

Web resources describing results of
PPI experiments,
design of such databases,
minimal information to describe PPIs

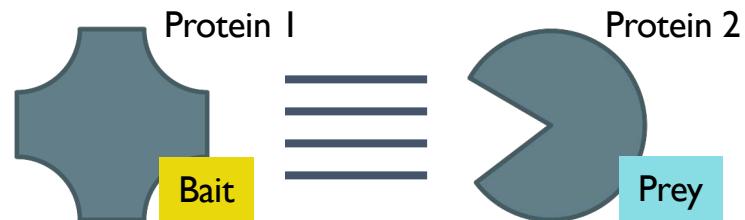
EMBO PPI December 2019
Natasha Wood

**Web resources describing results of
PPI experiments,
design of such databases,
minimal information to describe PPIs**

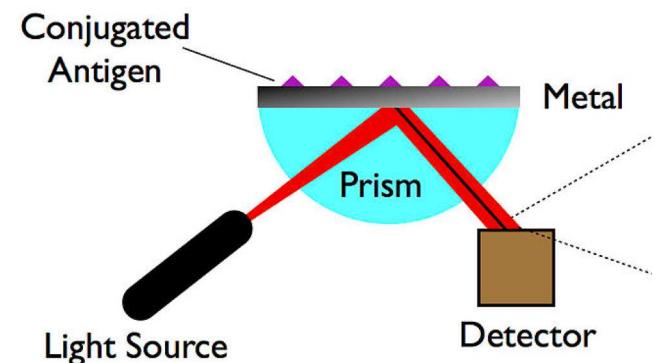
Web resources describing results of
PPI experiments,
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minimal information to describe PPIs

PPI Experiments

- Biochemical
 - Co-immunoprecipitation
 - Pull-down assays
 - Label transfer

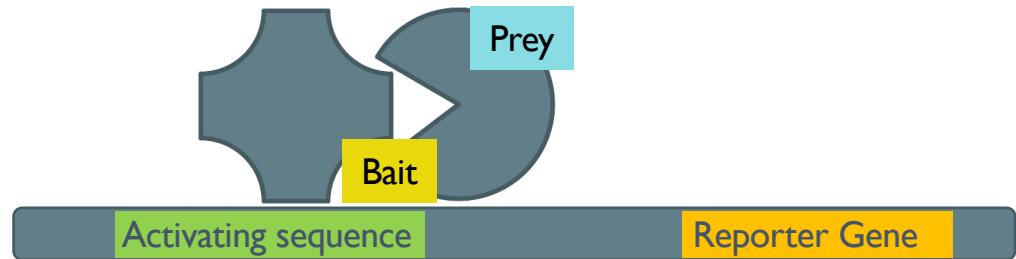


- Biophysical / Theoretical
 - Surface plasmon resonance (SPR)

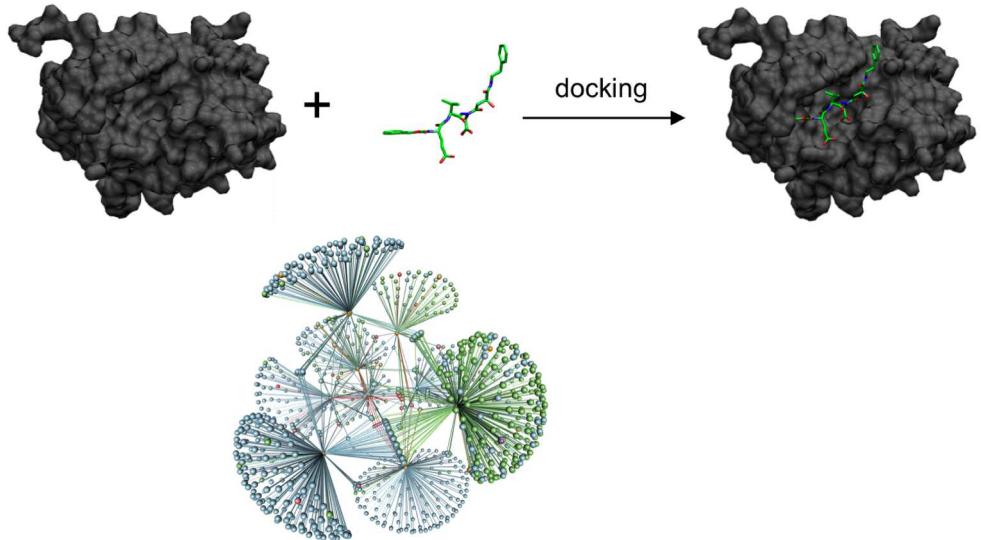


PPI Experiments

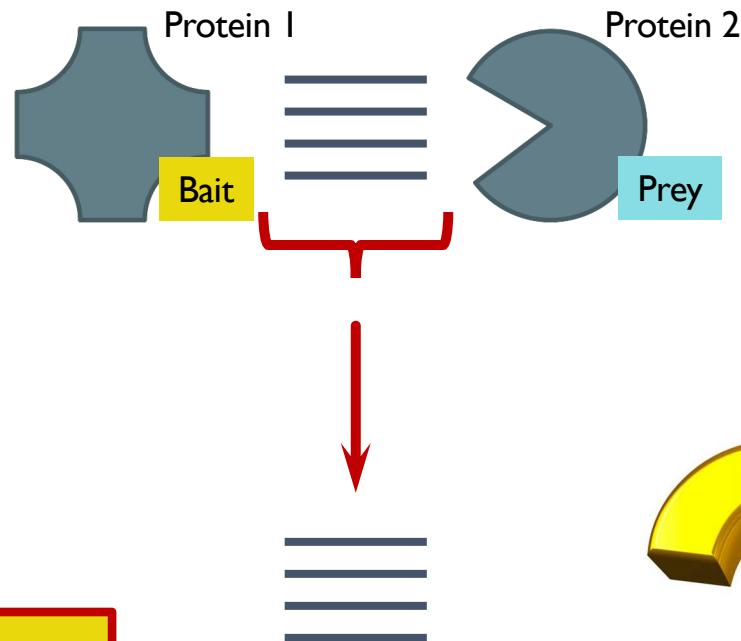
- Genetic
 - Yeast two-hybrid



- Computational
 - Docking
 - Network analysis



PPI Experiments



Different
interaction
types



PPI Types

- Weak or strong



- Direction



- Causality



- Permanent or Transient



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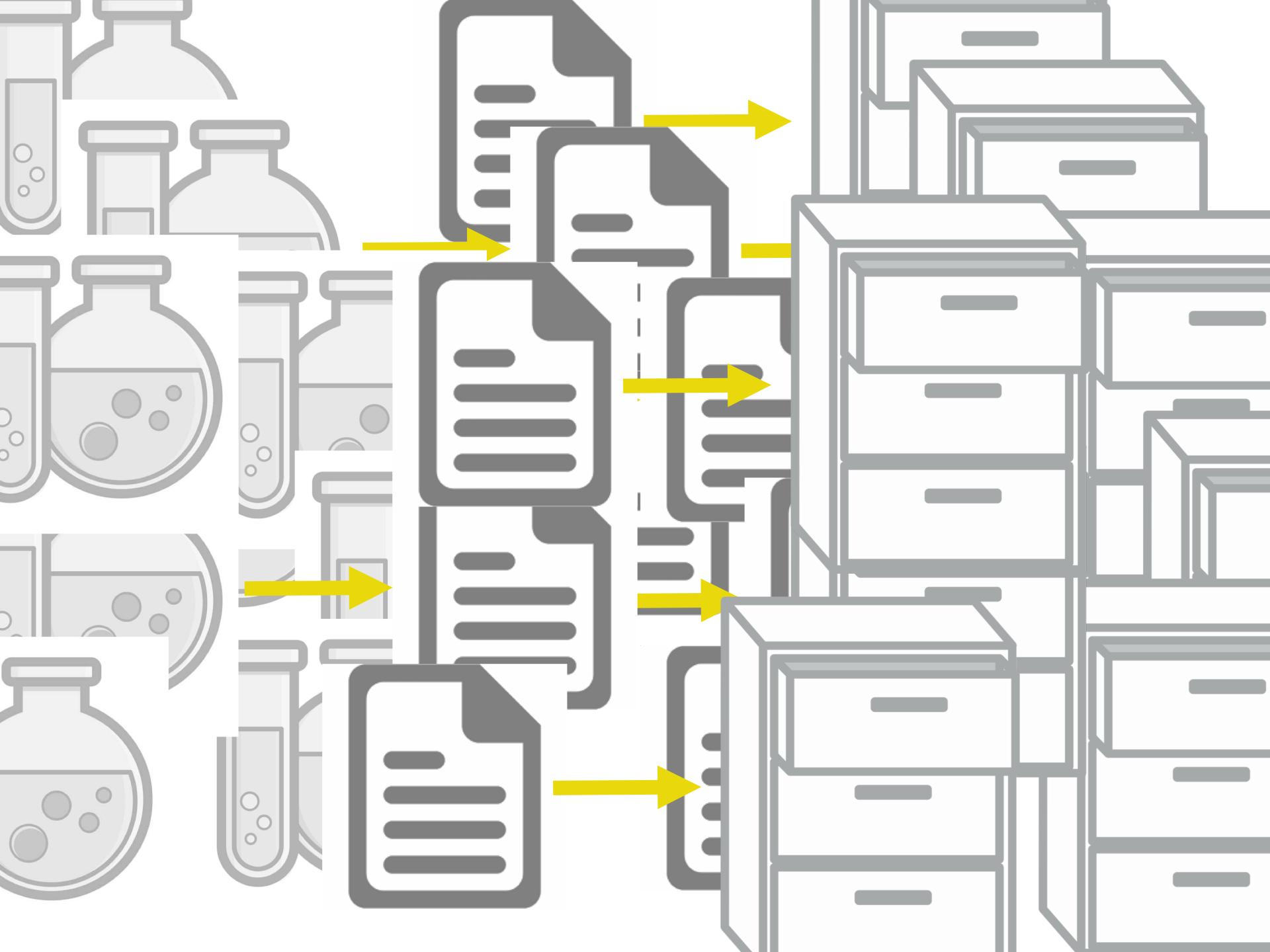
**Web resources describing results of
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minimal information to describe PPIs**

