# Resource Summary Report

Generated by RRID on Sep 8, 2026

## GM24385

RRID:CVCL_1C78
Type: Cell Line

### Proper Citation

Coriell Cat# GM24385, RRID:CVCL_1C78

### Cell Line Information

**URL:** https://web.expasy.org/cellosaurus/CVCL_1C78

**Proper Citation:** Coriell Cat# GM24385, RRID:CVCL_1C78

**Description:** Cell line GM24385 is a Transformed cell line with a species of origin Homo sapiens (Human)

**Sex:** Male

**Defining Citation:** PMID:27271295, PMID:35819189, PMID:37751688

**Comments:** Population: Caucasian., Part of: Personal Genome Project (PGP) cell line collection., Part of: Genome in a Bottle (GIAB) consortium samples.

**Category:** Transformed cell line

**Organism:** Homo sapiens (Human)

**Name:** GM24385

**Synonyms:** GM24385*B, HG002

**Cross References:** BioSample:SAMN03283347, Coriell:GM24385, Wikidata:Q54853746

**ID:** CVCL_1C78

**Vendor:** Coriell

**Catalog Number:** GM24385

**Record Creation Time:** 20220427T220204+0000

**Record Last Update:** 20260905T175950+0000

### Ratings and Alerts

No rating or validation information has been found for GM24385.

No alerts have been found for GM24385.

## Data and Source Information

**Source:** Cellosaurus

## Usage and Citation Metrics

We found 13 mentions in open access literature.

**Listed below are recent publications.** The full list is available at RRID .


Wu B, et al. (2026) Z-Calling: a tool for A/Z (2,6-diaminopurine) base calling and dZ-DNA detection using PacBio HiFi reads. Communications biology, 9(1).

Daniels CA, et al. (2025) Characterization of subclonal variants in HG002 Genome in a Bottle reference material as a resource for benchmarking variant callers. Cell genomics, 101104.

Elliott MJ, et al. (2025) Ultrasensitive Detection and Monitoring of Circulating Tumor DNA Using Structural Variants in Early-Stage Breast Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(8), 1520.

Wagner J, et al. (2025) Small variant benchmark from a complete assembly of X and Y chromosomes. Nature communications, 16(1), 497.

Maslan A, et al. (2024) Mapping protein-DNA interactions with DiMeLo-seq. Nature protocols, 19(12), 3697.

Chen K, et al. (2023) Individualized tumor-informed circulating tumor DNA analysis for postoperative monitoring of non-small cell lung cancer. Cancer cell, 41(10), 1749.

Jarvis ED, et al. (2022) Semi-automated assembly of high-quality diploid human reference genomes. Nature, 611(7936), 519.

Walker K, et al. (2022) The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. F1000Research, 11, 530.

Deshpande AS, et al. (2022) Identifying synergistic high-order 3D chromatin conformations from genome-scale nanopore concatemer sequencing. Nature biotechnology, 40(10), 1488.

Wagner J, et al. (2022) Benchmarking challenging small variants with linked and long reads. Cell genomics, 2(5).

Olson ND, et al. (2022) PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. Cell genomics, 2(5).

Wagner J, et al. (2022) Curated variation benchmarks for challenging medically relevant autosomal genes. Nature biotechnology, 40(5), 672.

Zhang L, et al. (2019) Assessment of human diploid genome assembly with 10x Linked-Reads data. GigaScience, 8(11).