Resource Summary Report

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Biomolecular Object Network Databank

RRID:SCR_007433
Type: Tool

Proper Citation

Biomolecular Object Network Databank (RRID:SCR_007433)

Resource Information

URL: http://bond.unleashedinformatics.com/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented May 10, 2017. A pilot effort that has developed a centralized, web-based biospecimen locator that presents biospecimens collected and stored at participating Arizona hospitals and biospecimen banks, which are available for acquisition and use by researchers. Researchers may use this site to browse, search and request biospecimens to use in qualified studies. The development of the ABL was guided by the Arizona Biospecimen Consortium (ABC), a consortium of hospitals and medical centers in the Phoenix area, and is now being piloted by this Consortium under the direction of ABRC. You may browse by type (cells, fluid, molecular, tissue) or disease. Common data elements decided by the ABC Standards Committee, based on data elements on the National Cancer Institute"s (NCI"s) Common Biorepository Model (CBM), are displayed. These describe the minimum set of data elements that the NCI determined were most important for a researcher to see about a biospecimen. The ABL currently does not display information on whether or not clinical data is available to accompany the biospecimens. However, a requester has the ability to solicit clinical data in the request. Once a request is approved, the biospecimen provider will contact the requester to discuss the request (and the requester"s questions) before finalizing the invoice and shipment. The ABL is available to the public to browse. In order to request biospecimens from the ABL, the researcher will be required to submit the requested required information. Upon submission of the information, shipment of the requested biospecimen(s) will be dependent on the scientific and institutional review approval. Account required. Registration is open to everyone.. Documented on August 19,2019.BOND, which requires registration of a free account, is a resource used to perform cross-database searches of available sequence, interaction, complex and pathway information. BOND integrates a range of component databases including GenBank and BIND, the Biomolecular Interaction Network Database. BOND contains 70+ million biological sequences, 33,000 structures, 38,000 GO terms, and over 200,000 human curated interactions contained in BIND, and is open access. BOND serves the interests of the developing global interactome effort encompassing the genomic,

proteomic and metabolomic research communities. BOND is the first open access search resource to integrate sequence and interaction information. BOND integrates BLAST functionality, and contains a well-documented API. BOND also stores annotation links for sequences, including links to Genome Ontology descriptions, MedLine abstracts, taxon identifiers, associated structures, redundant sequences, sequence neighbors, conserved domains, data base cross-references, Online Mendalian Inheritance in Man identifiers, LocusLink identifiers and complete genomes. BIND on BOND The Biomolecular Interaction Network Database (BIND), a component database of BOND, is a collection of records documenting molecular interactions. The contents of BIND include high-throughput data submissions and hand-curated information gathered from the scientific literature. BIND is an interaction database with three classifications for molecular associations: molecules that associate with each other to form interactions, molecular complexes that are formed from one or more interaction(s) and pathways that are defined by a specific sequence of two or more interactions.Interactions A BIND record represents an interaction between two or more objects that is believed to occur in a living organism. A biological object can be a protein, DNA, RNA, ligand, molecular complex, gene, photon or an unclassified biological entity. BIND records are created for interactions which have been shown experimentally and published in at least one peer-reviewed journal. A record also references any papers with experimental evidence that support or dispute the associated interaction. Interactions are the basic units of BIND and can be linked together to form molecular complexes or pathways. The BIND interaction viewer is a tool to visualize and analyze molecular interactions, complexes and pathways. The BIND interaction viewer uses Ontoglyphs to display information about a protein via attributes such as molecular function, biological process and sub-cellular localization. Ontoglyphs allow to graphically and interactively explore interaction networks, by visualizing interactions in the context of 34 functional, 25 binding specificity and 24 sub-cellular localization Ontoglyphs categories. We will continue to provide an open access version of BOND, providing its subscribers with free, unlimited access to a core content set. But we are confident you will soon want to upgrade to BONDplus.

Synonyms: BOND

Resource Type: data or information resource, database

Keywords: gene, genes, genome, annotation, binding specificity, biological process, complex, dna, genomes, genomic, human, interaction, interactome, ligand, metabolomic, molecular, molecular complex, molecular function, molecular interaction, mouse, ontoglyphs, ontology terms, pathway, photon, protein, protein-protein interactions, proteomic, rna, sequence, structure, sub-cellular localization, taxonomy, unclassified biological entity

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Biomolecular Object Network Databank

Resource ID: SCR_007433

Alternate IDs: nif-0000-00571

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260729T044146+0000

Ratings and Alerts

No rating or validation information has been found for Biomolecular Object Network Databank.

No alerts have been found for Biomolecular Object Network Databank.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Vastrad B, et al. (2020) Bioinformatics analyses of significant genes, related pathways, and candidate diagnostic biomarkers and molecular targets in SARS-CoV-2/COVID-19. Gene reports, 21, 100956.

Lim CY, et al. (2015) Effect of co-administration of Angelicae gigantis radix and Lithospermi radix on rat hepatic injury induced by carbon tetrachloride. Pharmacognosy magazine, 11(42), 395.

Frantzi M, et al. (2014) Clinical proteomic biomarkers: relevant issues on study design & technical considerations in biomarker development. Clinical and translational medicine, 3(1), 7.

Croze E, et al. (2013) Interferon-beta-1b-induced short- and long-term signatures of treatment activity in multiple sclerosis. The pharmacogenomics journal, 13(5), 443.

Wang J, et al. (2013) WEB-based GEne SeT AnaLysis Toolkit (WebGestalt): update 2013. Nucleic acids research, 41(Web Server issue), W77.

Arias CR, et al. (2012) Biomarker identification for prostate cancer and lymph node metastasis from microarray data and protein interaction network using gene prioritization method. TheScientificWorldJournal, 2012, 842727.

Peng CH, et al. (2012) Feature Identification of Compensatory Gene Pairs without Sequence Homology in Yeast. Comparative and functional genomics, 2012, 653174.

Zhang M, et al. (2012) Prediction and analysis of the protein interactome in Pseudomonas aeruginosa to enable network-based drug target selection. PloS one, 7(7), e41202.

Isserlin R, et al. (2011) The Biomolecular Interaction Network Database in PSI-MI 2.5. Database : the journal of biological databases and curation, 2011, baq037.

Kuo HC, et al. (2011) Discovering amino acid patterns on binding sites in protein complexes. Bioinformation, 6(1), 10.

De Las Rivas J, et al. (2010) Protein-protein interactions essentials: key concepts to building and analyzing interactome networks. PLoS computational biology, 6(6), e1000807.

Ravi D, et al. (2009) A network of conserved damage survival pathways revealed by a genomic RNAi screen. PLoS genetics, 5(6), e1000527.

Lehne B, et al. (2009) Protein-protein interaction databases: keeping up with growing interactomes. Human genomics, 3(3), 291.

Fu W, et al. (2009) Human immunodeficiency virus type 1, human protein interaction database at NCBI. Nucleic acids research, 37(Database issue), D417.

Park D, et al. (2008) MassNet: a functional annotation service for protein mass spectrometry data. Nucleic acids research, 36(Web Server issue), W491.

Lu X, et al. (2007) Hubs in biological interaction networks exhibit low changes in expression in experimental asthma. Molecular systems biology, 3, 98.

Tsui IF, et al. (2007) Public databases and software for the pathway analysis of cancer genomes. Cancer informatics, 3, 379.