ppi









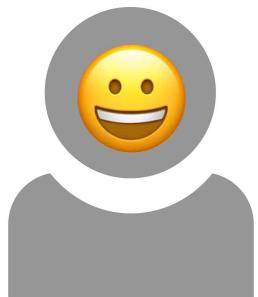
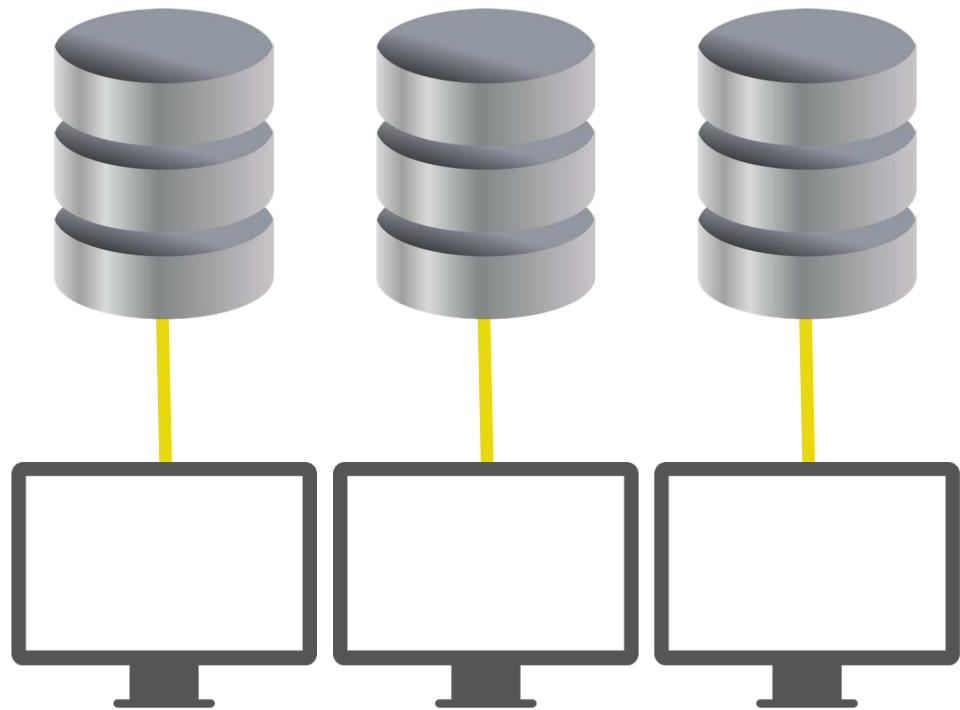
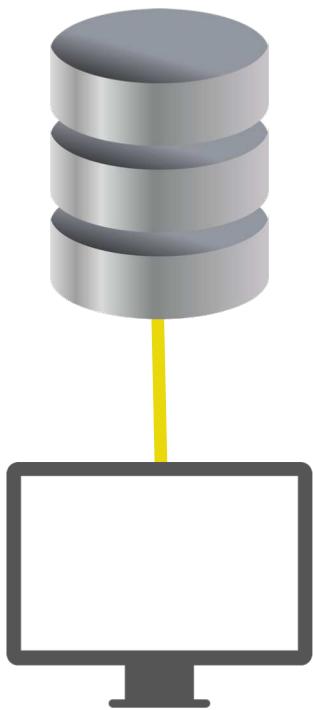
Protein features (in PPIs)

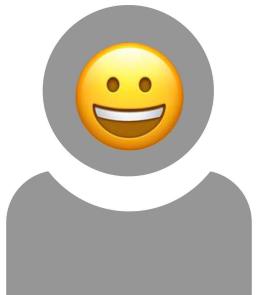
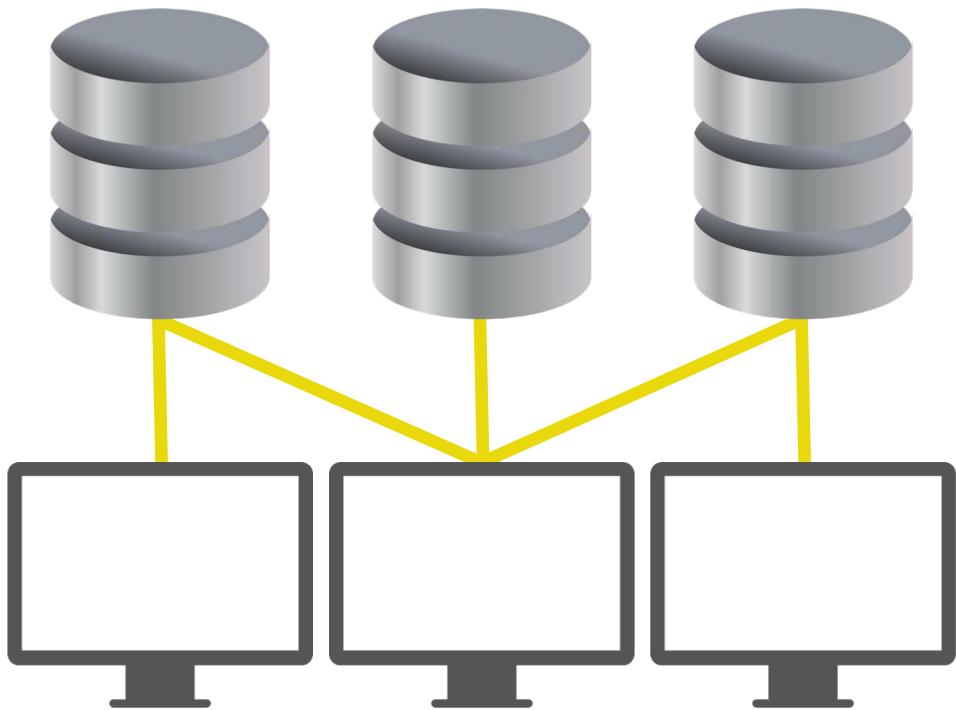
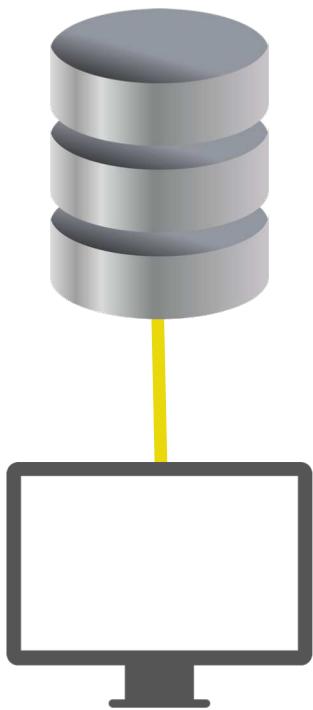


- Protein sequence and structure
 - Discover motifs that predict protein function
- Conserved sequences / evolutionary history
 - Identify key regulatory residues
- Expression profile
 - Regulation of expression and cell-type specificity
- Intracellular localisation
 - Implies certain protein function
- Post-translational modifications
 - Localisation, activation and function often related to phosphorylation, acylation, glycosylation and ubiquitination

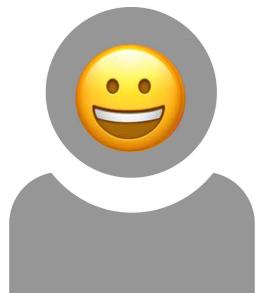
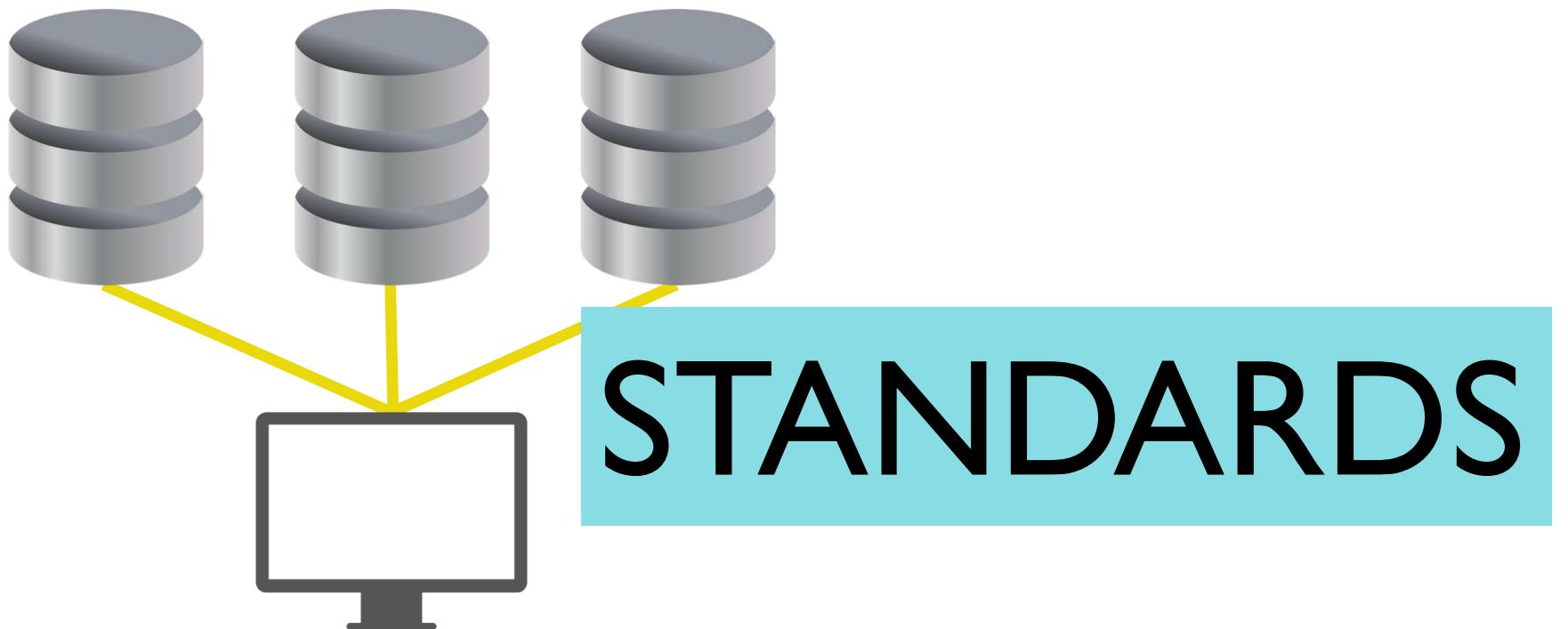
PPIs: what the researcher wants

- Combine results from multiple experiments
- Find out how many interactions exist in a specific organism
- Cross-search interactions between organisms
- View interactions and associated data in different ways
- Combine experimental data and predicted PPI networks





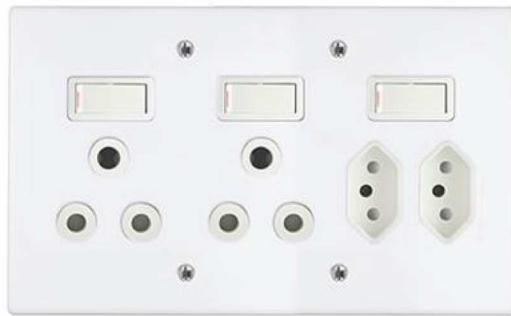
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STANDARDS



STANDARDS



STANDARDS

HOW STANDARDS PROLIFERATE:
(SEE: A/C CHARGERS, CHARACTER ENCODINGS, INSTANT MESSAGING, ETC)

SITUATION:
THERE ARE
14 COMPETING
STANDARDS.

