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

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: 20250428T054025+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 37 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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

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

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.

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

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.

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.

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

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

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.

Aschenbrenner D, et al. (2023) Pathogenic Interleukin-10 Receptor Alpha Variants in Humans - Balancing Natural Selection and Clinical Implications. Journal of clinical immunology, 43(2), 495.

Yang ZH, et al. (2023) Identification of a psychiatric risk gene NISCH at 3p21.1 GWAS locus mediating dendritic spine morphogenesis and cognitive function. BMC medicine, 21(1), 254.

Yu L, et al. (2022) Identification of novel ?-globin inducers among all potential erythroid druggable targets. Blood advances, 6(11), 3280.

Federico A, et al. (2022) The integration of large-scale public data and network analysis uncovers molecular characteristics of psoriasis. Human genomics, 16(1), 62.

Jiang J, et al. (2022) Systematic illumination of druggable genes in cancer genomes. Cell reports, 38(8), 110400.

Spielmann N, et al. (2022) Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. Nature cardiovascular research, 1(2), 157.

Behzadi P, et al. (2022) Worldwide Protein Data Bank (wwPDB): A virtual treasure for research in biotechnology. European journal of microbiology & immunology, 11(4), 77.

Ding X, et al. (2022) Inhibition of CDK8/19 Mediator kinase potentiates HER2-targeting drugs and bypasses resistance to these agents in vitro and in vivo. Proceedings of the National Academy of Sciences of the United States of America, 119(32), e2201073119.