

Resource Summary Report

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PINT

RRID:SCR_007856

Type: Tool

Proper Citation

PINT (RRID:SCR_007856)

Resource Information

URL: <http://www.bioinfodatabase.com/pint/>

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Description: A protein-protein interactions thermodynamic database which contains data of several thermodynamic parameters along with sequence and structural information experimental conditions and literature information. Each entry contains numerical data for features of the interacting proteins such as the free energy change, dissociation constant, association constant, enthalpy change, and heat capacity change. PINT includes: the name and source of the proteins involved in binding, SWISS-PROT and Protein Data Bank (PDB) codes, secondary structure and solvent accessibility of residues at mutant positions, measuring methods, and experimental conditions such as buffers, ions and additives, and literature information. PINT is cross-linked with other related databases such as PIR, SWISS-PROT, PDB and the NCBI PUBMED literature database.

Abbreviations: PINT

Synonyms: Protein-protein Interactions Thermodynamic Database

Resource Type: data or information resource, database

Keywords: database, protein protein interaction, thermodynamic, protein structure, protein database, FASEB list

Resource Name: PINT

Resource ID: SCR_007856

Alternate IDs: nif-0000-03291

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260804T043333+0000

Ratings and Alerts

No rating or validation information has been found for PINT.

No alerts have been found for PINT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 116 mentions in open access literature.

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

Sayour NV, et al. (2025) Effects of sex and obesity on immune checkpoint inhibition-related cardiac systolic dysfunction in aged mice. Basic research in cardiology, 120(1), 207.

Salomonsson J, et al. (2025) Dynamic networks connect the USP14 active site region with the proteasome interaction surface. Protein science : a publication of the Protein Society, 34(4), e70077.

Jeong MK, et al. (2025) Stable Open-Shell Conjugated Terpolymer with Extended NIR Absorption for Organic Photodetectors Detecting Beyond 1000 nm. ACS applied materials & interfaces, 17(17), 25591.

Saxe P, et al. (2025) SEAMM: A Simulation Environment for Atomistic and Molecular Modeling. The journal of physical chemistry. A, 129(30), 6973.

Betz V, et al. (2025) [Presentation of a new pre-emptive endoscopic treatment concept in duodenal interventions exemplified by an iatrogenic duodenal perforation after percutaneous transrenal nephrostomy. German version]. Chirurgie (Heidelberg, Germany), 96(7), 593.

Viswanatha R, et al. (2025) Higher resolution pooled genome-wide CRISPR knockout screening in Drosophila cells using integration and anti-CRISPR (IntAC). Nature communications, 16(1), 6498.

Thublaor T, et al. (2025) Novel Method for Determining Standard Enthalpy and Entropy of Volatilisation of Chromia Exposed to Humidified Oxygen at 298 K Based on Transport Theory of Multicomponent Gas Mixtures. Entropy (Basel, Switzerland), 27(2).

Feng K, et al. (2025) Initial nucleation of nanodroplets in viscoelastic tissue driven by ultrasound: A theoretical simulation. Ultrasonics sonochemistry, 115, 107285.

Langille J, et al. (2025) Quantized Convolutional Neural Networks Robustness under Perturbation. F1000Research, 14, 419.

Papp LA, et al. (2025) Transcriptome changes of fission yeast cells exposed to fumonisin B1 or co-cultured with *Fusarium verticillioides*. *Applied microbiology and biotechnology*, 109(1), 211.

Jensen KS, et al. (2025) N-terminal acetylation of superoxide dismutase 1 accelerates amyloid formation without general destabilization of the apo state. *Protein science : a publication of the Protein Society*, 34(9), e70267.

Rocchi M, et al. (2024) A patient-specific echogenic soft robotic left ventricle embedded into a closed-loop cardiovascular simulator for advanced device testing. *APL bioengineering*, 8(2), 026114.

Salomonsson J, et al. (2024) Transient interdomain interactions in free USP14 shape its conformational ensemble. *Protein science : a publication of the Protein Society*, 33(5), e4975.

Nguyen CQ, et al. (2024) Cohort profile of a prospective cohort study among middle-aged community-dwellers in rural Vietnam: The Khánh Hòa cardiovascular study. *PloS one*, 19(12), e0312525.

Stenström O, et al. (2024) Ligand-induced protein transition state stabilization switches the binding pathway from conformational selection to induced fit. *Proceedings of the National Academy of Sciences of the United States of America*, 121(14), e2317747121.

Sako K, et al. (2024) Bipartite binding interface recruiting HP1 to chromosomal passenger complex at inner centromeres. *The Journal of cell biology*, 223(9).

Bohl V, et al. (2024) The *Listeria monocytogenes* persistence factor ClpL is a potent stand-alone disaggregase. *eLife*, 12.

Theisen FF, et al. (2024) Molecular switching in transcription through splicing and proline-isomerization regulates stress responses in plants. *Nature communications*, 15(1), 592.

Tran NT, et al. (2024) Intrauterine inflammation and postnatal intravenous dopamine alter the neurovascular unit in preterm newborn lambs. *Journal of neuroinflammation*, 21(1), 142.

Raum HN, et al. (2024) Proton Transfer Kinetics in Histidine Side Chains Determined by pH-Dependent Multi-Nuclear NMR Relaxation. *Journal of the American Chemical Society*, 146(32), 22284.