14?! RIDICULOUS!
WE NEED TO DEVELOP
ONE UNIVERSAL STANDARD
THAT COVERS EVERYONE'S
USE CASES.

YEAH!



SOON:

SITUATION:
THERE ARE
15 COMPETING
STANDARDS.

PSI – Proteomics Standards Initiative



Proteomics Standards Initiative defines community standards for data representation in proteomics and interactomics to facilitate data comparison, exchange and verification.

HUPO Initiative



translating
the code of life

PSI

- **Minimum Information Specification**
 - the minimum information required for the useful reporting of experimental results
 - Minimum information about a proteomics experiment (MIAPE) document
- **Formal exchange format**
 - usually an XML format, capable of representing at least the Minimum Information, and normally significant additional detail
- **Controlled vocabularies**
- **Support for implementation of the standard in publicly available tools**

PSI

- Minimum Information Specification
 - the minimum information required for the useful reporting of experimental results
 - Minimum information about a proteomics experiment (MIAPE) document



“formal list of the items of information that should be provided when describing particular analytical techniques employed in a proteomics experiment, the data generated and any analyses performed”

PSI

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Controlled Vocabularies

A formal **ontology** is a **controlled vocabulary** expressed in an **ontology** representation language

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Ontology Lookup Service

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Welcome to the EMBL-EBI Ontology Lookup Service.

Search OLS... 

Examples: [diabetes](#), [GO:0098743](#)

Looking for a particular ontology? 

About OLS

The Ontology Lookup Service (OLS) is a repository for biomedical ontologies that aims to provide a single point of access to the latest ontology versions. You can browse the ontologies through the website as well as programmatically via the OLS API. OLS is developed and maintained by the [Samples, Phenotypes and Ontologies Team \(SPOT\)](#) at EMBL-EBI.

Related Tools

In addition to OLS the SPOT team also provides the OxO, Zooma and Webulous services. [OxO](#) provides cross-ontology mappings between terms from different ontologies. [Zooma](#) is a service to assist in mapping data to ontologies in OLS and [Webulous](#) is a tool for building ontologies from spreadsheets.

Contact Us

For feedback, enquiries or suggestion about OLS or to request a new ontology please contact [ols-support @ ebi.ac.uk](mailto:ols-support@ebi.ac.uk). For bugs or problems with the code or API please report on [GitHub issue](#) For announcements relating to OLS, such as new releases and new features sign up to the [OLS announce mailing list](#).

Data Content

Updated 29 Nov 2019 05:25

- 240 ontologies
- 5,709,654 terms
- 26,896 properties
- 484,519 individuals

Tweets by @EBIOLS

 [EBISPOT OLS](#) @EBIOLS Replying to @EBIOLS SERVICE UPDATE: OLS is back to normal

  Dec 6, 2018

 [EBISPOT OLS](#) @EBIOLS SERVICE UPDATE: OLS is having a

<https://www.ebi.ac.uk/ols/index>

Controlled Vocabularies

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Tweets by [@EBIOLS](#) 

 **EBISPORT OLS**
@EBIOLS

Replies to @EBIOLS

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  Dec 6, 2018

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@EBIOLS

SERVICE UPDATE: OLS is having a

<https://www.ebi.ac.uk/ols/index>

Controlled Vocabularies

OLS > Molecular Interactions Controlled Vocabulary [MI](#) > [MI:0000](#) 

molecular interaction

 http://purl.obolibrary.org/obo/MI_0000 

Search MI 

Controlled vocabularies originally created for protein protein interactions, extended to other molecules interactions. [PMID:14755292]

Controlled Vocabularies

OLS > Molecular Interactions Controlled Vocabulary  > MI:0000 

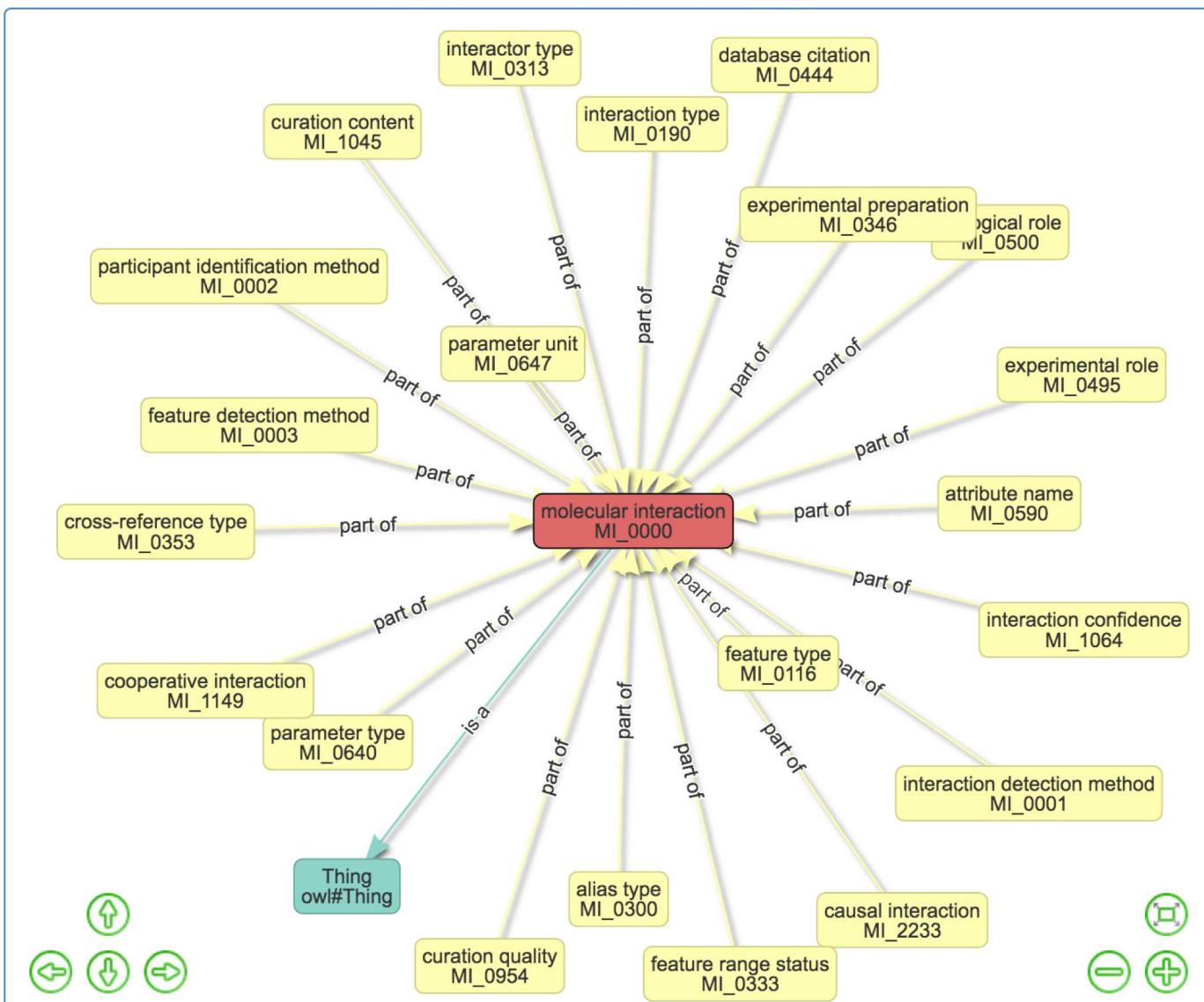
molecular interaction

 http://purl.obolibrary.org/obo/MI_0000 

Search MI 

Controlled vocabularies originally created for protein protein interactions, extended to other molecules interactions. [PMID:14755292]

https://www.ebi.ac.uk/ols/ontologies/mi/terms?iri=http%3A%2F%2Fpurl.obolibrary.org%2Fobo%2FMI_0000

