Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 23, 2025

Human Cancer Protein Interaction Network

RRID:SCR_008116
Type: Tool

Proper Citation

Human Cancer Protein Interaction Network (RRID:SCR_008116)

Resource Information

URL: http://nesg.org:9090/HCPIN/

Proper Citation: Human Cancer Protein Interaction Network (RRID:SCR_008116)

Description: The Human Cancer Pathway Protein Interaction Network (HCPIN) was constructed as a step toward better integrating protein three-dimensional (3D) structural information in cancer systems biology. It was constructed by analysis of several classical cancer-associated signaling pathways and their physical protein-protein interactions. The HCPIN Website provides a comprehensive description of this biomedically important multipathway network together with experimental and homology models of HCPIN proteins useful for cancer biology research.

Synonyms: HCPIN

Resource Type: data or information resource, database

Funding:

Resource Name: Human Cancer Protein Interaction Network

Resource ID: SCR_008116

Alternate IDs: nif-0000-20855

Record Creation Time: 20220129T080245+0000

Record Last Update: 20250523T054654+0000

Ratings and Alerts

No rating or validation information has been found for Human Cancer Protein Interaction Network.

No alerts have been found for Human Cancer Protein Interaction Network.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Huskova A, et al. (2022) Model of abasic site DNA cross-link repair; from the architecture of NEIL3 DNA binding domains to the X-structure model. Nucleic acids research, 50(18), 10436.

Lux V, et al. (2020) Molecular Mechanism of LEDGF/p75 Dimerization. Structure (London, England : 1993), 28(12), 1288.

Began J, et al. (2020) Rhomboid intramembrane protease YqgP licenses bacterial membrane protein quality control as adaptor of FtsH AAA protease. The EMBO journal, 39(10), e102935.

Dinesh DC, et al. (2020) Structural basis of RNA recognition by the SARS-CoV-2 nucleocapsid phosphoprotein. PLoS pathogens, 16(12), e1009100.

North JP, et al. (2018) Cell of origin and mutation pattern define three clinically distinct classes of sebaceous carcinoma. Nature communications, 9(1), 1894.

Gemperle J, et al. (2017) Structural characterization of CAS SH3 domain selectivity and regulation reveals new CAS interaction partners. Scientific reports, 7(1), 8057.

Buchner L, et al. (2015) Increased reliability of nuclear magnetic resonance protein structures by consensus structure bundles. Structure (London, England : 1993), 23(2), 425.

Mareuil F, et al. (2015) Improved reliability, accuracy and quality in automated NMR structure calculation with ARIA. Journal of biomolecular NMR, 62(4), 425.

Aramini JM, et al. (2015) The RAS-Binding Domain of Human BRAF Protein Serine/Threonine Kinase Exhibits Allosteric Conformational Changes upon Binding HRAS. Structure (London, England : 1993), 23(8), 1382.

Mao B, et al. (2014) Protein NMR structures refined with Rosetta have higher accuracy relative to corresponding X-ray crystal structures. Journal of the American Chemical Society,

136(5), 1893.

Stark JL, et al. (2014) Structure and function of human DnaJ homologue subfamily a member 1 (DNAJA1) and its relationship to pancreatic cancer. Biochemistry, 53(8), 1360.

Murphy GS, et al. (2012) Increasing sequence diversity with flexible backbone protein design: the complete redesign of a protein hydrophobic core. Structure (London, England : 1993), 20(6), 1086.

Acton TB, et al. (2011) Preparation of protein samples for NMR structure, function, and small-molecule screening studies. Methods in enzymology, 493, 21.

Mao B, et al. (2011) Improved technologies now routinely provide protein NMR structures useful for molecular replacement. Structure (London, England : 1993), 19(6), 757.

Jha RK, et al. (2010) Computational design of a PAK1 binding protein. Journal of molecular biology, 400(2), 257.

Raman S, et al. (2010) Accurate automated protein NMR structure determination using unassigned NOESY data. Journal of the American Chemical Society, 132(1), 202.

Wu B, et al. (2010) NleG Type 3 effectors from enterohaemorrhagic Escherichia coli are U-Box E3 ubiquitin ligases. PLoS pathogens, 6(6), e1000960.

Van Voorhis WC, et al. (2009) The role of medical structural genomics in discovering new drugs for infectious diseases. PLoS computational biology, 5(10), e1000530.

Burley SK, et al. (2008) Contributions to the NIH-NIGMS Protein Structure Initiative from the PSI Production Centers. Structure (London, England : 1993), 16(1), 5.

von Grotthuss M, et al. (2008) 3D-Fun: predicting enzyme function from structure. Nucleic acids research, 36(Web Server issue), W303.