Resource Summary Report

Generated by Kravitz on Sep 10, 2026

SIDER

RRID:SCR_004321
Type: Tool

Proper Citation

SIDER (RRID:SCR_004321)

Resource Information

URL: http://sideeffects.embl.de/

Proper Citation: SIDER (RRID:SCR_004321)

Description: Database containing information on marketed medicines and their recorded adverse drug reactions. The information is extracted from public documents and package inserts. The available information include side effect frequency, drug and side effect classifications as well as links to further information, for example drug-target relations. The SIDER Side Effect Resource represents an effort to aggregate dispersed public information on side effects. To our knowledge, no such resource exist in machine-readable form despite the importance of research on drugs and their effects. The creation of this resource was motivated by the many requests for data that we received related to our paper (Campillos, Kuhn et al., Science, 2008, 321(5886):263-6.) on the utilization of side effects for drug target prediction. Inclusion of side effects as readouts for drug treatment should have many applications and we hope to be able to enhance the respective research with this resource. You may browse the drugs by name, browse the side effects by name, download the current version of SIDER, or use the search interface.

Abbreviations: SIDER

Synonyms: Side Effect Resource, SIDER: Side Effect Resource

Resource Type: data or information resource, database

Defining Citation: PMID:20087340

Keywords: medicine, drug, side effect, adverse drug reaction, drug-target, phenotype, bio.tools, FASEB list

Resource Name: SIDER

Resource ID: SCR_004321

Alternate IDs: r3d100012791, nlx_33359, OMICS_01588, biotools:sider

Alternate URLs: https://bio.tools/sider, https://doi.org/10.17616/R3J226

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260905T133123+0000

Ratings and Alerts

No rating or validation information has been found for SIDER.

No alerts have been found for SIDER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 410 mentions in open access literature.

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

Cai C, et al. (2026) A unified multi-scale deep learning framework for molecular property prediction that bridges molecular structures and fingerprinting. Communications chemistry, 9(1).

Hong H, et al. (2026) A hierarchical interaction message net for accurate molecular property prediction. Communications chemistry, 9(1).

Patidar P, et al. (2026) An integrative analysis of genetic factors reveals dysregulation of cytokines, immune signaling, and T cell activity as the underlying immune mechanisms in autoimmune immune thrombocytopenia. Thrombosis journal, 24(1), 25.

Nygren S, et al. (2026) RAG-based architectures for drug side effect retrieval using compact LLMs. Scientific reports, 16(1).

Zhang Y, et al. (2026) MolGramTreeNet: A multimodal molecular property prediction model via grammar tree-constrained molecular representation. iScience, 29(3), 114928.

Xie C, et al. (2026) MMPCS: multi-view molecular pretraining based on consistency information and specific information. Bioinformatics (Oxford, England), 42(2).

Zhang W, et al. (2026) Task-specific pre-training for molecular property prediction. Briefings in bioinformatics, 27(1).

Wu S, et al. (2026) Enhanced drug disease association prediction through multimodal data integration and meta path guided global local feature fusion. Scientific reports, 16(1).

Pala MA, et al. (2026) Graph-Aware AURALSTM: An Attentive Unified Representation Architecture with BiLSTM for Enhanced Molecular Property Prediction. Molecular diversity, 30(2), 1709.

Zheng W, et al. (2026) Signal detection of drug-induced esophageal ulcer across 20 years of real-world study: Focus on 49 high-risk medicines. The Journal of international medical research, 54(3), 3000605261426764.

Fan H, et al. (2026) A Bond-Level Sequence Framework for Molecular Representation Learning with Structural Constraints. Molecules (Basel, Switzerland), 31(11).

Zhao J, et al. (2026) MolProphecy: Bridging medicinal chemists' knowledge and molecular pre-trained models via a multi-modal framework. Journal of advanced research, 85, 577.

Rjoob K, et al. (2026) A multimodal vision knowledge graph of cardiovascular disease. Nature cardiovascular research, 5(1), 18.

Khodadadi AghGhaleh M, et al. (2026) ConvAHKG: Action-based hybrid knowledge graph with a dual-channel convolutional approach for drug repurposing. Scientific reports, 16(1).

Mun V, et al. (2026) CheMLT-F: multitask learning in biochemistry through transformer fusion. Journal of cheminformatics, 18(1).

Huang T, et al. (2026) Explainable drug side effect prediction in central neural system via biologically informed graph neural network. Translational psychiatry, 16(1).

Yang L, et al. (2026) Multimodal Collaborative Modeling of Molecular Structures and Biomedical Text for Accurate Drug-Drug Interaction Extraction. Biomedicines, 14(6).

Jeon W, et al. (2025) Predicting Drug-Side Effect Relationships From Parametric Knowledge Embedded in Biomedical BERT Models: Methodological Study With a Natural Language Processing Approach. JMIR medical informatics, 13, e67513.

He M, et al. (2025) Prediction of adverse drug reactions based on pharmacogenomics combination features: a preliminary study. Frontiers in pharmacology, 16, 1448106.

Abbasi SH, et al. (2025) Acute cardiovascular effects associated with the use of prescription medications: A Danish nationwide screening study. British journal of clinical pharmacology, 91(7), 1947.