, CLDB:cl1639, CLDB:cl1641, CLDB:cl1642, CLDB:cl1643, CLDB:cl1644, CLDB:cl4910, Abcam:ab257304, Abcam:ab275467, AddexBio:C0015002/46, ArrayExpress:E-MTAB-38, ArrayExpress:E-MTAB-2706, ArrayExpress:E-MTAB-2770, ArrayExpress:E-MTAB-6919, ATCC:HB-8065, BCRC:60025, BCRJ:0103, BioGRID_ORCS_Cell_line:809, BioSample:SAMN01821557, BioSample:SAMN01821681, BioSample:SAMN03472183, BioSample:SAMN10988201, cancercellines:CVCL_0027, CCRID:1101HUM-PUMC000035, CCRID:3101HUMSCSP510, CCRID:3101HUMTCHu72, CCRID:4201HUM-CCTCC00024, CCRID:5301HUM-KCB05007YJ, CCTCC:GDC0024, Cell_Model_Passport:SIDM00904, CGH-DB:9068-4, ChEMBL-Cells:ChEMBL3307718, ChEMBL-Targets:ChEMBL395, CLS:300198, Cosmic:690746, Cosmic:724821, Cosmic:852774, Cosmic:869169, Cosmic:869298, Cosmic:871510, Cosmic:873392, Cosmic:873713, Cosmic:928138, Cosmic:932989, Cosmic:934550, Cosmic:945158, Cosmic:948062, Cosmic:979732, Cosmic:999850, Cosmic:1060080, Cosmic:1187331, Cosmic:1351511, Cosmic:1499246, Cosmic:1518227, Cosmic:1628386, Cosmic:2162525, Cosmic:2301556, Cosmic:2321029, Cosmic:2560244, Cosmic:2668285, Cosmic:2674233, Cosmic:2773180, DepMap:ACH-000739, DSMZ:ACC-180, DSMZCellDive:ACC-180, ECACC:85011430, EGA:EGAS00001000610, ENCODE:ENCBS002KIX, ENCODE:ENCBS005KKO, ENCODE:ENCBS005NKZ, ENCODE:ENCBS006INV, ENCODE:ENCBS009AVS, ENCODE:ENCBS011BYX, ENCODE:ENCBS011NDE, ENCODE:ENCBS012DTZ, ENCODE:ENCBS013LLU, ENCODE:ENCBS015PAC, ENCODE:ENCBS016WDR, ENCODE:ENCBS017VYZ, ENCODE:ENCBS018BAD, ENCODE:ENCBS018WXY, ENCODE:ENCBS019LAC, ENCODE:ENCBS019QTJ, ENCODE:ENCBS019XED, ENCODE:ENCBS020YDI, ENCODE:ENCBS021UTC, ENCODE:ENCBS023JBH, ENCODE:ENCBS024EHA, ENCODE:ENCBS025AAW, ENCODE:ENCBS030GWA, ENCODE:ENCBS030ZIT, ENCODE:ENCBS033QJG, ENCODE:ENCBS034ENA, ENCODE:ENCBS034PYO, ENCODE:ENCBS035IIS, ENCODE:ENCBS038OUO, ENCODE:ENCBS038ZQB, ENCODE:ENCBS039DPC, ENCODE:ENCBS039XPI, ENCODE:ENCBS040DES, ENCODE:ENCBS040EJF, ENCODE:ENCBS040QBA, ENCODE:ENCBS041GAW, ENCODE:ENCBS042JDA, ENCODE:ENCBS044VWV, ENCODE:ENCBS045GOD,

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ID: CVCL_0027

Record Creation Time: 20250131T200406+0000

Record Last Update: 20250131T201626+0000

Ratings and Alerts

No rating or validation information has been found for Hep-G2.

Warning: Problematic cell line: Misclassified. Originally thought to be a hepatocellular carcinoma cell line but shown to be from an hepatoblastoma (PubMed=19751877).

Registration: International Depository Authority, American Type Culture Collection (ATCC); HB-8065.

Omics: Virome analysis using proteomics., Omics: Transcriptome analysis by RNAseq., Omics: Transcriptome analysis by microarray., Omics: SNP array analysis., Omics: Secretome proteome analysis., Omics: Protein expression by reverse-phase protein arrays., Omics: miRNA expression profiling., Omics: Metabolome analysis., Omics: Genome sequenced., Omics: DNA methylation analysis., Omics: Deep quantitative proteome analysis., Omics: Deep proteome analysis., Omics: Deep phosphoproteome analysis., Omics: Deep exome analysis., Omics: Deep antibody staining analysis., Omics: H4K20me1 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: 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: CTCF ChIP-seq epigenome analysis., Population: Caucasian., Part of: TCGA-110-CL cell line panel., Part of: MD Anderson Cell Lines Project., Part of: Liver Cancer Model Repository (LIMORE)., Part of: JFCR45 cancer cell line panel., Part of: ENCODE project common cell types; tier 1., Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE)., Problematic cell line: Misclassified. Originally thought to be a hepatocellular carcinoma cell line but shown to be from an hepatoblastoma (PubMed=19751877)..., Group: Patented cell line. **Warning:** Problematic cell line: Misclassified. Originally thought to be a hepatocellular carcinoma cell line but shown to be from an hepatoblastoma (PubMed=19751877).