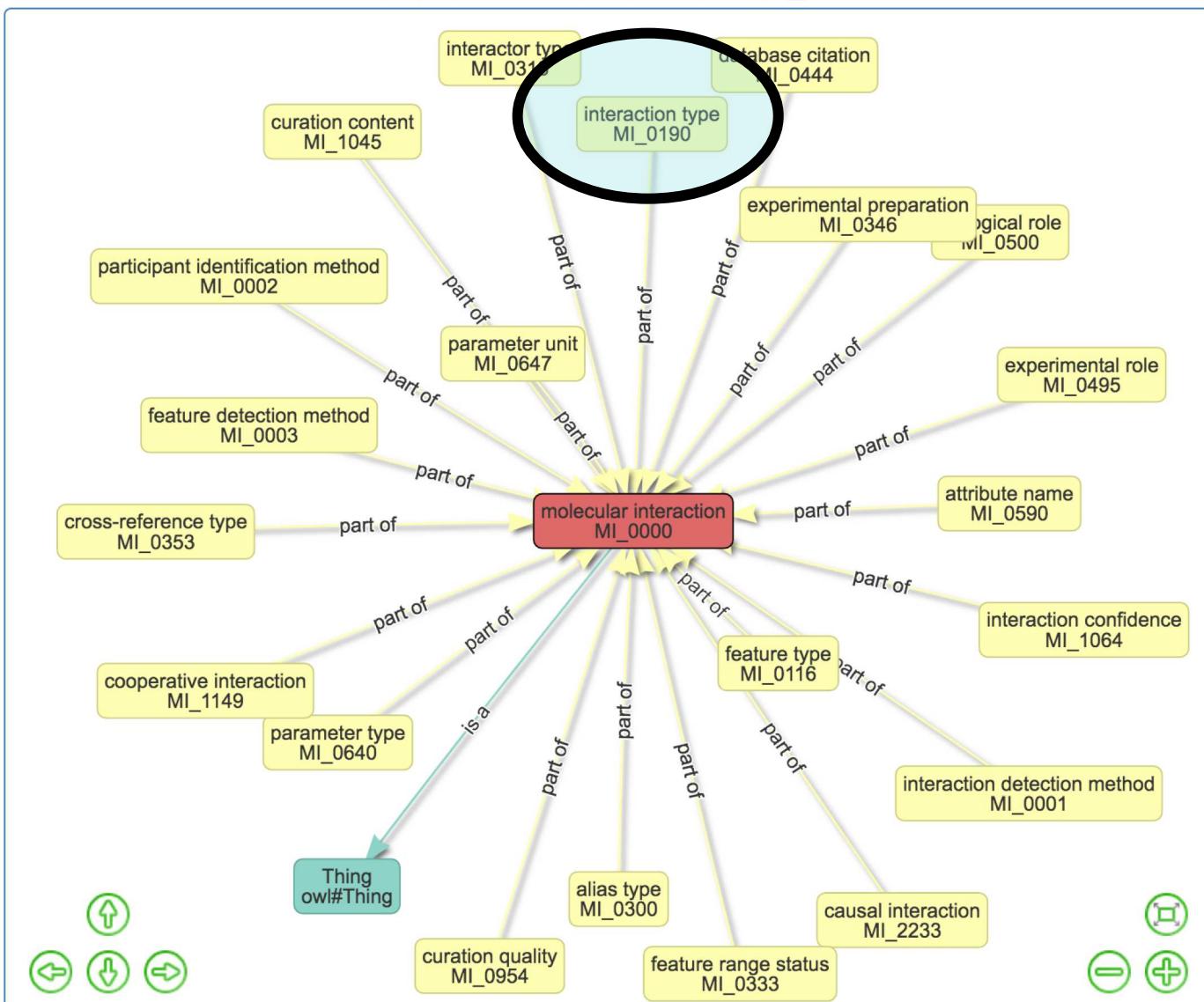


LEGEND

Relationship	Color	Visibility
Extended nodes (*)	Red	-
is a	Teal	<input checked="" type="checkbox"/>
part of	Yellow	<input checked="" type="checkbox"/>
Select/Deselect all	Grey	<input type="checkbox"/>

List of extended nodes (*):

- molecular interaction (MI_0000)



LEGEND

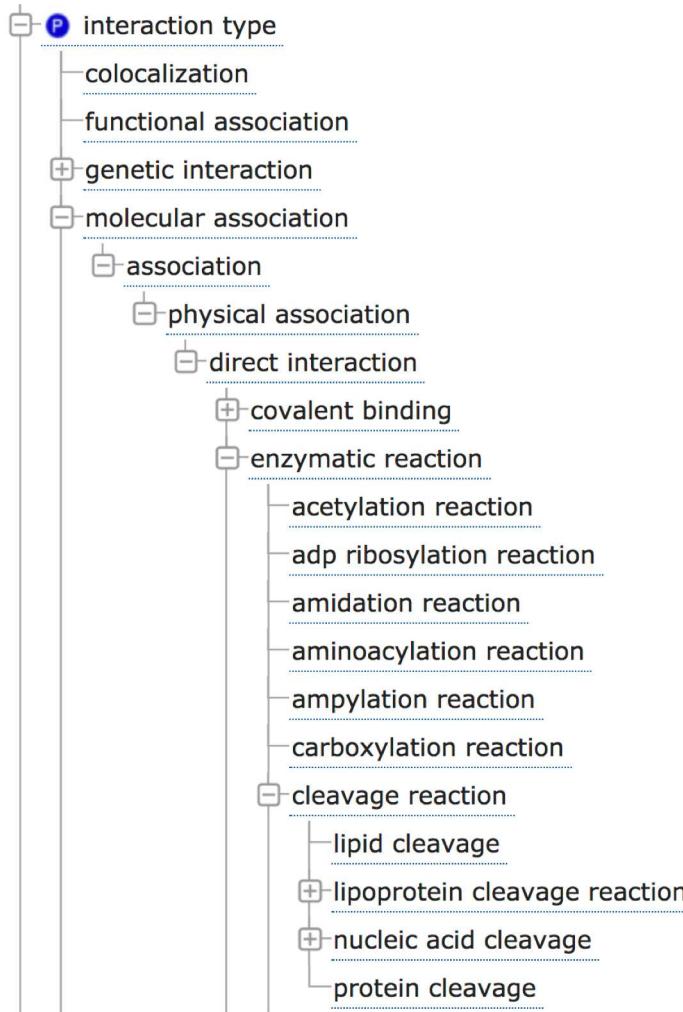
Relationship	Color	Visibility
Extended nodes (*)		-
is a		<input checked="" type="checkbox"/>
part of		<input checked="" type="checkbox"/>
Select/Deselect all		<input type="checkbox"/>

List of extended nodes (*):

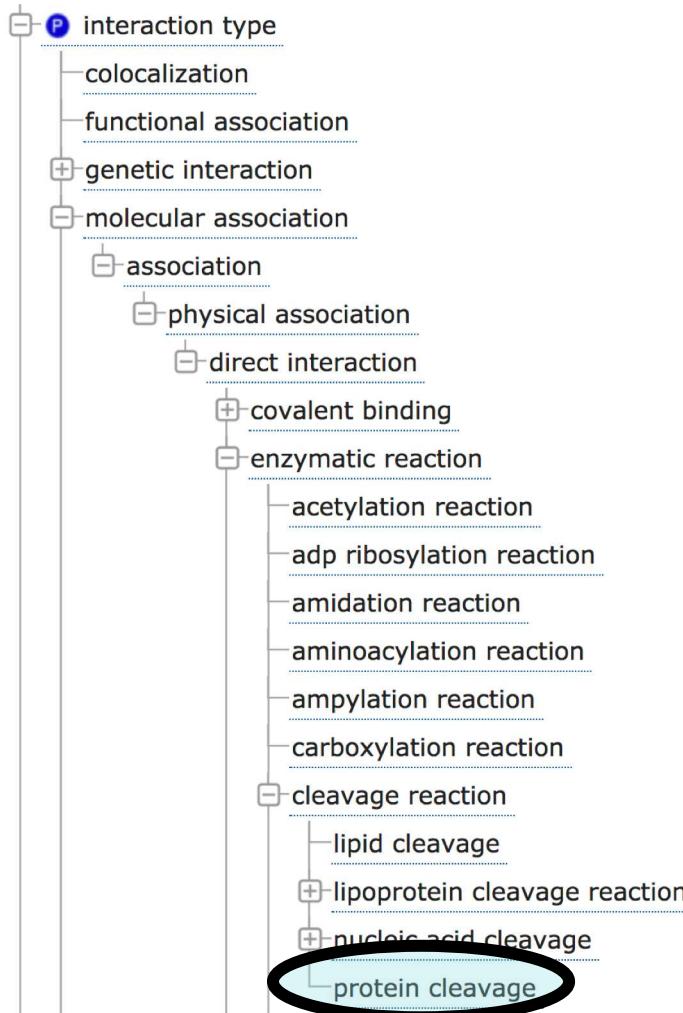
- molecular interaction (MI_0000)



Controlled Vocabularies



Controlled Vocabularies



Controlled Vocabularies

Tree view Term history

- molecular interaction
 - interaction type
 - P molecular association
 - association
 - physical association
 - direct interaction
 - enzymatic reaction
 - cleavage reaction
 - protein cleavage

Graph view
Reset tree
Show all siblings

Term info

Subsets
PSI-MI_slim

definition
Covalent modification of a polypeptide occurring during its maturation or its proteolytic degradation.

has obo namespace
PSI-MI

id
MI:0570

PSI

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HUPO-PSI Working groups and Outputs

Working Groups	Guidelines	v.	Formats	v.	Controlled Vocabularies	v.
Molecular Interactions	MIMIx	1.1.2	PSI-MI XML	2.5.4	PSI-MI CV	2.5.0
	MIABE	1.0.0	PSI-MI XML	3.0.0		
Group charter	MIAPAR	1.0.0	MITAB	2.7	PAR CV	n/a
Mass Spectrometry			mzML	1.1.0	PSI-MS	4.0.15
	Mass spectrometry (MIAPE-MS)	2.98	TraML	1.0.0		
Group charter	Identification (MIAPE-MSI)	1.1	<i>mzData (deprecated)</i>	1.05	XLMOD	1.1.0
	Mass spectrometry Quantification (MIAPE-Quant)	1.0	mzIdentML	1.2.0		
Proteomics Informatics			mzQuantML	1.0.1	XLMOD	4.0.15
			mzTab	1.0.0		
Group charter			proBed	1.0.0	qcML	(PSI spec. under construction)
			proBAM	1.0.0		
Quality Control			PEFF (under review)		sepCV	1.0.0
			qcML			
Group charter	Gel electrophoresis (MIAPE-GE)	1.4	GelML	1.1.0	sepCV	1.0.0
	Gel informatics (MIAPE-GI)	1.0				
Protein separations	Column chromatography (MIAPE-CC)	1.1			sepCV	1.0.0
	Capillary electrophoresis (MIAPE-CE)	0.9.3	spML	1.0.0		
(Inactive)	Phosphoproteomics (MIASSPE)	0.9.				

HUPO-PSI Working groups and Outputs

Working Groups	Guidelines	v.	Formats	v.	Controlled Vocabularies	v.
Molecular Interactions	MIMIx	1.1.0	PSI-MI XML	2.5.4	PSI-MI CV	2.5.0
	MIABE	1.0.0	PSI-MI XML	3.0.0		
Group charter	MIAPAR	1.0.0	MIAPAR	2.7	PAR CV	n/a
Mass Spectrometry	Mass spectrometry (MIAPE-MS)	2.98	mzML	1.1.0		
Group charter	Identification (MIAPE-MSI)	1.1	mzData (deprecated)	1.0.0	PSI-MS	4.0.15
Proteomics Informatics	Mass spectrometry Quantification (MIAPE-Quant)	1.0	mzIdentML	1.0.5		
			mzQuantML	1.2.0		
Group charter			mzTab	1.0.1	XLMod	1.1.0
			proBed	1.0.0		
			proBAM	1.0.0		
			PEFF (under review)			
Quality Control			qcML			
Group charter			(PSI spec. under construction)			
Protein separations (Inactive)	Gel electrophoresis (MIAPE-GE)	1.4	GelML	1.1.0	sepCV	1.0.0
	Gel informatics (MIAPE-GI)	1.0				
	Column chromatography (MIAPE-CC)	1.1				
	Capillary electrophoresis (MIAPE-CE)	0.9.3	spML	1.0.0		
	Phosphoproteomics (MIASSPE)	0.9.				

