

Resource Summary Report

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PolySearch

RRID:SCR_005291

Type: Tool

Proper Citation

PolySearch (RRID:SCR_005291)

Resource Information

URL: <http://wishart.biology.ualberta.ca/polysearch/index.htm>

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Description: A web-based tool that supports more than 50 different classes of queries against nearly a dozen different types of text, scientific abstract or bioinformatic databases. The typical query supported by PolySearch is Given X, find all Y"s where X or Y can be diseases, tissues, cell compartments, gene/protein names, SNPs, mutations, drugs and metabolites. PolySearch also exploits a variety of techniques in text mining and information retrieval to identify, highlight and rank informative abstracts, paragraphs or sentences.

Abbreviations: PolySearch

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Keywords: text mining, disease, gene, protein, drug, metabolite, snp, gene sequence, pathway, tissue, gene family, subcellular localization, organ

Resource Name: PolySearch

Resource ID: SCR_005291

Alternate IDs: OMICS_01194

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260905T133129+0000

Ratings and Alerts

No rating or validation information has been found for PolySearch.

No alerts have been found for PolySearch.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Davuluri S, et al. (2021) The molecular basis of gender disparities in smoking lung cancer patients. Life sciences, 267, 118927.

Wahab Khattak F, et al. (2021) Protein-Protein Interaction Analysis through Network Topology (Oral Cancer). Journal of healthcare engineering, 2021, 6623904.

Khan F, et al. (2021) IBDDb: a manually curated and text-mining-enhanced database of genes involved in inflammatory bowel disease. Database : the journal of biological databases and curation, 2021.

Dmitrzak-Weglarz M, et al. (2021) Common and Unique Genetic Background between Attention-Deficit/Hyperactivity Disorder and Excessive Body Weight. Genes, 12(9).

Foroutan A, et al. (2020) The Bovine Metabolome. Metabolites, 10(6).

Cabrera-Andrade A, et al. (2020) Gene Prioritization through Consensus Strategy, Enrichment Methodologies Analysis, and Networking for Osteosarcoma Pathogenesis. International journal of molecular sciences, 21(3).

Yang B, et al. (2019) A Proteomic Network Approach across the Kidney Stone Disease Reveals Endoplasmic Reticulum Stress and Crystal-Cell Interaction in the Kidney. Oxidative medicine and cellular longevity, 2019, 9307256.

Zhao Y, et al. (2019) Multi-omics integration reveals molecular networks and regulators of psoriasis. BMC systems biology, 13(1), 8.

Zhao Y, et al. (2019) Integrative Genomics Analysis Unravels Tissue-Specific Pathways, Networks, and Key Regulators of Blood Pressure Regulation. Frontiers in cardiovascular medicine, 6, 21.

Zyner KG, et al. (2019) Genetic interactions of G-quadruplexes in humans. eLife, 8.

Bhasuran B, et al. (2018) Automatic extraction of gene-disease associations from literature using joint ensemble learning. PloS one, 13(7), e0200699.

Kanwal A, et al. (2018) Construction and analysis of protein-protein interaction network correlated with ankylosing spondylitis. Gene, 638, 41.

Zhang X, et al. (2018) Nucleolar and Spindle Associated Protein 1 (NUSAP1) Inhibits Cell Proliferation and Enhances Susceptibility to Epirubicin In Invasive Breast Cancer Cells by Regulating Cyclin D Kinase (CDK1) and DLGAP5 Expression. Medical science monitor : international medical journal of experimental and clinical research, 24, 8553.

Jing Y, et al. (2017) Bufe Huoxue Capsule Attenuates PM2.5-Induced Pulmonary Inflammation in Mice. Evidence-based complementary and alternative medicine : eCAM, 2017, 1575793.

Sharma A, et al. (2017) In-Cardiome: integrated knowledgebase for coronary artery disease enabling translational research. Database : the journal of biological databases and curation, 2017.

Tejera E, et al. (2017) Consensus strategy in genes prioritization and combined bioinformatics analysis for preeclampsia pathogenesis. BMC medical genomics, 10(1), 50.

Gomez-Cabrero D, et al. (2016) From comorbidities of chronic obstructive pulmonary disease to identification of shared molecular mechanisms by data integration. BMC bioinformatics, 17(Suppl 15), 441.

Roy S, et al. (2015) Systematic Analysis of Integrated Gene Functional Network of Four Chronic Stress-related Lifestyle Disorders. Genome integrity, 6, 1.

Tsatsaronis G, et al. (2015) An overview of the BIOASQ large-scale biomedical semantic indexing and question answering competition. BMC bioinformatics, 16, 138.

Li P, et al. (2015) Identification of potential biomarkers to differentially diagnose solid pseudopapillary tumors and pancreatic malignancies via a gene regulatory network. Journal of translational medicine, 13, 361.