

Resource Summary Report

Generated by [dkNET](#) on Aug 22, 2026

HET-1A

RRID:CVCL_3702

Type: Cell Line

Proper Citation

CLS Cat# 305270, RRID:CVCL_3702

Cell Line Information

URL: https://web.expasy.org/cellosaurus/CVCL_3702

Proper Citation: CLS Cat# 305270, RRID:CVCL_3702

Description: Cell line HET-1A is a Transformed cell line with a species of origin Homo sapiens (Human)

Sex: Male

Defining Citation: [PMID:1703038](#), [PMID:7972006](#), [PMID:8504475](#), [PMID:10078940](#), [PMID:20139130](#), [PMID:20843300](#), [PMID:21127259](#), [PMID:28224081](#)

Comments: Caution: Indicated as originating from a 25 year old male in ATCC, but said to be derived from autopsy specimen from a 74 year old male., Population: African American., Group: Patented cell line.

Category: Transformed cell line

Organism: Homo sapiens (Human)

Name: HET-1A

Synonyms: Het-1A, HET1A, Het1A

Cross References: BTO:BTO_0004433, CLO:CLO_0003718, EFO:EFO_0022693, ATCC:CRL-2692, BioSample:SAMN03471766, ChEMBL-Cells:ChEMBL4295465, ChEMBL-Targets:ChEMBL4296426, CLS:305270, GEO:GSM1375723, GEO:GSM1375724, GEO:GSM1375725, GEO:GSM1375726, GEO:GSM1375735, GEO:GSM1375736, GEO:GSM1375737, GEO:GSM1375738, GEO:GSM1375747, GEO:GSM1375748, GEO:GSM1375749, GEO:GSM1375750, GEO:GSM1508954, GEO:GSM1508958, IARC_TP53:21630, IARC_TP53:23555, PubChem_Cell_line:CVCL_3702, Wikidata:Q54882925

ID: CVCL_3702

Vendor: CLS

Catalog Number: 305270

Record Creation Time: 20250423T100424+0000

Record Last Update: 20260816T002356+0000

Ratings and Alerts

No rating or validation information has been found for HET-1A.

Warning: Discontinued: ATCC; CRL-10209

Caution: Indicated as originating from a 25 year old male in ATCC, but said to be derived from autopsy specimen from a 74 year old male., Population: African American., Group: Patented cell line.

Data and Source Information

Source: [CelloSaurus](#)

Usage and Citation Metrics

We found 329 mentions in open access literature.

Listed below are recent publications. The full list is available at [dkNET](#) .

Liao H, et al. (2026) Ectopic CD11c Drives SMAD3-Mediated Aberrant Antigen Presentation and Epithelial-Mesenchymal Transition in Esophageal Squamous Cell Carcinoma. Cancer communications (London, England), 46, 0014.

Li X, et al. (2026) Spatio-Temporal Proteomic Landscape Reveals Early Warning Signals of Esophageal Squamous Cell Carcinoma Progression. Advanced science (Weinheim, Baden-Wurttemberg, Germany), e14343.

Zheng X, et al. (2026) Integrative bioinformatics and experiments identify RIBC2 as a key regulator in the esophageal cancer. PloS one, 21(2), e0340850.

Zhu L, et al. (2026) A Circulating GPNMB-Based Multimodal Model Integrates Tumor-Immune Crosstalk to Predict Immunotherapy Response in Esophageal Cancer. Cancer discovery, 16(7), 1360.

Yan H, et al. (2026) Integrative Transcriptomic and Single-Cell Analyses Identify ATP1A1 as a Prognostic and Immune-Associated Factor in Esophageal Cancer. International journal of genomics, 2026, 1461834.

Ma J, et al. (2026) Alcohol-Induced Metabolic Stress Sensed by m6A-Modified ChREBP Drives Immune Evasion in Esophageal Carcinogenesis. Cancer research.

Meng L, et al. (2026) The TNRC6B/circTNRC6B axis drives lymphovascular invasion and metastasis through an intragenic self-degradation loop. *Cell reports*, 45(7), 117606.

Yan R, et al. (2025) Delivery of cancer cell-derived extracellular vesicles modulates the morphology and gene expression of Barrett esophagus and duodenal organoids (Article). *Biochemical and biophysical research communications*, 769, 151976.

Gruden E, et al. (2025) The Endocannabinoid System Drives Eosinophil Infiltration During Eosinophilic Esophagitis. *Cellular and molecular gastroenterology and hepatology*, 19(8), 101515.

Chang J, et al. (2025) Single-cell multi-stage spatial evolutionary map of esophageal carcinogenesis. *Cancer cell*, 43(3), 380.

Deng Z, et al. (2025) Targeting TFAP2 γ condensation suppresses the development of esophageal squamous cell carcinoma. *Cell*.

García-Castillo J, et al. (2025) MicroRNA 196a contributes to the aggressiveness of esophageal adenocarcinoma through the MYC/TERT/NF κ B axis. *Molecular oncology*, 19(11), 3305.

Cao K, et al. (2024) Analysis of multiple programmed cell death-related prognostic genes and functional validations of necroptosis-associated genes in oesophageal squamous cell carcinoma. *EBioMedicine*, 99, 104920.

Wei L, et al. (2024) SP4 Facilitates Esophageal Squamous Cell Carcinoma Progression by Activating PHF14 Transcription and Wnt/ β -Catenin Signaling. *Molecular cancer research : MCR*, 22(1), 55.

Zhang R, et al. (2024) Plasma CircCYP24A1 as a Novel Biomarker of Esophageal Squamous Cell Carcinoma. *Technology in cancer research & treatment*, 23, 15330338241295313.

Qiu H, et al. (2024) Elaiophyllin targets EIF4B to suppress the growth of esophageal squamous cell carcinoma via the PI3K/AKT signaling pathway. *Cancer letters*, 611, 217401.

Zhou Q, et al. (2023) Circ-ATIC regulates esophageal squamous cell carcinoma growth and metastasis through miR-1294/PBX3 pathway. *Heliyon*, 9(1), e12916.

Hu Y, et al. (2023) lncRNA SSTR5-AS1 Predicts Poor Prognosis and Contributes to the Progression of Esophageal Cancer. *Disease markers*, 2023, 5025868.

Lu W, et al. (2023) Improving the Transduction Efficiency and Antitumor Effect of Conditionally Replicative Adenovirus by Application of 6-cyclohexyl Methyl- α -D-maltoside. *Molecules (Basel, Switzerland)*, 28(2).

Duan X, et al. (2023) Bioinformatics analysis of necroptosis-related lncRNAs and immune infiltration, and prediction of the prognosis of patients with esophageal carcinoma. *Experimental and therapeutic medicine*, 26(1), 331.