PSI Molecular Interaction XML



HUPO Proteomics Standards Initiative

[ABOUT](#)[GROUPS ▾](#)[SPECIFICATIONS ▾](#)[DISCUSS](#)[USERS](#)[EVENTS](#)[PUBLICATIONS](#)

PSI-MI XML Specification

Proteomics Standards Initiative
Molecular Interaction XML Format Documentation
Version 2.5

Released 2005, Last maintenance update to version 2.5.4

Version 3.0

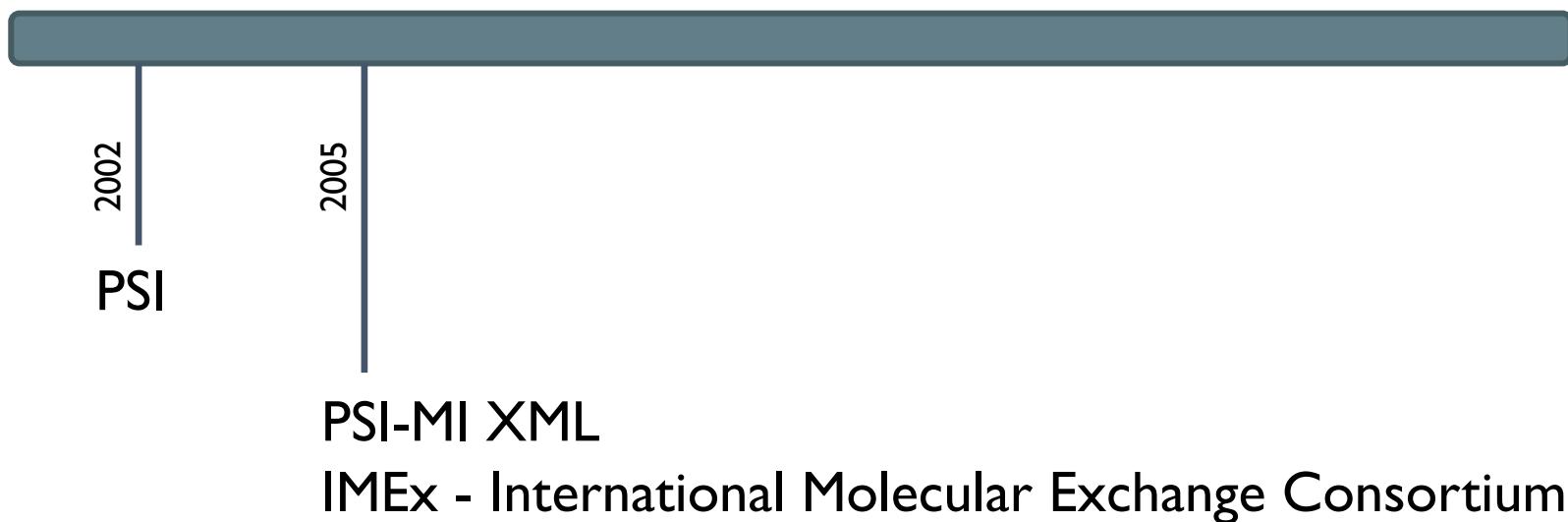
Available for use now, estimated formal release - Spring 2016

P-Standards-...



P-Standards-I...

“The aims of IMEx are to coordinate curation to avoid redundant work on the same data, increase curation coverage and synchronize curation strategies to ensure consistency of data across all IMEx member databases.”



P-Standards-l...

BMC Biology



Software

Open Access

Broadening the horizon – level 2.5 of the HUPO-PSI format for molecular interactions

Samuel Kerrien^{*1}, Sandra Orchard¹, Luisa Montecchi-Palazzi¹,
Bruno Aranda¹, Antony F Quinn¹, Nisha Vinod¹, Gary D Bader^{2,3},
Ioannis Xenarios⁴, Jérôme Wojcik⁴, David Sherman⁵, Mike Tyers³,
John J Salama⁶, Susan Moore^{6,7}, Arnaud Ceol⁸, Andrew Chatr-aryamontri⁸,
Matthias Oesterheld⁹, Volker Stümpflen⁹, Lukasz Salwinski¹⁰,
Jason Nerothin¹⁰, Ethan Cerami¹¹, Michael E Cusick¹², Marc Vidal¹²,
Michael Gilson¹³, John Armstrong¹⁴, Peter Woppard¹⁴, Christopher Hogue¹⁵,
David Eisenberg¹⁰, Gianni Cesareni⁸, Rolf Apweiler¹ and
Henning Hermjakob¹

Address: ¹European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK, ²Banting & Best Department of Medical Research and Terrence Donnelly Centre for Cellular & Biomolecular Research, University of Toronto, 160 College Street, Toronto, Ontario, Canada, ³Samuel Lunenfeld Research Institute, Mount Sinai Hospital, 600 University Avenue, Toronto, Ontario, Canada, ⁴Merck Serono, 9 chemin des Mines, 1211 Geneva, Switzerland, ⁵Laboratoire Bordelais de Recherche en Informatique, ENSI Electronique, Informatique et Radiocomm. de Bordeaux France, ⁶The Blueprint Initiative of Mount Sinai Hospital, 600 University Avenue, Toronto, ON, M5G 1X5, Canada, ⁷National University of Singapore, Office of Life Sciences (OLS), Centre for Life Sciences, Singapore, ⁸Department of Biology, University of Rome Tor Vergata, Via della Ricerca Scientifica, Rome, Italy, ⁹Institute for Bioinformatics, GSF – National Research Center for Environment and Health, Neuherberg, Germany, ¹⁰UCLA-DOE Institute for Genomics & Proteomics, UCLA, LA, USA, ¹¹Computational Biology Center, Memorial Sloan-Kettering Cancer Center 1275 York Avenue, Box 460, New York, NY, USA, ¹²Center for Cancer Systems Biology (CCSB) and Department of Cancer, Biology, Dana-Farber Cancer Institute, and Department of Genetics, Harvard Medical School, Boston, MA, USA, ¹³Center for Advanced Research in Biotechnology, University of Maryland Biotechnology Institute, Rockville, MD, USA, ¹⁴Glaxo Smithkline Medicines Research Centre, Gunnels Wood Road, Stevenage, Herts, UK and ¹⁵Dept. of Biochemistry, University of Toronto, Toronto, Ontario, Canada

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* Corresponding author

Published: 9 October 2007

BMC Biology 2007, 5:44 doi:10.1186/1741-7007-5-44

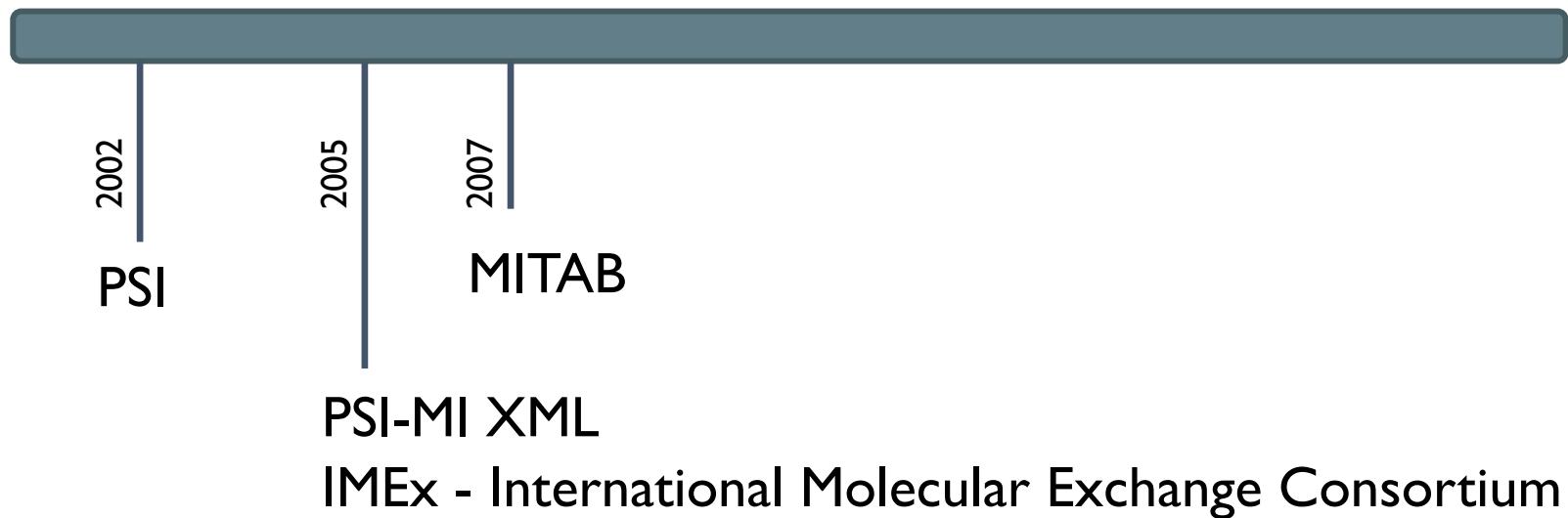
Received: 19 February 2007

Accepted: 9 October 2007

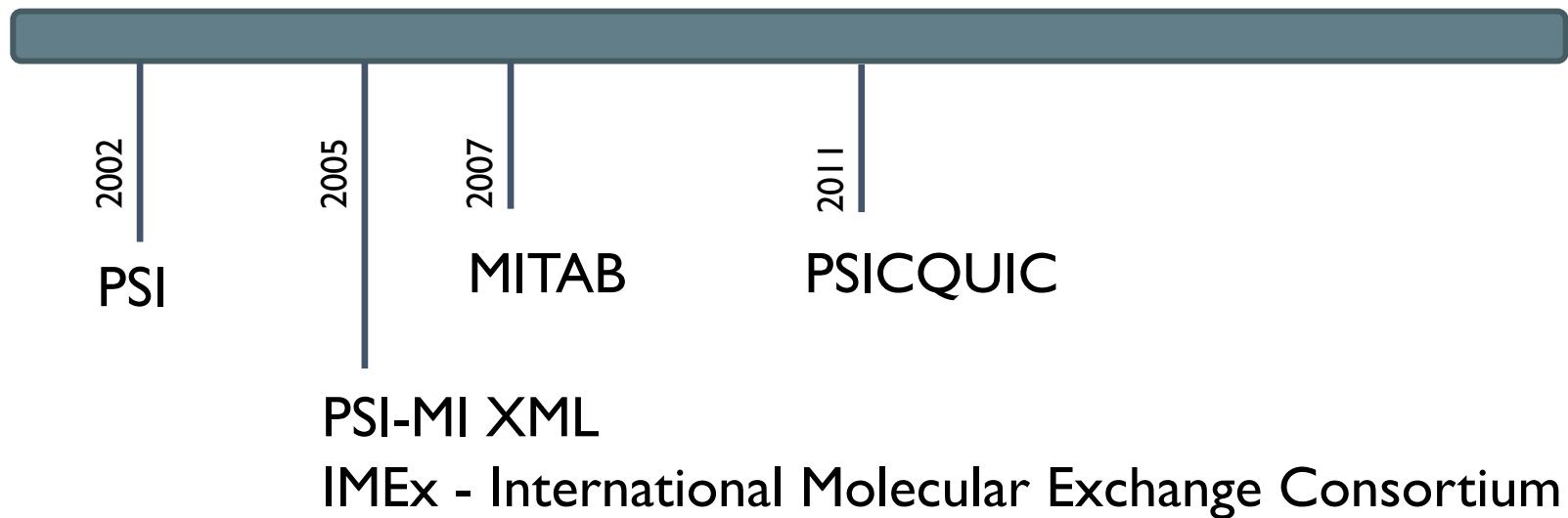
P-Standards-I...

