

Resource Summary Report

Generated by [dkNET](#) on Aug 14, 2026

MetaMap

RRID:SCR_015031

Type: Tool

Proper Citation

MetaMap (RRID:SCR_015031)

Resource Information

URL: <https://metamap.nlm.nih.gov/>

Proper Citation: MetaMap (RRID:SCR_015031)

Description: Program to map biomedical text to the UMLS Metathesaurus and to discover Metathesaurus concepts referred to in text based on symbolic, natural-language processing and computational-linguistic techniques.

Synonyms: MetaMap 2016, MetaMap 2016v2

Resource Type: software resource, text-mining software, software application

Keywords: text mining, biomedical text

Funding: NLM

Availability: Free, Account required

Resource Name: MetaMap

Resource ID: SCR_015031

License: UMLS Metathesaurus License

License URLs: <https://metamap.nlm.nih.gov/MMTnCs.shtml>

Record Creation Time: 20220129T080323+0000

Record Last Update: 20260814T042907+0000

Ratings and Alerts

No rating or validation information has been found for MetaMap.

No alerts have been found for MetaMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 343 mentions in open access literature.

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

Kayira AB, et al. (2026) Natural Language Processing of Clinical Notes for Cancer Research and Patient Care Prior to Widespread Adoption of Generative AI: Scoping Review. JMIR AI, 5, e73481.

Zhang G, et al. (2026) A neural-symbolic AI agent system for biomedical concept mapping. NPJ digital medicine, 9(1).

Chen YW, et al. (2026) Enhanced Prediction of Atrial Fibrillation in Patients With Ischemic Stroke Through Electronic Medical Records and Text Mining: Algorithm Development and Validation. JMIR medical informatics, 14, e78117.

Liu X, et al. (2026) Safetyome and specialized panels for over 3,000 phenotypes: a systematic and translational approach using human genetics and pharmacology. Toxicological sciences : an official journal of the Society of Toxicology, 209(3).

Jung S, et al. (2025) Clinical Terminology Mapping Service Based on Information Retrieval. Methods of information in medicine, 64(1-02), 31.

Forrest N, et al. (2025) A Dynamic Time Warping Extension to Consensus Weight-Based Cachexia Criteria Improves Prediction of Cancer Patient Outcomes. JCSM communications, 8(1), e107.

Nejat P, et al. (2025) Optimizing Digital Management of Research and Collaboration With Academic Information Manager. Mayo Clinic proceedings. Digital health, 3(2), 100222.

Hu YH, et al. (2025) An Intelligent Trial Eligibility Screening Tool Using Natural Language Processing With a Block-Based Visual Programming Interface: Development and Usability Study. JMIR medical informatics, 13, e80072.

Wang L, et al. (2025) DrugCombo: an informatics bridge for anticancer drug combination Phase I trial design. Database : the journal of biological databases and curation, 2025.

Huang H, et al. (2025) An open-source multi-semantic annotation dataset and automated recognition tool for viral carcinogenesis factors. Database : the journal of biological databases and curation, 2025.

Forrest N, et al. (2025) Natural language processing algorithms identify wild-type isocitrate dehydrogenase gliomas in electronic health records. Neuro-oncology advances, 7(1), vdaf111.

Xin Y, et al. (2025) Improving topic modeling performance on social media through semantic relationships within biomedical terminology. PloS one, 20(2), e0318702.

Haaker TS, et al. (2025) Approaches for extracting daily dosage from free-text prescription signatures in heart failure with reduced ejection fraction: a comparative study. JAMIA open, 8(1), ooae153.

Tayebi Arasteh S, et al. (2024) Enhancing diagnostic deep learning via self-supervised pretraining on large-scale, unlabeled non-medical images. European radiology experimental, 8(1), 10.

Kamp H, et al. (2024) Utility of in vivo metabolomics to support read-across for UVCB substances under REACH. Archives of toxicology, 98(3), 755.

Roberts K, et al. (2024) Natural language processing of clinical notes enables early inborn error of immunity risk ascertainment. The journal of allergy and clinical immunology. Global, 3(2), 100224.

Nédellec C, et al. (2024) TaeC: A manually annotated text dataset for trait and phenotype extraction and entity linking in wheat breeding literature. PloS one, 19(6), e0305475.

Gutiérrez-Sacristán A, et al. (2024) Development and validation of an open-source pipeline for automatic population of case report forms from electronic health records: a pediatric multi-center prospective study. EBioMedicine, 108, 105337.

Zhou H, et al. (2024) Complementary and Integrative Health Information in the literature: its lexicon and named entity recognition. Journal of the American Medical Informatics Association : JAMIA, 31(2), 426.

Song L, et al. (2024) Centrifuger: lossless compression of microbial genomes for efficient and accurate metagenomic sequence classification. Genome biology, 25(1), 106.