

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

[PINdb](#)

RRID:SCR_003348

Type: Tool

Proper Citation

PINdb (RRID:SCR_003348)

Resource Information

URL: <http://pin.mskcc.org>

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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 September 2, 2016. Relational database containing the compositions of multi-protein complexes in the nucleus of budding yeast and human cells. Its content is limited to information curated from the proteomics literature and primarily comprises of components of the general transcription and DNA repair machinery. In addition to database browsing and searching capabilities, the PINdb web portal also includes user-friendly interactive tools for comparative analysis of the composition of multiple protein complexes and for clustering and visualizing network of protein complexes. Currently, PINdb contains mostly protein

complexes that may be involved in gene transcription. To facilitate comparative analyses and identification of protein complexes, the compositional information is integrated with standardized gene nomenclature, annotation and protein sequences from public databases. The PINdb web interface provides a number of tools for (1) comparison of protein complexes, (2) search for a protein complex by its published name or by a partial list of its components and (3) browsing specific subsets or a functional classification of the complexes.

Abbreviations: PINdb, PIN

Synonyms: Proteins Interacting in the Nucleus Database

Resource Type: data or information resource, database

Defining Citation: [PMID:15087322](#)

Keywords: nuclear protein complex, protein interaction, targeted proteomics, network visualization, protein, nucleus, proteomics, protein complex, gene transcription

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PINdb

Resource ID: SCR_003348

Alternate IDs: nif-0000-03290

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260821T193659+0000

Ratings and Alerts

No rating or validation information has been found for PINdb.

No alerts have been found for PINdb.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Yang Q, et al. (2021) Simulating human behavioral changes in livestock production systems during an epidemic: The case of the US beef cattle industry. PloS one, 16(6), e0253498.

Cao B, et al. (2018) Detection of Protein Complexes Based on Penalized Matrix Decomposition in a Sparse Protein-Protein Interaction Network. *Molecules* (Basel, Switzerland), 23(6).

Narula K, et al. (2013) Comparative analyses of nuclear proteome: extending its function. *Frontiers in plant science*, 4, 100.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. *Nucleic acids research*, 33(Database issue), D5.