- PSI-MI XML
 - “...the PSI-MI XML schema to enable the description of interactions between a wider range of molecular types, for example nucleic acids, chemical entities, and molecular complexes.”
- MITAB
 - “Additionally, a simpler, tab-delimited format **MITAB2.5** has been developed for the benefit of users who require only minimal information in an easy to access configuration.”

P-Standards-...



P-Standards-I...



P-Standards-I...

nature|methods

Correspondence | Published: 29 June 2011

PSICQUIC and PSISCORE: accessing and scoring molecular interactions

Bruno Aranda✉, Hagen Blankenburg [...] Henning Hermjakob

Nature Methods 8, 528–529 (2011) | Download Citation ↓

PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe

PSICQUIC is an effort from the HUPO Proteomics Standard Initiative (HUPO-PSI) to standardise the access to molecular interaction databases programmatically.

PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe

- I. A standard web service with a well-defined list of methods, accessible using SOAP or REST
 - Simple Object Access Protocol (SOAP)
 - Representational State Transfer (REST)
2. A common query language
 - Molecular Interactions Query Language (MIQL)

The **PSICQUIC Registry** contains the list of PSICQUIC services available, their tags, and their current status.

PSICQUIC Registry

Home Documentation About PSICQUIC Registry

Registry

Total: **11,405,049** Interactions from **33** PSICQUIC Services, of which **10** are currently down.

Filter:

Name	Status	Interactions	Version	URLs	Description	Restricted	Tags
APID Interactomes	🔴	0	-	SOAP: http://cicblade.dep.usal.es/psicquic-ws/webservices/psicquic REST: http://cicblade.dep.usal.es/psicquic-ws/webservices/current/search/ REST example		NO	protein-protein imported spoke expansion clustered
BioGrid	🟢	1,513,281	1.3.14	SOAP: http://tyersrest.tyerslab.com:8805/psicquic/webservices/psicquic REST: http://tyersrest.tyerslab.com:8805/psicquic/webservices/current/search/ REST example		NO	protein-protein internally-curated rapid curation spoke expansion evidence
BIND	🔴	0	-	SOAP: http://webservice.baderlab.org:8480/psicquic-ws/webservices/psicquic REST: http://webservice.baderlab.org:8480/psicquic-ws/webservices/current/search/ REST example		NO	protein-protein smallmolecule-protein nucleicacid-protein spoke expansion clustered
BindingDB	🟢	1,011,029	v1.3	SOAP: http://bindingdb.org/psicquic-ws REST: http://bindingdb.org/psicquic-ws/webservices/psicquic/current/search/ REST example		NO	smallmolecule-protein internally-curated evidence spoke expansion experimentally-observed
BAR	🟢	115,325	1.4.0	SOAP: http://bar.utoronto.ca:9090/psicquic/webservices/psicquic REST: http://bar.utoronto.ca:9090/psicquic/webservices/current/search/ REST example		NO	protein-protein imported spoke expansion predicted internally-curated

PSICQUIC View

Input Form **Browse** Help

Search

Feedback

Input Form > Browse

11,405,049 binary interactions found for search term *

- APID Interactomes [↗](#)
- BindingDB [↗](#) - 1,011,029
- DIP-IMEx [↗](#)
- GeneMANIA [↗](#)
- InnateDB [↗](#) - 33,295
- iRefindex [↗](#) - 3,194,377
- MINT [↗](#) - 131,735
- Spike [↗](#)
- ZINC [↗](#)

- BAR [↗](#) - 115,325
- BioGrid [↗](#) - 1,513,281
- DrugBank [↗](#)
- HPIDb [↗](#) - 5,062
- InnateDB-All [↗](#) - 578,350
- MatrixDB [↗](#) - 65,000
- MPIDB [↗](#) - 1,750
- TopFind [↗](#)

- bhf-ucl [↗](#) - 4,019
- ChEMBL [↗](#) - 628,504
- EBI-GOA-miRNA [↗](#) - 1,996
- I2D [↗](#) - 817,915
- IntAct [↗](#) - 752,488
- MBInfo [↗](#) - 638
- Reactome [↗](#) - 141,996
- UniProt [↗](#) - 21,951

- BIND [↗](#)
- DIP [↗](#)
- EBI-GOA-nonIntAct [↗](#) - 73,995
- IMEx [↗](#) - 795,499
- Interoporc [↗](#)
- mentha [↗](#) - 1,272,096
- Reactome-Fls [↗](#) - 209,988
- VirHostNet [↗](#) - 34,760

Status of the service

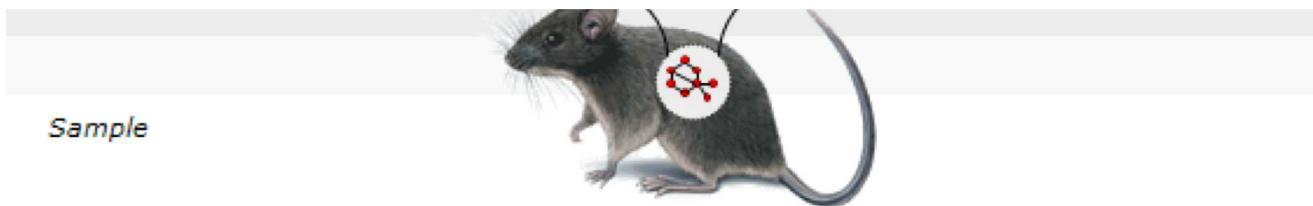
- ONLINE
- OFFLINE
- WARNING: Time out
- ERROR: Unexpected Error

11,405,049 selected interactions

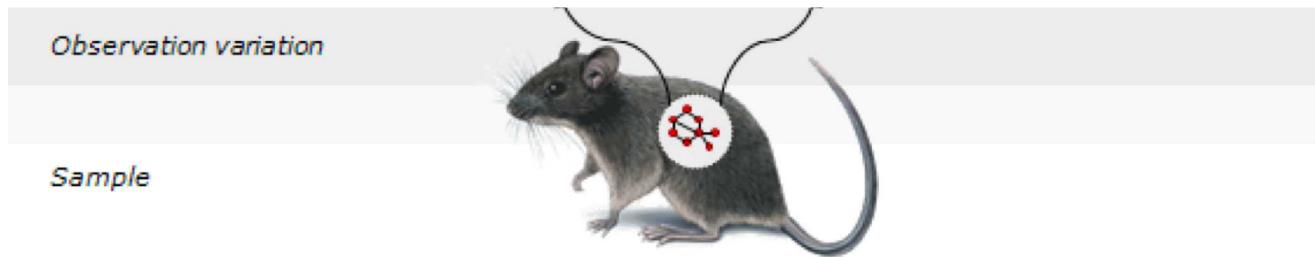
To many interactions to cluster. Please reduce the number to less than 5000 interactions.

version: 1.4.11

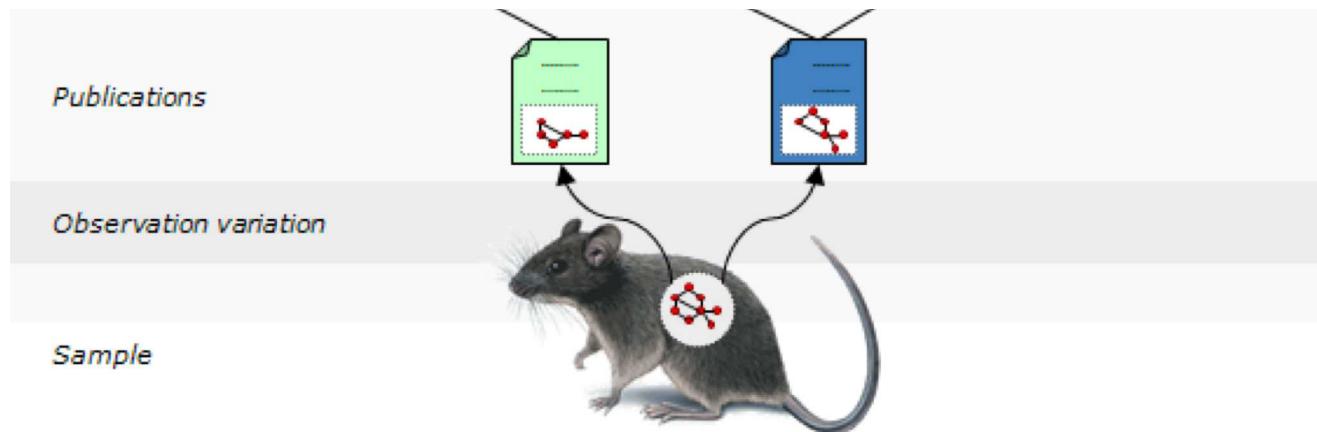
PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe



