

Resource Summary Report

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BioBERT

RRID:SCR_017547

Type: Tool

Proper Citation

BioBERT (RRID:SCR_017547)

Resource Information

URL: <https://github.com/dmis-lab/biobert>

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Description: Pre-trained biomedical language representation model for biomedical text mining. This repository provides fine-tuning codes of BioBERT, language representation model for biomedical domain, especially designed for biomedical text mining tasks such as biomedical named entity recognition, relation extraction, question answering, etc.

Synonyms: Bidirectional Encoder Representations from Transformers for Biomedical Text Mining

Resource Type: software application, software resource

Defining Citation: [DOI:10.1093/bioinformatics/btz682](https://doi.org/10.1093/bioinformatics/btz682)

Keywords: Pretrained, biomedical, language, representation, model, text, mining, bio.tools

Funding: National Research Foundation of Korea

Availability: Free, Available for download, Freely available

Resource Name: BioBERT

Resource ID: SCR_017547

Alternate IDs: biotools:biobERT

Alternate URLs: <https://github.com/naver/biobert-pretrained>, <https://bio.tools/BioBERT>

License: Apache License

Record Creation Time: 20220129T080335+0000

Ratings and Alerts

No rating or validation information has been found for BioBERT.

No alerts have been found for BioBERT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 45 mentions in open access literature.

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

Althabiti S, et al. (2025) Predicting Behavioral Determinants of Health from Clinical Text Using Transformer Models and BiLSTM. medRxiv : the preprint server for health sciences.

Xu Y, et al. (2025) A multimodal knowledge-enhanced whole-slide pathology foundation model. Nature communications, 16(1), 11406.

Happi Happi BG, et al. (2025) GRU-SCANET: unleashing the power of GRU-based sinusoidal capture network for precision-driven named entity recognition. Bioinformatics advances, 5(1), vbaf096.

Rodin D, et al. (2025) Medical Cannabis Library: development of a curated database for research articles on cannabis therapeutic activity. Journal of cannabis research, 7(1), 39.

Raciti D, et al. (2025) Characterization and automated classification of sentences in the biomedical literature: a case study for biocuration of gene expression and protein kinase activity. Database : the journal of biological databases and curation, 2025.

Saadh MJ, et al. (2025) Advanced machine learning framework for enhancing breast cancer diagnostics through transcriptomic profiling. Discover oncology, 16(1), 334.

Hier DB, et al. (2025) A simplified retriever to improve accuracy of phenotype normalizations by large language models. Frontiers in digital health, 7, 1495040.

Jimenez-Maggiora GA, et al. (2025) Artificial intelligence-enabled safety monitoring in Alzheimer's disease clinical trials. The journal of prevention of Alzheimer's disease, 12(1), 100002.

Zhang S, et al. (2025) SCATrans: semantic cross-attention transformer for drug-drug interaction predication through multimodal biomedical data. BMC bioinformatics, 26(1), 157.

Schoenmaker L, et al. (2025) Toward Assay-Aware Bioactivity Model(er)s: Getting a Grip on Biological Context. *Journal of chemical information and modeling*, 65(13), 7013.

Theodoropoulos C, et al. (2025) Reduction of supervision for biomedical knowledge discovery. *BMC bioinformatics*, 26(1), 225.

Ghelfi A, et al. (2025) Hayai-Annotation: A functional gene prediction tool that integrates orthologs and gene ontology for network analysis in plant species. *Computational and structural biotechnology journal*, 27, 117.

Li N, et al. (2024) Drug-target interaction prediction using knowledge graph embedding. *iScience*, 27(6), 109393.

Gonzalez Hernandez F, et al. (2024) Named entity recognition of pharmacokinetic parameters in the scientific literature. *Scientific reports*, 14(1), 23485.

Kim K, et al. (2024) Multifaceted Natural Language Processing Task-Based Evaluation of Bidirectional Encoder Representations From Transformers Models for Bilingual (Korean and English) Clinical Notes: Algorithm Development and Validation. *JMIR medical informatics*, 12, e52897.

Huang DL, et al. (2024) A Combined Manual Annotation and Deep-Learning Natural Language Processing Study on Accurate Entity Extraction in Hereditary Disease Related Biomedical Literature. *Interdisciplinary sciences, computational life sciences*, 16(2), 333.

Sharma T, et al. (2024) Exploring COVID-related relationship extraction: Contrasting data sources and analyzing misinformation. *Heliyon*, 10(5), e26973.

Alamro H, et al. (2024) BioBBC: a multi-feature model that enhances the detection of biomedical entities. *Scientific reports*, 14(1), 7697.

Rehana H, et al. (2024) Evaluating GPT and BERT models for protein-protein interaction identification in biomedical text. *Bioinformatics advances*, 4(1), vbae133.

Rehana H, et al. (2023) Evaluation of GPT and BERT-based models on identifying proteinprotein interactions in biomedical text. *ArXiv*.