Resource Summary Report

Generated by RRID on Apr 8, 2025

DrugCentral

RRID:SCR_015663
Type: Tool

Proper Citation

DrugCentral (RRID:SCR_015663)

Resource Information

URL: http://drugcentral.org/

Proper Citation: DrugCentral (RRID:SCR_015663)

Description: Database of drug information created and maintained by the Division of Translational Informatics at University of New Mexico. It provides information on active ingredients chemical entities, pharmaceutical products, drug mode of action, indications, and pharmacologic action.

Synonyms: Drug Central, DrugCentral: Online Drug Compendium

Resource Type: data or information resource, web application, database, software resource

Defining Citation: PMID:27789690

Keywords: drug, chemical, pharmaceutical, active ingredient, translational informatics, FASEB list

Funding: NIH 1U54CA189205-01

Availability: Freely Available, Free, Available for download

Resource Name: DrugCentral

Resource ID: SCR_015663

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Record Creation Time: 20220129T080326+0000

Record Last Update: 20250407T220234+0000

Ratings and Alerts

No rating or validation information has been found for DrugCentral.

No alerts have been found for DrugCentral.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 104 mentions in open access literature.

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

Li VOK, et al. (2025) DeepDrug as an expert guided and AI driven drug repurposing methodology for selecting the lead combination of drugs for Alzheimer's disease. Scientific reports, 15(1), 2093.

Zhang R, et al. (2025) Proteome-Wide Identification and Comparison of Drug Pockets for Discovering New Drug Indications and Side Effects. Molecules (Basel, Switzerland), 30(2).

Zhai Y, et al. (2025) Network pharmacology: a crucial approach in traditional Chinese medicine research. Chinese medicine, 20(1), 8.

Batth TS, et al. (2024) Streamlined analysis of drug targets by proteome integral solubility alteration indicates organ-specific engagement. Nature communications, 15(1), 8923.

Kim J, et al. (2024) 5-aminosalicylic acid suppresses osteoarthritis through the OSCAR-PPAR? axis. Nature communications, 15(1), 1024.

Lichtenberg FR, et al. (2024) Do newer drugs treat fewer diseases, controlling for time since launch? Evidence from France and the U.S. Journal of pharmaceutical policy and practice, 17(1), 2357604.

Li J, et al. (2024) Single-cell and bulk RNA-sequence identi?ed ?broblasts signature and CD8 + T-cell - ?broblast subtype predicting prognosis and immune therapeutic response of bladder cancer, based on machine learning: bioinformatics multi-omics study. International journal of surgery (London, England), 110(8), 4911.

Wang Z, et al. (2024) VarCards2: an integrated genetic and clinical database for ACMG-AMP variant-interpretation guidelines in the human whole genome. Nucleic acids research, 52(D1), D1478.

Wei J, et al. (2024) Predicting drug-protein interactions by preserving the graph information of multi source data. BMC bioinformatics, 25(1), 10.

García Sánchez N, et al. (2024) Protein sequence analysis in the context of drug repurposing. BMC medical informatics and decision making, 24(1), 122.

Wang Y, et al. (2024) Effects of dipeptidyl peptidase 4 inhibitors on the risk of acute respiratory failure in patients with type 2 diabetes mellitus: a meta-analysis of cardiovascular outcomes trials. Endocrine journal, 71(12), 1175.

Guan Y, et al. (2024) Comprehensive analysis revealed the immunoinflammatory targets of rheumatoid arthritis based on intestinal flora, miRNA, transcription factors, and RNA-binding proteins databases, GSEA and GSVA pathway observations, and immunoinfiltration typing. Hereditas, 161(1), 6.

Otero-Carrasco B, et al. (2024) Identifying patterns to uncover the importance of biological pathways on known drug repurposing scenarios. BMC genomics, 25(1), 43.

Tu R, et al. (2024) Drug Repurposing using consilience of Knowledge Graph Completion methods. bioRxiv : the preprint server for biology.

Gualdi F, et al. (2024) Predicting gene disease associations with knowledge graph embeddings for diseases with curtailed information. NAR genomics and bioinformatics, 6(2), lqae049.

Lalagkas PN, et al. (2024) Shared etiology of Mendelian and complex disease supports drug discovery. BMC medical genomics, 17(1), 228.

Sadegh S, et al. (2023) Lacking mechanistic disease definitions and corresponding association data hamper progress in network medicine and beyond. Nature communications, 14(1), 1662.

Jamir E, et al. (2023) Polypharmacology guided drug repositioning approach for SARS-CoV2. PloS one, 18(8), e0289890.

Elkashlan M, et al. (2023) A review of SARS-CoV-2 drug repurposing: databases and machine learning models. Frontiers in pharmacology, 14, 1182465.

Zhou WZ, et al. (2023) CHDbase: A Comprehensive Knowledgebase for Congenital Heart Disease-related Genes and Clinical Manifestations. Genomics, proteomics & bioinformatics, 21(1), 216.