

Resource Summary Report

Generated by [NIF](#) on Sep 10, 2026

GM12878

RRID:CVCL_7526

Type: Cell Line

Proper Citation

RRID:CVCL_7526

Cell Line Information

URL: https://web.expasy.org/cellosaurus/CVCL_7526

Proper Citation: RRID:CVCL_7526

Description: Cell line GM12878 is a Transformed cell line with a species of origin Homo sapiens (Human)

Sex: Female

Defining Citation: [PMID:17122850](#), [PMID:19043577](#), [PMID:20856902](#), [PMID:21418647](#), [PMID:23325432](#), [PMID:23676674](#), [PMID:24185094](#), [PMID:24380390](#), [PMID:26621101](#), [PMID:26719794](#), [PMID:27271295](#), [PMID:27792722](#), [PMID:29116076](#), [PMID:29431738](#), [PMID:30485824](#), [PMID:31273215](#), [PMID:31401124](#), [PMID:36094314](#)

Comments: Population: Caucasian; Utah residents with ancestry from Northern and Western Europe., Part of: International Genome Sample Resource (1000 genomes project) cell lines., Part of: Genome in a Bottle (GIAB) consortium samples., Part of: Genetic Testing Reference Material (GeT-RM) samples., Part of: ENCODE project common cell types; tier 1., Part of: CEPH/Utah pedigree cell line collection.

Category: Transformed cell line

Organism: Homo sapiens (Human)

Name: GM12878

Synonyms: GM-12878, HG001

Cross References: BTO:BTO_0006353, CLO:CLO_0022851, EFO:EFO_0002784, 4DN:4DNSRH17RFKR, 4DN:4DNSRVWZS4XO, ArrayExpress:E-MTAB-1511, ArrayExpress:E-MTAB-5835, BioGRID_ORCS_Cell_line:203, BioSample:SAMN00000339, BioSample:SAMN00801888, BioSample:SAMN03492678, CLS:305439, Coriell:GM12878, ENCODE:ENCBS004QBB, ENCODE:ENCBS011ZCV,

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ID: CVCL_7526

Record Creation Time: 20220427T220039+0000

Record Last Update: 20260905T175708+0000

Ratings and Alerts

No rating or validation information has been found for GM12878.

No alerts have been found for GM12878.

Data and Source Information

Source: [CelloSaurus](#)

Usage and Citation Metrics

We found 1427 mentions in open access literature.

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

Kempynck N, et al. (2026) CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species. *Nature methods*, 23(5), 946.

Bruckner I, et al. (2026) Extrachromosomal microDNA Signature as a Candidate Biomarker in Pediatric Acute Lymphoblastic Leukemia. *Cancer research communications*, 6(1), 143.

Xu W, et al. (2026) Single-nucleus chromatin accessibility and gene expression co-profiling by ISSAAC-seq. *Nature protocols*.

Liao Y, et al. (2026) PRELID1 and VDAC3 Coordinate a Senescence-Like State in Germinal Center B Cells to Promote IL-7-Driven Antitumor Immunity in Colorectal Cancer. *Advanced science (Weinheim, Baden-Wuerttemberg, Germany)*, 13(23), e21951.

Sigalova OM, et al. (2026) Modeling cis-regulatory variation in human brain enhancers across a large Parkinson's Disease cohort. *bioRxiv : the preprint server for biology*.

Lee M, et al. (2026) LINE-1 Locus Transcription Nucleates Oncogenic Chromatin Architecture. *Cancer discovery*, 16(4), 800.

Stewart JA, et al. (2026) High-fidelity rare structural variant detection with HiFiRE3 reduced representation via restriction enzyme ends. *bioRxiv : the preprint server for*

biology.

Vaidya P, et al. (2025) Molecular Characterization of Polyomavirus-Positive and Negative Merkel Cell Carcinoma. *Cancers*, 17(21).

Komiya T, et al. (2025) Novel MAML2 Fusions in Human Malignancy. *Cancers*, 17(19).

Chen Y, et al. (2025) Reconstruction of diploid higher-order human 3D genome interactions from noisy Pore-C data using Dip3D. *Nature structural & molecular biology*, 32(7), 1305.

Goldberg DC, et al. (2025) Scalable screening of ternary-code DNA methylation dynamics associated with human traits. *Cell genomics*, 5(9), 100929.

Wilson TE, et al. (2024) Replication stress induces POLQ-mediated structural variant formation throughout common fragile sites after entry into mitosis. *Nature communications*, 15(1), 9582.

Hansen TJ, et al. (2024) Human gene regulatory evolution is driven by the divergence of regulatory element function in both cis and trans. *Cell genomics*, 4(4), 100536.

Kolekar P, et al. (2024) SJPedPanel: A Pan-Cancer Gene Panel for Childhood Malignancies to Enhance Cancer Monitoring and Early Detection. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(18), 4100.

Bravo JI, et al. (2024) An eQTL-based approach reveals candidate regulators of LINE-1 RNA levels in lymphoblastoid cells. *PLoS genetics*, 20(6), e1011311.

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

Kalef-Ezra E, et al. (2023) Single-cell somatic copy number variants in brain using different amplification methods and reference genomes. *bioRxiv : the preprint server for biology*.

Harris HL, et al. (2023) Chromatin alternates between A and B compartments at kilobase scale for subgenic organization. *Nature communications*, 14(1), 3303.

Wang B, et al. (2023) DFHiC: a dilated full convolution model to enhance the resolution of Hi-C data. *Bioinformatics (Oxford, England)*, 39(5).

Kim S, et al. (2023) Chromatin structure and context-dependent sequence features control prime editing efficiency. *bioRxiv : the preprint server for biology*.