IntAct: Quick tour

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Systems
Proteins
Beginner
0.5 hour

This quick tour provides a brief introduction to the EBI's molecular interactions database, IntAct.

Learning objectives:

- Basic understanding of IntAct and how it can help you to find information on molecular interactions
- Knowing where to find out more about IntAct

What is IntAct?

IntAct [2] is a central, public repository where molecular interactions data can be stored and accessed. We are populating IntAct both with submitted data and with data from the scientific literature. The database makes extensive use of controlled vocabularies, which allow consistent description of the experimental detail that was used to generate the data. To support generalised queries, these vocabularies have a hierarchical structure and, where possible, existing reference systems such as the NCBI [3] taxonomy database or the Gene Ontology [4] (GO) are used. In addition, IntAct provides a complete, open source database and analysis system for molecular interactions: it can be locally installed and adapted to the needs of the local organisation. This reduces development time and encourages researchers to build consistent interaction datasets by using the same infrastructure and annotation [5] system. When you query data in IntAct you also access over 16 million interactions in a further 15 data resources via our PSICQUIC [6] (Protemics Standard Initiative Common QUery InterfaCe) service or a consistently annotated, non-redundant, experimentally determined subset from the IMEx Consortium [7].

Why do we need IntAct?

Molecular interactions provide a valuable resource for the elucidation of cellular function, and protein interaction studies have been the focus of much recent biomolecular research. Experiments vary from large-scale systems that generate sizeable datasets, for example two-hybrid systems or tandem affinity purification [8], to an in-depth analysis of a single interaction in which the interacting domains, or even the individual amino acid [9] residues, can be identified. The IntAct database makes these detailed data available both for search over the web and for local download. Additional data, curated to the same level of detail, are available from our IMEx partners. These data are available via the PSICQUIC service, along with many other data types, including predictive interactions, interologues and the results of text-mining-based approaches for inferring molecular interactions.

What can I do with IntAct?

- Find the molecules that interact with your protein of interest.
- Probe more deeply into individual experiments to gain both a degree of confidence in the specific interaction and its functional consequence.
Graphically display interaction networks.

Query across additional resources via PSICQUIC.

Rapidly transfer data into Cytoscape for further analysis.

Visualise minimal connecting networks for protein sets.

Download data in PSI-MI XML [10] and tabular formats.

Searching and visualising data in IntAct

IntAct data: inputs

Figure 1a. Sources of the data in IntAct. Data are submitted directly by individuals, submitted from high-throughput protein–protein interaction projects, or from molecular-interaction data from publications.
high-throughput projects, or derived from the scientific literature. The submitted information is curated by professionals with a background in the molecular life sciences. Information in IntAct is cross-referenced to other data resources, both from within and from beyond EMBL-EBI.

**IntAct data: outputs**

![Diagram of IntAct data access](image)

**Figure 1b.** Different ways to access the data in IntAct. You can browse the IntAct website, download your search results, or download the entire IntAct system and all its data. You can then add your own data to your local version of IntAct, and submit these data to IntAct so that others can access them. Finally, you can access all the information in IntAct, plus additional data, via the IMEx [11] and PSICQUIC websites.

**Getting data from IntAct**

**Quick search**
Simply type in the protein, gene or chemical name of your molecule of interest, or a UniProtKB [12] or ChEBI [13] accession [14] number, to see a binary view of all of the known interaction partners of that molecule. Drill down to see the details of any one piece of interaction evidence. View selected interactions in a simple graphical interface or export to Cytoscape [15] at the click of a button. Advanced search options are available for more complex queries.

Data download

The IntAct [16] project co-develops and supports the PSI-MI standard (see information box) and provides both a web service and a simple URL-based interface that allow direct computational access to retrieve interaction networks in PSI-MI format. Additionally, all files can be accessed and downloaded from the FTP site [17] for local installation.

What is the PSI-MI format?
The PSI-MI format (Proteomics [18] Standards Initiative Molecular Interaction format) is a community standard data model for representing and exchanging molecular interaction data. It has been jointly developed by members of the Proteomics Standards Initiative [19] (PSI), a work group of the Human Proteome Organization [20] (HUPO), and is supported by major protein interaction data providers.

Submitting data to IntAct

We actively encourage the submission of data from external users, particularly if the submitter intends to publish all or part of the information in question. An accession [14] number will be supplied for inclusion in a paper, and the data can be held in confidence until the publication date. Contact the IntAct help desk [21] if you are interested in using this service and to discuss the most appropriate submission format.

Your feedback

Please tell us what you thought about this course. Your feedback is invaluable and helps us to improve our courses and thus enhance your learning experience.

Get help and support on IntAct

References


Orchard, S. et al. (2007) Submit your interaction data the IMEx way: a step by step guide to trouble-free deposition. [26] Proteomics [18], 7, suppl 1, 28–34

**Support**

- For support, submission and related enquiries, email the [IntAct help desk](#) [21].

**Collaborators**

IntAct is hosted by the [European Bioinformatics institute](#) [27], a part of the [European Molecular Biology Laboratory](#) [28].

IntAct is a member of [The International Molecular Exchange (IMEx) Consortium](#) [7] – a group of major public interaction data providers intending to share [curation](#) [29] effort and exchange completed records on molecular interaction data, similar to successful global collaborations for protein and DNA sequences and for macromolecular structures. The current partner databases are DIP, IntAct, MINT, Molecular Connections, MatrixDB, InnateDB, I2D and MPIDB, and the consortium is open to the participation of additional partners.

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**Contributors**

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Sandra Orchard leads the Molecular Interaction Team, responsible for developing resources enabling the network analysis of large-scale datasets as well as supplying basic interaction data and information about protein complexes. She is responsible for the production and maintenance of the IntAct Molecular Interaction database and the Complex Portal. She has previously contributed to the
annotation of the UniProtKB, InterPro and GOA databases. She also applies her experience to provide hands-on training in several resources, including UniProtKB, InterPro, IntAct and Reactome.

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