# Resource Summary Report

Generated by ASWG on Aug 5, 2026

## IntAct

RRID:SCR_006944
Type: Tool

### Proper Citation

IntAct (RRID:SCR_006944)

### Resource Information

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

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**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:** storage service resource, data repository, service resource, database, data or information 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:** 20260805T044143+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 1892 mentions in open access literature.

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

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.

Namuli KL, et al. (2026) Unbiased human genomic characterization of polyglutamine disorder genes to guide biological understanding and therapeutic strategies. HGG advances, 7(1), 100547.

Chen Q, et al. (2026) SMAD7 regulates the canonical Wnt signaling through TGF-? cascade crosstalk and SMAD7/?-CATENIN transcription factor complex formation during tooth regeneration. International journal of oral science, 18(1), 2.

Ding M, et al. (2025) Identification of a Novel Gene ARNT2 for Osteogenic Differentiation of Mesenchymal Stem Cells. Calcified tissue international, 116(1), 100.

van Hooff JJE, et al. (2025) Repeated duplications and losses shaped SMC complex evolution from archaeal ancestors to modern eukaryotes. Cell reports, 44(7), 115855.

Marino GB, et al. (2025) GeneSetCart: assembling, augmenting, combining, visualizing, and analyzing gene sets. GigaScience, 14.

Van Horn S, et al. (2025) Transcriptomic Dysregulation in Animal Models of Attention-Deficit Hyperactivity Disorder and Nicotine Dependence Suggests Shared Neural Mechanisms. Brain and behavior, 15(3), e70444.

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.

Frommelt F, et al. (2025) The solute carrier superfamily interactome. Molecular systems biology, 21(6), 632.

Phan A, et al. (2025) A longitudinal analysis of function annotations of the human proteome reveals consistently high biases. Database : the journal of biological databases and curation, 2025.

Shalaby KS, et al. (2025) SynDRep: a synergistic partner prediction tool based on knowledge graph for drug repurposing. Bioinformatics advances, 5(1), vbaf092.

Yang C, et al. (2025) European and African ancestry-specific plasma protein-QTL and metabolite-QTL analyses identify ancestry-specific T2D effector proteins and metabolites. Nature communications, 16(1), 7412.

Noh SG, et al. (2025) Co-regulation of Nr1d1 and Ppar? in age-related changes of lipid metabolism and its modulation by calorie restriction. Aging, 17(7), 1810.

Su TY, et al. (2025) A quantitative comparison of the deleteriousness of missense and nonsense mutations using the structurally resolved human protein interactome. Protein science : a publication of the Protein Society, 34(6), e70155.

Wang Y, et al. (2025) A Network-Driven Framework for Drug Response Precision Prediction of Acute Myeloid Leukemia. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(36), e06447.

Wang P, et al. (2025) Molecular characterization of breast cancer and multiple primary malignancies: the latest application using unmarked quantitative proteomics. International journal of surgery (London, England), 111(11), 7746.

Helmke PS, et al. (2025) Refining Drug-Induced Cholestasis Prediction: An Explainable Consensus Model Integrating Chemical and Biological Fingerprints. Journal of chemical information and modeling, 65(11), 5301.

Fuchs R, et al. (2025) Functional and Structural Determinants of Long- and Short-Term Evolution of Herpesvirus Proteins. Molecular biology and evolution, 42(10).

Jiang L, et al. (2025) Graph neural network integrated with pretrained protein language model for predicting human-virus protein-protein interactions. Briefings in bioinformatics, 26(5).

Veinstein M, et al. (2025) A simple workflow to identify novel small linear motif (SLiM)-mediated interactions with AlphaFold. Briefings in bioinformatics, 26(5).