Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 25, 2025

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

Funding:

Availability: Available to the research community

Resource Name: PINT

Resource ID: SCR_007856

Alternate IDs: nif-0000-03291

Record Creation Time: 20220129T080244+0000

Record Last Update: 20250525T032316+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 105 mentions in open access literature.

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

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).

Kushibiki H, et al. (2024) Tryptophan metabolism and small fibre neuropathy: a correlation study. Brain communications, 6(2), fcae103.

Villardi HGD, et al. (2024) Experimental study, simulation and technical-economic feasibility of an interesterification plant for hydrocarbons synthesis by using plastics and frying oil waste. Scientific reports, 14(1), 10240.

Li R, et al. (2024) A longitudinal evaluation of personalized intrinsic network topography and cognitive decline in Parkinson's disease. The European journal of neuroscience, 60(1), 3795.

Aspholm EE, et al. (2024) Structural basis of substrate recognition and allosteric activation of the proapoptotic mitochondrial HtrA2 protease. Nature communications, 15(1), 4592.

Rejnowicz E, et al. (2024) Exploring the dynamics and interactions of the N-myc transactivation domain through solution nuclear magnetic resonance spectroscopy. The Biochemical journal, 481(21), 1535.

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

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

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.

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.

Fierro MA, et al. (2024) PEXEL is a proteolytic maturation site for both exported and non-exported Plasmodium proteins. mSphere, 9(2), e0039323.

Young WJ, et al. (2024) Genome-Wide Interaction Analyses of Serum Calcium on Ventricular Repolarization Time in 125?393 Participants. Journal of the American Heart Association, 13(17), e034760.

Wayment-Steele HK, et al. (2024) The conformational landscape of fold-switcher KaiB is tuned to the circadian rhythm timescale. Proceedings of the National Academy of Sciences of the United States of America, 121(45), e2412293121.

Sarre R, et al. (2024) Structural dynamics of human deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase). Scientific reports, 14(1), 26081.

Lin J, et al. (2024) Long non-coding RNA LINC-PINT as a novel prognostic biomarker in human cancer: a meta-analysis and machine learning. Scientific reports, 14(1), 7483.

Wernersson S, et al. (2023) Cosolvent Dimethyl Sulfoxide Influences Protein-Ligand Binding Kinetics via Solvent Viscosity Effects: Revealing the Success Rate of Complex Formation Following Diffusive Protein-Ligand Encounter. Biochemistry, 62(1), 44.