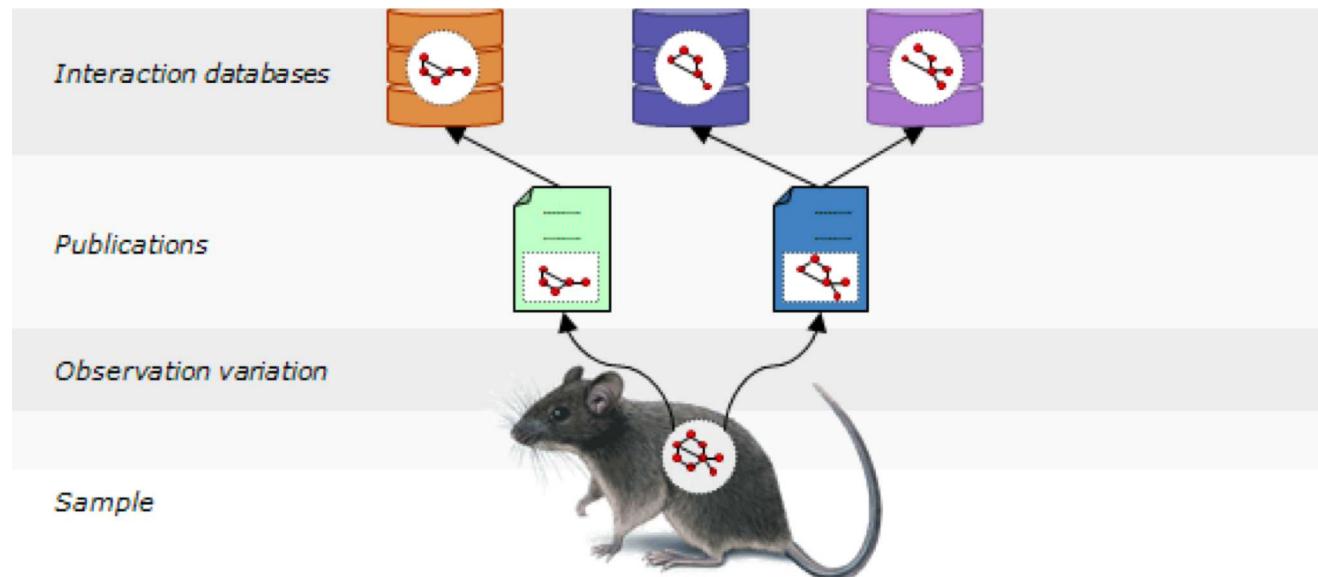
PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe



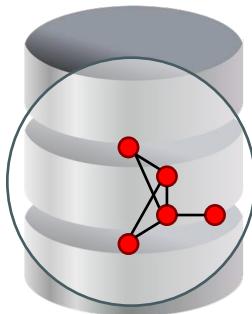
PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe



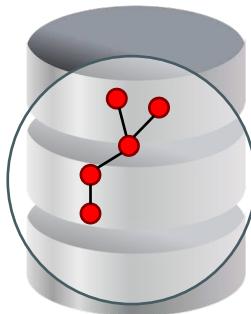
PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe



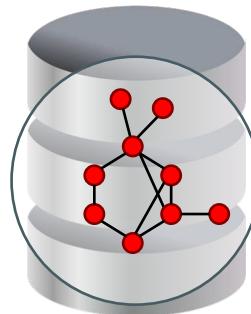
Interaction
Databases

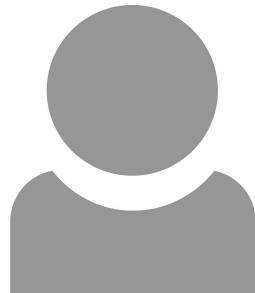
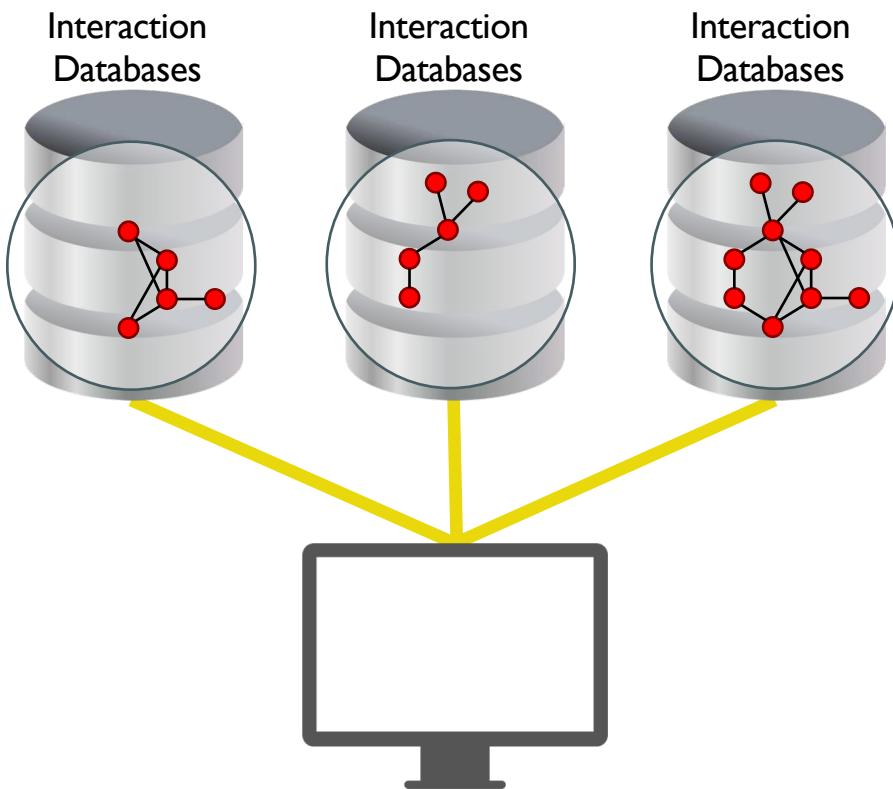


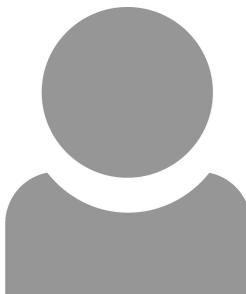
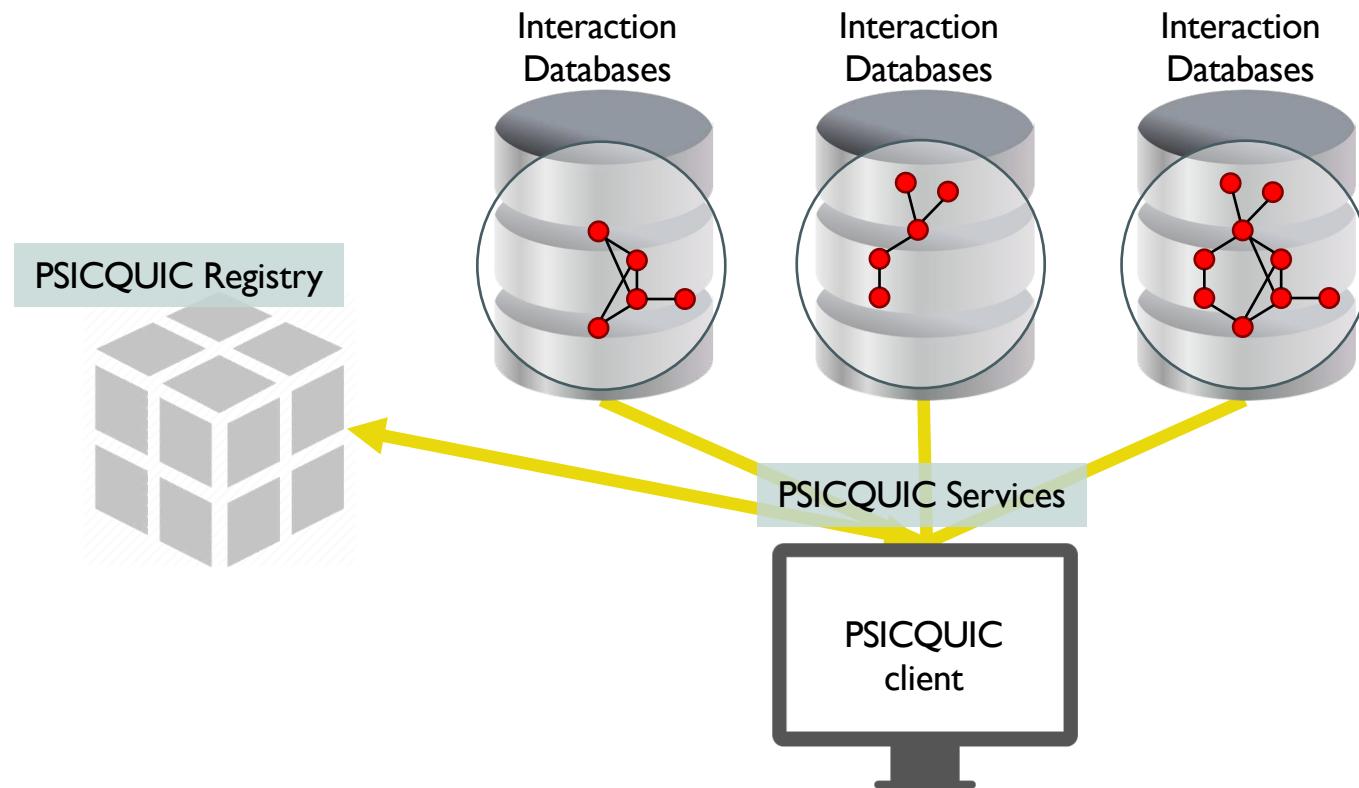
Interaction
Databases

