Resource Summary Report

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Illuminating the Druggable Genome

RRID:SCR_016924
Type: Tool

Proper Citation

Illuminating the Druggable Genome (RRID:SCR_016924)

Resource Information

URL: https://pharos.nih.gov/

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Description: Program to improve understanding of properties and functions of proteins that are currently unannotated within three most commonly drug protein families: targeted G-protein coupled receptors, ion channels, and protein kinases. Includes Data and Resource Generating Centers (DRGC), Knowledge Management Center (KMC), and Resource Dissemination and Outreach Center (RDOC).

Abbreviations: IDG

Synonyms: Pharos, Illuminating the Druggable Genome, IDG, Illuminating Druggable Genome

Resource Type: organization portal, data repository, portal, data or information resource, storage service resource, consortium, service resource

Keywords: understudied, target, protein, G protein, coupled, receptor, ion, channel, kinase, bio.tools

Funding: NIH Common Fund

Resource Name: Illuminating the Druggable Genome

Resource ID: SCR_016924

Alternate IDs: biotools:pharos

Alternate URLs: https://pharos.nih.gov/, https://bio.tools/pharos, https://darkmatter.ucsf.edu/about

Old URLs: https://druggablegenome.net

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260804T043658+0000

Ratings and Alerts

No rating or validation information has been found for Illuminating the Druggable Genome.

No alerts have been found for Illuminating the Druggable Genome.

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 RRID .

Zhao C, et al. (2025) Identification of Tumor-Specific Surface Proteins Enables Quantification of Extracellular Vesicle Subtypes for Early Detection of Pancreatic Ductal Adenocarcinoma. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(21), e2414982.

Chen Y, et al. (2025) Semi-inductive dataset construction and framework optimization for practical drug target interaction prediction with ScopeDTI. Nature communications, 16(1), 11509.

Hazelwood E, et al. (2025) Multi-tissue expression and splicing data prioritise anatomical subsite- and sex-specific colorectal cancer susceptibility genes. Nature communications, 16(1), 5043.

Percudani R, et al. (2025) Predicting Protein Function in the AI and Big Data Era. Biochemistry, 64(11), 2345.

Poluektov YM, et al. (2025) Mechanisms mediating effects of cardiotonic steroids in mammalian blood cells. Frontiers in pharmacology, 16, 1520927.

Yoo H, et al. (2025) Exploring neurokinin-1 receptor antagonism for depression with structurally differentiated inhibitors. Experimental & molecular medicine, 57(11), 2699.

Yu Q, et al. (2025) scMalignantFinder distinguishes malignant cells in single-cell and spatial transcriptomics by leveraging cancer signatures. Communications biology, 8(1), 504.

Kapoor A, et al. (2025) SCOPE: Revealing Hidden Mechanisms in Phenotypic Screens Through Target and Pathway Enrichment. bioRxiv : the preprint server for biology.

Suhre K, et al. (2024) Genetic associations with ratios between protein levels detect new pQTLs and reveal protein-protein interactions. Cell genomics, 4(3), 100506.

Malone SG, et al. (2024) Alcohol use disorder and body mass index show genetic pleiotropy and shared neural associations. medRxiv : the preprint server for health sciences.

Sinkala M, et al. (2024) Machine learning and bioinformatic analyses link the cell surface receptor transcript levels to the drug response of breast cancer cells and drug off-target effects. PloS one, 19(2), e0296511.

Munson BP, et al. (2024) De novo generation of multi-target compounds using deep generative chemistry. Nature communications, 15(1), 3636.

Cao X, et al. (2024) Analysis of 3760 hematologic malignancies reveals rare transcriptomic aberrations of driver genes. Genome medicine, 16(1), 70.

Teixeira SK, et al. (2024) Genetic determinants of blood pressure and heart rate identified through ENU-induced mutagenesis with automated meiotic mapping. Science advances, 10(9), eadj9797.

Comajuncosa-Creus A, et al. (2024) Comprehensive detection and characterization of human druggable pockets through binding site descriptors. Nature communications, 15(1), 7917.

Lundgaard AT, et al. (2023) BALDR: A Web-based platform for informed comparison and prioritization of biomarker candidates for type 2 diabetes mellitus. PLoS computational biology, 19(8), e1011403.

Ganji M, et al. (2023) Discovery of potential FGFR3 inhibitors via QSAR, pharmacophore modeling, virtual screening and molecular docking studies against bladder cancer. Journal of translational medicine, 21(1), 111.

Banerjee A, et al. (2023) The First Pituitary Proteome Landscape From Matched Anterior and Posterior Lobes for a Better Understanding of the Pituitary Gland. Molecular & cellular proteomics : MCP, 22(1), 100478.

Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution-A practical guide. PloS one, 18(2), e0279597.

Coral DE, et al. (2023) A phenome-wide comparative analysis of genetic discordance between obesity and type 2 diabetes. Nature metabolism, 5(2), 237.