

Resource Summary Report

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

LightGBM

RRID:SCR_021697

Type: Tool

Proper Citation

LightGBM (RRID:SCR_021697)

Resource Information

URL: <https://lightgbm.readthedocs.io/en/latest/>

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Description: Software tool as gradient boosting framework that uses tree based learning algorithms. Designed to be distributed and efficient with advantages:Faster training speed and higher efficiency;Lower memory usage;Better accuracy;Support of parallel, distributed, and GPU learning;Capable of handling large scale data.

Resource Type: software resource

Keywords: Gradient boosting framework

Availability: Free, Available for download, Freely available

Resource Name: LightGBM

Resource ID: SCR_021697

Alternate URLs: <https://github.com/Microsoft/LightGBM/blob/master/docs/index.rst>

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260815T182654+0000

Ratings and Alerts

No rating or validation information has been found for LightGBM.

No alerts have been found for LightGBM.

Data and Source Information

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Moradmand H, et al. (2025) Graph feature selection for enhancing radiomic stability and reproducibility across multiple institutions in head and neck cancer. Scientific reports, 15(1), 27995.

Harrigan CF, et al. (2025) Damage and Misrepair Signatures: Compact Representations of Pan-cancer Mutational Processes. bioRxiv : the preprint server for biology.

Kagan D, et al. (2025) Network-based anomaly detection algorithm reveals proteins with major roles in human tissues. GigaScience, 14.

Ma Q, et al. (2024) Machine Learning Reveals Impacts of Smoking on Gene Profiles of Different Cell Types in Lung. Life (Basel, Switzerland), 14(4).

Kawai M, et al. (2024) Early detection of pancreatic cancer by comprehensive serum miRNA sequencing with automated machine learning. British journal of cancer, 131(7), 1158.

Özgür S, et al. (2024) A machine learning approach to predict foot care self-management in older adults with diabetes. Diabetology & metabolic syndrome, 16(1), 244.

Xu Y, et al. (2023) Characterization of chromatin accessibility patterns in different mouse cell types using machine learning methods at single-cell resolution. Frontiers in genetics, 14, 1145647.

Boudanga Z, et al. (2023) An innovative medical waste management system in a smart city using XAI and vehicle routing optimization. F1000Research, 12, 1060.

Ma QL, et al. (2023) Machine Learning Classification of Time since BNT162b2 COVID-19 Vaccination Based on Array-Measured Antibody Activity. Life (Basel, Switzerland), 13(6).

Sharma A, et al. (2023) VirulentPred 2.0: An improved method for prediction of virulent proteins in bacterial pathogens. Protein science : a publication of the Protein Society, 32(12), e4808.

Zheng HL, et al. (2023) A data-driven interpretable ensemble framework based on tree models for forecasting the occurrence of COVID-19 in the USA. Environmental science and pollution research international, 30(5), 13648.

Ren J, et al. (2023) Identification of Genes Associated with the Impairment of Olfactory and Gustatory Functions in COVID-19 via Machine-Learning Methods. Life (Basel, Switzerland), 13(3).

Li J, et al. (2023) Identification of genes related to immune enhancement caused by heterologous ChAdOx1-BNT162b2 vaccines in lymphocytes at single-cell resolution with machine learning methods. *Frontiers in immunology*, 14, 1131051.

Ren JX, et al. (2023) Identification of Gene Markers Associated with COVID-19 Severity and Recovery in Different Immune Cell Subtypes. *Biology*, 12(7).

Li S, et al. (2022) Improving preeclampsia risk prediction by modeling pregnancy trajectories from routinely collected electronic medical record data. *NPJ digital medicine*, 5(1), 68.

Kalyakulina A, et al. (2022) Disease classification for whole-blood DNA methylation: Meta-analysis, missing values imputation, and XAI. *GigaScience*, 11.

Yang L, et al. (2022) Identification of protein-protein interaction associated functions based on gene ontology and KEGG pathway. *Frontiers in genetics*, 13, 1011659.

Zhang YH, et al. (2022) Subcellular Localization Prediction of Human Proteins Using Multifeature Selection Methods. *BioMed research international*, 2022, 3288527.

Susi D, et al. (2022) Identification of decompensation episodes in chronic heart failure patients based solely on heart sounds. *Frontiers in cardiovascular medicine*, 9, 1009821.

Ding S, et al. (2022) Predicting Heart Cell Types by Using Transcriptome Profiles and a Machine Learning Method. *Life (Basel, Switzerland)*, 12(2).