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Omics: Virome analysis using proteomics., Omics: Transcriptome analysis by RNAseq., Omics: Transcriptome analysis by microarray., Omics: SNP array analysis., Omics: Secretome proteome analysis., Omics: Protein expression by reverse-phase protein arrays., Omics: miRNA expression profiling., Omics: Metabolome analysis., Omics: Genome sequenced., Omics: DNA methylation analysis., Omics: Deep quantitative proteome analysis., Omics: Deep proteome analysis., Omics: Deep phosphoproteome analysis., Omics: Deep exome analysis., Omics: Deep antibody staining analysis., Omics: H4K20me1 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: 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: CTCF ChIP-seq epigenome analysis., Population: Caucasian., Part of: TCGA-110-CL cell line panel., Part of: MD Anderson Cell Lines Project., Part of: Liver Cancer Model Repository (LIMORE)., Part of: JFCR45 cancer cell line panel., Part of: ENCODE project common cell types; tier 1., Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE)., Problematic cell line: Misclassified. Originally thought to be a hepatocellular carcinoma cell line but shown to be from an hepatoblastoma (PubMed=19751877).., Group: Patented cell line. **Warning:** Discontinued: RCB; RCB0459

Omics: Virome analysis using proteomics., Omics: Transcriptome analysis by RNAseq., Omics: Transcriptome analysis by microarray., Omics: SNP array analysis., Omics: Secretome proteome analysis., Omics: Protein expression by reverse-phase protein arrays., Omics: miRNA expression profiling., Omics: Metabolome analysis., Omics: Genome sequenced., Omics: DNA methylation analysis., Omics: Deep quantitative proteome analysis., Omics: Deep proteome analysis., Omics: Deep phosphoproteome analysis., Omics: Deep exome analysis., Omics: Deep antibody staining analysis., Omics: H4K20me1

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: 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: CTCF ChIP-seq epigenome analysis., Population: Caucasian., Part of: TCGA-110-CL cell line panel., Part of: MD Anderson Cell Lines Project., Part of: Liver Cancer Model Repository (LIMORE)., Part of: JFCR45 cancer cell line panel., Part of: ENCODE project common cell types; tier 1., Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE)., Problematic cell line: Misclassified. Originally thought to be a hepatocellular carcinoma cell line but shown to be from an hepatoblastoma (PubMed=19751877)..., Group: Patented cell line.

Data and Source Information

Source: [Cellosaurus](#)

Usage and Citation Metrics

We found 22212 mentions in open access literature.

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

Champagne J, et al. (2025) Adoptive T cell therapy targeting an inducible and broadly shared product of aberrant mRNA translation. *Immunity*, 58(1), 247.

Liu X, et al. (2024) USP7 reduces the level of nuclear DICER, impairing DNA damage response and promoting cancer progression. *Molecular oncology*, 18(1), 170.

Singh AK, et al. (2024) Development of a [89Zr]Zr-labeled Human Antibody using a Novel Phage-displayed Human scFv Library. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(7), 1293.

Chen Y, et al. (2024) Functionalized tetrahedral DNA frameworks for the capture of circulating tumor cells. *Nature protocols*.

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Ma RK, et al. (2024) DNAJB1-PRKACA fusion protein-regulated LINC00473 promotes tumor growth and alters mitochondrial fitness in fibrolamellar carcinoma. *PLoS genetics*, 20(3), e1011216.

Ma D, et al. (2024) cGAS suppresses hepatocellular carcinoma independent of its cGAMP synthase activity. *Cell death and differentiation*, 31(6), 722.

Xu C, et al. (2024) Systematic dissection of sequence features affecting binding specificity of

a pioneer factor reveals binding synergy between FOXA1 and AP-1. *Molecular cell*, 84(15), 2838.

Chen Z, et al. (2024) SIGLEC15, negatively correlated with PD-L1 in HCC, could induce CD8+ T cell apoptosis to promote immune evasion. *Oncoimmunology*, 13(1), 2376264.

Kato H, et al. (2024) Histone methyltransferase SUV420H1/KMT5B contributes to poor prognosis in hepatocellular carcinoma. *Cancer science*, 115(2), 385.

Arora C, et al. (2024) The landscape of cancer-rewired GPCR signaling axes. *Cell genomics*, 4(5), 100557.

Rutkowska A, et al. (2024) Synergistic Effects of PARP Inhibition and Cholesterol Biosynthesis Pathway Modulation. *Cancer research communications*, 4(9), 2427.

Hu Y, et al. (2024) Protocol for preparing metabolically reprogrammed human CAR T cells and evaluating their in vitro effects. *STAR protocols*, 5(4), 103333.

Tian S, et al. (2024) Design, performance, processing, and validation of a pooled CRISPR perturbation screen for bacterial toxins. *Nature protocols*.

Liu K, et al. (2024) Thymosin β 1 reverses oncolytic adenovirus-induced M2 polarization of macrophages to improve antitumor immunity and therapeutic efficacy. *Cell reports. Medicine*, 5(10), 101751.

Damiecki M, et al. (2024) Mitochondrial apolipoprotein MIC26 is a metabolic rheostat regulating central cellular fuel pathways. *Life science alliance*, 7(12).

Hamamoto K, et al. (2024) Unveiling the physiological impact of ESCRT-dependent autophagosome closure by targeting the VPS37A ubiquitin E2 variant-like domain. *Cell reports*, 43(12), 115016.

Nieto-Romero V, et al. (2024) Restored glyoxylate metabolism after AGXT gene correction and direct reprogramming of primary hyperoxaluria type 1 fibroblasts. *iScience*, 27(4), 109530.

Yi SA, et al. (2024) mTORC1-CTLH E3 ligase regulates the degradation of HMG-CoA synthase 1 through the Pro/N-degron pathway. *Molecular cell*, 84(11), 2166.

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.