

Resource Summary Report

Generated by [dkNET](#) on Sep 4, 2026

HET-1A

RRID:CVCL_3702

Type: Cell Line

Proper Citation

ATCC Cat# CRL-2692, RRID:CVCL_3702

Cell Line Information

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

Proper Citation: ATCC Cat# CRL-2692, 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: ATCC

Catalog Number: CRL-2692

Record Creation Time: 20220427T220336+0000

Record Last Update: 20260904T013945+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.

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.

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

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.

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.