Resource Summary Report

Generated by dkNET on Sep 16, 2026

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

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, r3d100010671, nif-0000-03026

Alternate URLs: https://doi.org/10.17616/R3QS4R

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260912T195648+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 1955 mentions in open access literature.

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

Silveira ALPA, et al. (2026) The Role of NLRP1, AIM2 and MEFV Inflammasomes in the High-Intensity Interval Training of Individuals With Obesity. Immunology, 178(1), 109.

Kazmirchuk TDD, et al. (2026) Developing an artificial intelligence-generated peptide targeting platelet-type von Willebrand disease. Blood advances, 10(1), 248.

Palollathil A, et al. (2026) Integrative phosphoproteomic analysis reveals co-regulatory phosphorylation networks of rhotekin in cancer progression. Discover oncology, 17(1).

Zhang Y, et al. (2026) Integrated IP-MS and Optoproteomics Reveal Dynamic Remodeling of Protein Interaction Networks During NLRP3 Inflammasome Activation. Molecular & cellular proteomics : MCP, 25(7), 101595.

Anzoom N, et al. (2026) Modeling the Effects of Single Nucleotide Polymorphisms (SNPs) on the Structure and Function of the Human RET Gene: An In Silico Study. Human mutation, 2026, 8848146.

Palollathil A, et al. (2026) Integrative phosphoproteomic analysis identifies functional roles of TRPM7 phosphosites in oncogenesis. Frontiers in bioinformatics, 6, 1757645.

Shivani , et al. (2026) Hydrogen sulfide modulates gene networks in hypoxia/reoxygenation-stressed trophoblasts: insights from transcriptome profiling. Frontiers in bioinformatics, 6, 1785302.

Xu Y, et al. (2026) Quantitative Phosphoproteomics Identifies Myofibrillar Protein Phosphorylation Mediated by Pyruvate Kinase M2 in Beef. Foods (Basel, Switzerland), 15(7).

Karthick V, et al. (2026) Quantum-augmented graph differential geometry enhances accuracy in protein-protein interaction prediction. Scientific reports, 16(1).

Pankivskyi S, et al. (2026) U2AF2 controls alternative splicing in speckle-proximal regions in an RS domain-dependent manner. Nucleic acids research, 54(5).

Wienholts K, et al. (2026) The perioperative microbiome of patients undergoing rectal cancer surgery: A pilot study. Colorectal disease : the official journal of the Association of Coloproctology of Great Britain and Ireland, 28(2), e70397.

Noh SG, et al. (2026) Calorie Restriction Modulates Gene Expression of Il19 and Il24 during Renal Aging. Annals of geriatric medicine and research, 30(1), 28.

Guo J, et al. (2026) Response and degradation of indole-3-aceticacid by the plant growth-promoting rhizobacteria Variovorax boronicumulans. Applied microbiology and biotechnology, 110(1), 43.

Vinogradov-Talyah E, et al. (2026) Human clearance systems have a layered architecture across tissues and cell types that supports varied proteome compositions. Autophagy, 22(1), 145.

Palollathil A, et al. (2026) Proteome-Wide Analysis of Functional Phosphosites in the FGFR Family of Proteins: Insights from Large-Scale Phosphoproteomic Analysis. Proteomes, 14(1).

Silveira ALPA, et al. (2026) The effects of high-intensity interval training on NLRP3 inflammasome and monocyte chemokine receptors in individuals with obesity. PloS one, 21(2), e0343214.

Saghaei S, et al. (2026) VirJenDB: a FAIR (meta)data and bioinformatics platform for all viruses. Nucleic acids research, 54(D1), D912.

Lambourne L, et al. (2026) Experimental assessment of AI-based interactome mapping. Nature communications, 17(1).

Sun P, et al. (2026) MiR-31 suppresses lung adenocarcinoma cell proliferation through CDK1 and E2F2-mediated cell cycle arrest. Discover oncology, 17(1), 251.

Li C, et al. (2026) Integrative analysis of proteomics and metabolomics reveals amino acid metabolism disorder in adriamycin-resistant acute myeloid leukemia cells. Scientific reports, 16(1), 4902.