Resource Summary Report

Generated by NIF on Apr 26, 2025

IntAct

RRID:SCR_006944
Type: Tool

Proper Citation

IntAct (RRID:SCR_006944)

Resource Information

URL: http://www.ebi.ac.uk/intact

Proper Citation: IntAct (RRID:SCR_006944)

Description: Open source database system and analysis tools for molecular interaction data. All interactions are derived from literature curation or direct user submissions. Direct user submissions of molecular interaction data are encouraged, which may be deposited prior to publication in a peer-reviewed journal. The IntAct Database contains (Jun. 2014): * 447368 Interactions * 33021 experiments * 12698 publications * 82745 Interactors IntAct provides a two-tiered view of the interaction data. The search interface allows the user to iteratively develop complex queries, exploiting the detailed annotation with hierarchical controlled vocabularies. Results are provided at any stage in a simplified, tabular view. Specialized views then allows "zooming in" on the full annotation of interactions, interactors and their properties. IntAct source code and data are freely available.

Abbreviations: IntAct

Synonyms: IntAct

Resource Type: service resource, storage service resource, data or information resource, data repository, database

Defining Citation: PMID:24234451, PMID:22121220, PMID:19850723, PMID:17145710, PMID:14681455

Keywords: protein domain, motif, protein interaction, molecular interaction, interaction, protein, binary interaction, complex, data set, protein-protein interaction, pathway, small molecule-protein, nucleic acid-protein, small molecule, nucleic acid, protein binding, chromatin, cancer, apoptosis, molecular biology, virus, source code, isoform, gold standard

Funding: European Union contract FP7-HEALTH-2007-223411;
European Union contract FP7-HEALTH-2007-200767

Availability: Apache License, v2, (software), Creative Commons Attribution License, (data), The community can contribute to this resource

Resource Name: IntAct

Resource ID: SCR_006944

Alternate IDs: OMICS_01918, nif-0000-03026

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250426T055909+0000

Ratings and Alerts

No rating or validation information has been found for IntAct.

No alerts have been found for IntAct.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1815 mentions in open access literature.

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

Malaymar Pinar D, et al. (2025) Nuclear Factor I Family Members are Key Transcription Factors Regulating Gene Expression. Molecular & cellular proteomics : MCP, 24(1), 100890.

Jia X, et al. (2025) Exploring vimentin's role in breast cancer via PICK1 alternative polyadenylation and the miR-615-3p-PICK1 interaction. BioFactors (Oxford, England), 51(1), e2147.

Zhou YQ, et al. (2025) Proteomic characterization of molecular mechanisms of paraquat-induced lung injury in a mouse model. Respiratory research, 26(1), 1.

Miller D, et al. (2025) Pooled PPIseq: Screening the SARS-CoV-2 and human interface with a scalable multiplexed protein-protein interaction assay platform. PloS one, 20(1), e0299440.

Ni T, et al. (2025) Integrated Transcriptome Analysis Reveals Novel Molecular Signatures for Schizophrenia Characterization. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2407628.

Trang KB, et al. (2025) 3D genomic features across >50 diverse cell types reveal insights into the genomic architecture of childhood obesity. eLife, 13.

Chen P, et al. (2025) A Proteomic Study Based on Home Quarantine Model Identifies NQO1 and Inflammation Pathways Involved in Adenoid Hypertrophy. Journal of inflammation research, 18, 723.

Gui A, et al. (2025) Protein lactylation within the nucleus independently predicts the prognosis of non?specific triple?negative breast cancer. Oncology letters, 29(2), 72.

Panni S, et al. (2025) Integrated Analysis of microRNA Targets Reveals New Insights into Transcriptional-Post-Transcriptional Regulatory Cross-Talk. Biology, 14(1).

Kiouri DP, et al. (2025) Structure-Based Approaches for Protein-Protein Interaction Prediction Using Machine Learning and Deep Learning. Biomolecules, 15(1).

Maley S, et al. (2024) Validity of postmortem computed tomography for use in forensic odontology identification casework. Forensic science, medicine, and pathology, 20(1), 43.

Captur G, et al. (2024) Novel Multiplexed Plasma Biomarker Panel Has Diagnostic and Prognostic Potential in Children With Hypertrophic Cardiomyopathy. Circulation. Genomic and precision medicine, 17(3), e004448.

van Zwam MC, et al. (2024) IntAct: A nondisruptive internal tagging strategy to study the organization and function of actin isoforms. PLoS biology, 22(3), e3002551.

Zhang Z, et al. (2024) Acanthopanax senticosus improves cognitive impairment in Alzheimer's disease by promoting the phosphorylation of the MAPK signaling pathway. Frontiers in immunology, 15, 1383464.

Holfeld A, et al. (2024) Systematic identification of structure-specific protein-protein interactions. Molecular systems biology, 20(6), 651.

Hembree WC, et al. (2024) Effect of Distal Tibiofibular Destabilization and Syndesmosis Compression on the Flexibility Kinematics of the Ankle Bones: An In Vitro Human Cadaveric Model. Foot & ankle orthopaedics, 9(2), 24730114241255356.

Xiong G, et al. (2024) Integrated transcriptome and proteome analysis reveals the unique

molecular features and nutritional components on the muscles in Chinese Taihe black-bone silky fowl chicken. PloS one, 19(3), e0299385.

Sun F, et al. (2024) TurboID-based proteomic profiling reveals proxitome of ASK1 and CUL1 of the SCF ubiquitin ligase in plants. The New phytologist, 244(6), 2127.

Treccarichi S, et al. (2024) Implications of a De Novo Variant in the SOX12 Gene in a Patient with Generalized Epilepsy, Intellectual Disability, and Childhood Emotional Behavioral Disorders. Current issues in molecular biology, 46(7), 6407.

Mehryary F, et al. (2024) STRING-ing together protein complexes: corpus and methods for extracting physical protein interactions from the biomedical literature. Bioinformatics (Oxford, England), 40(9).