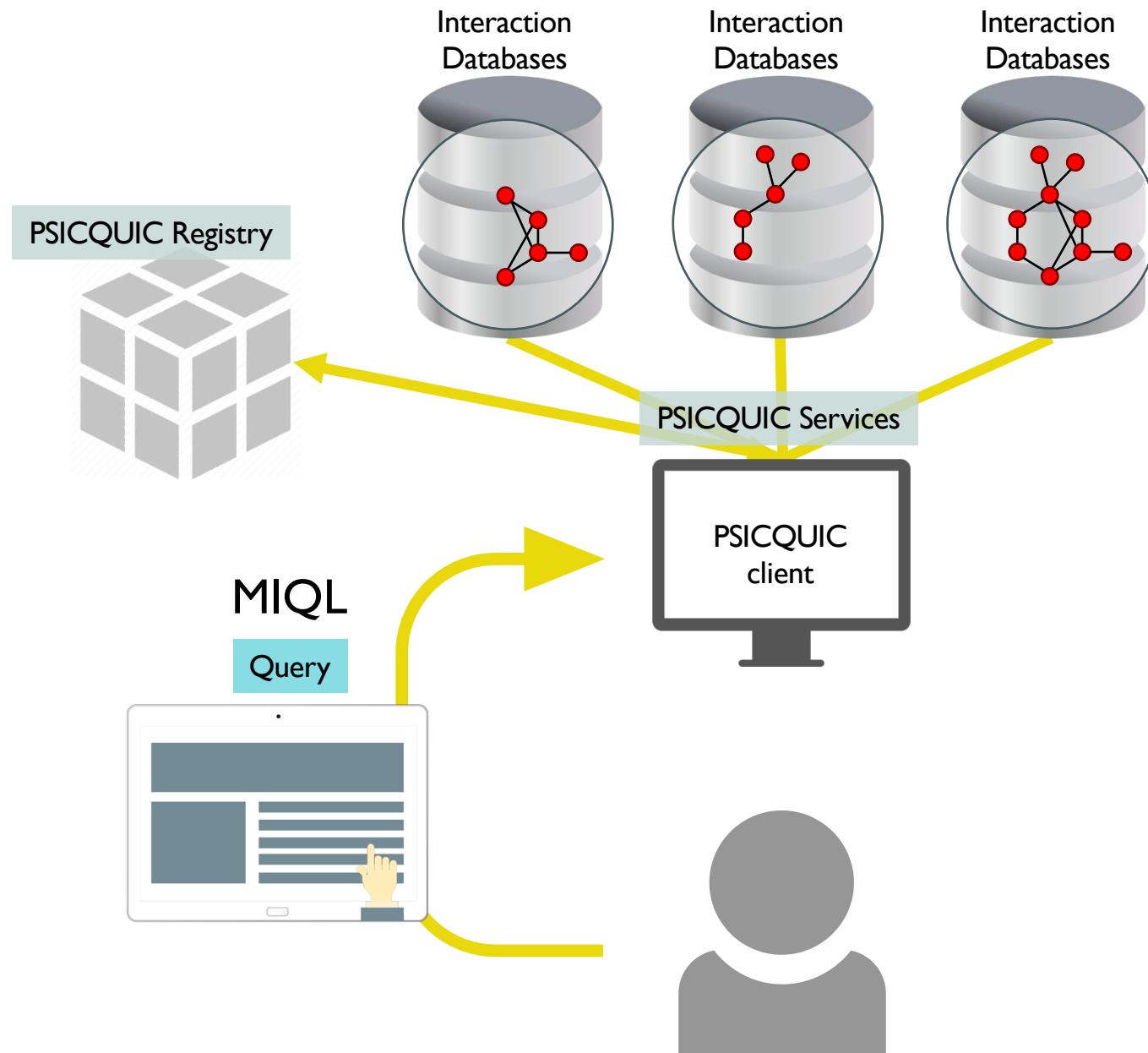


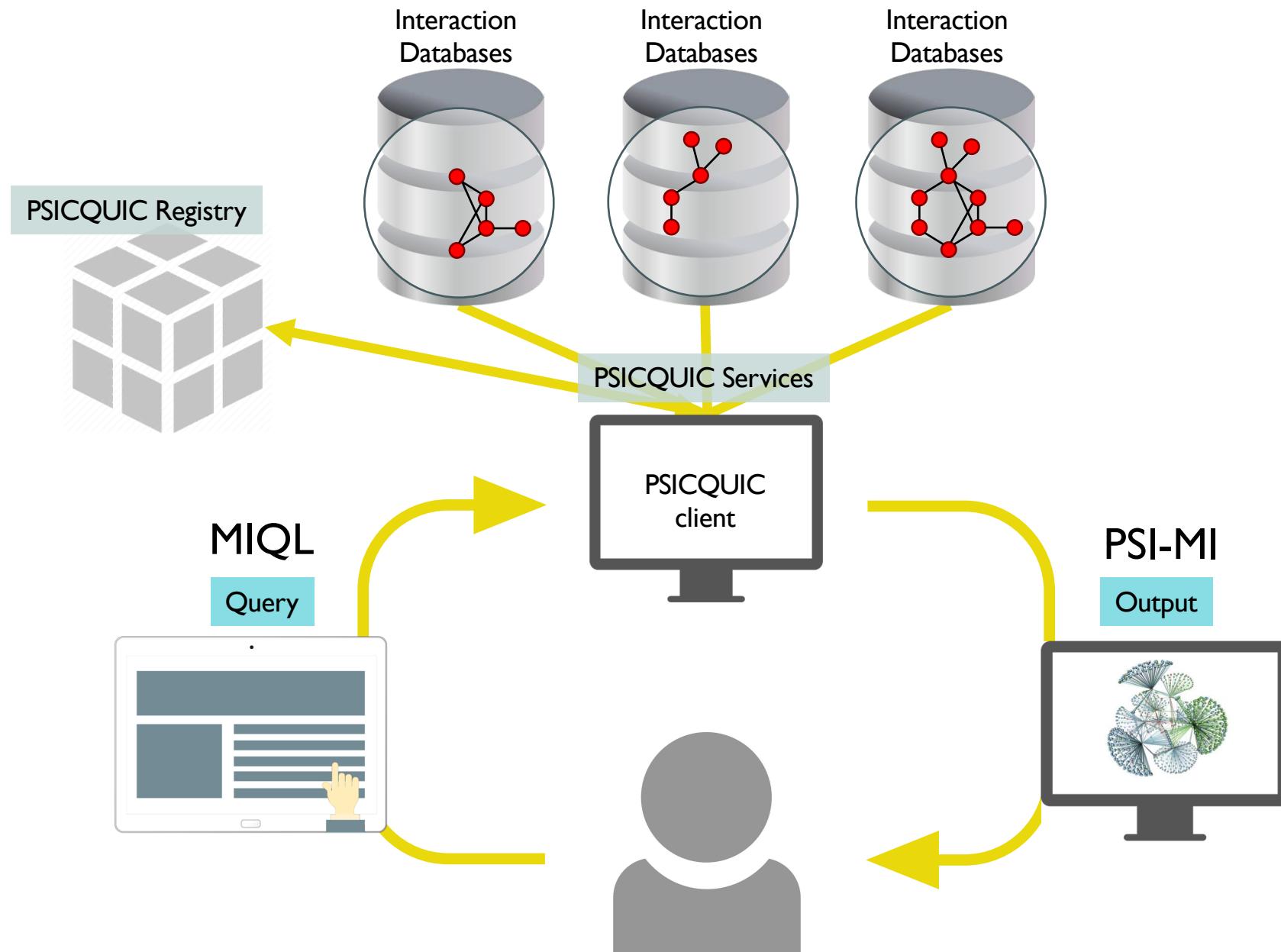
Interaction
Databases

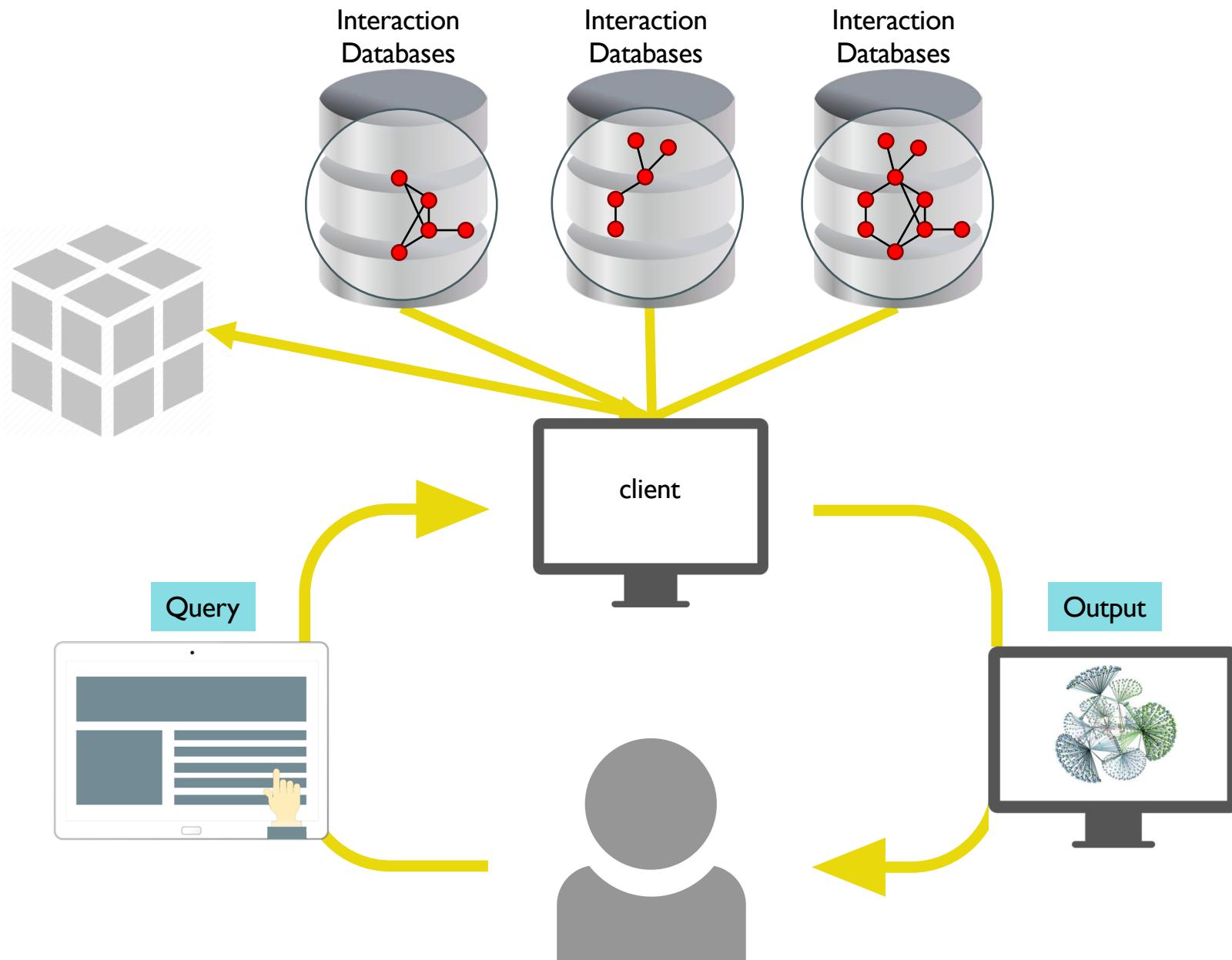




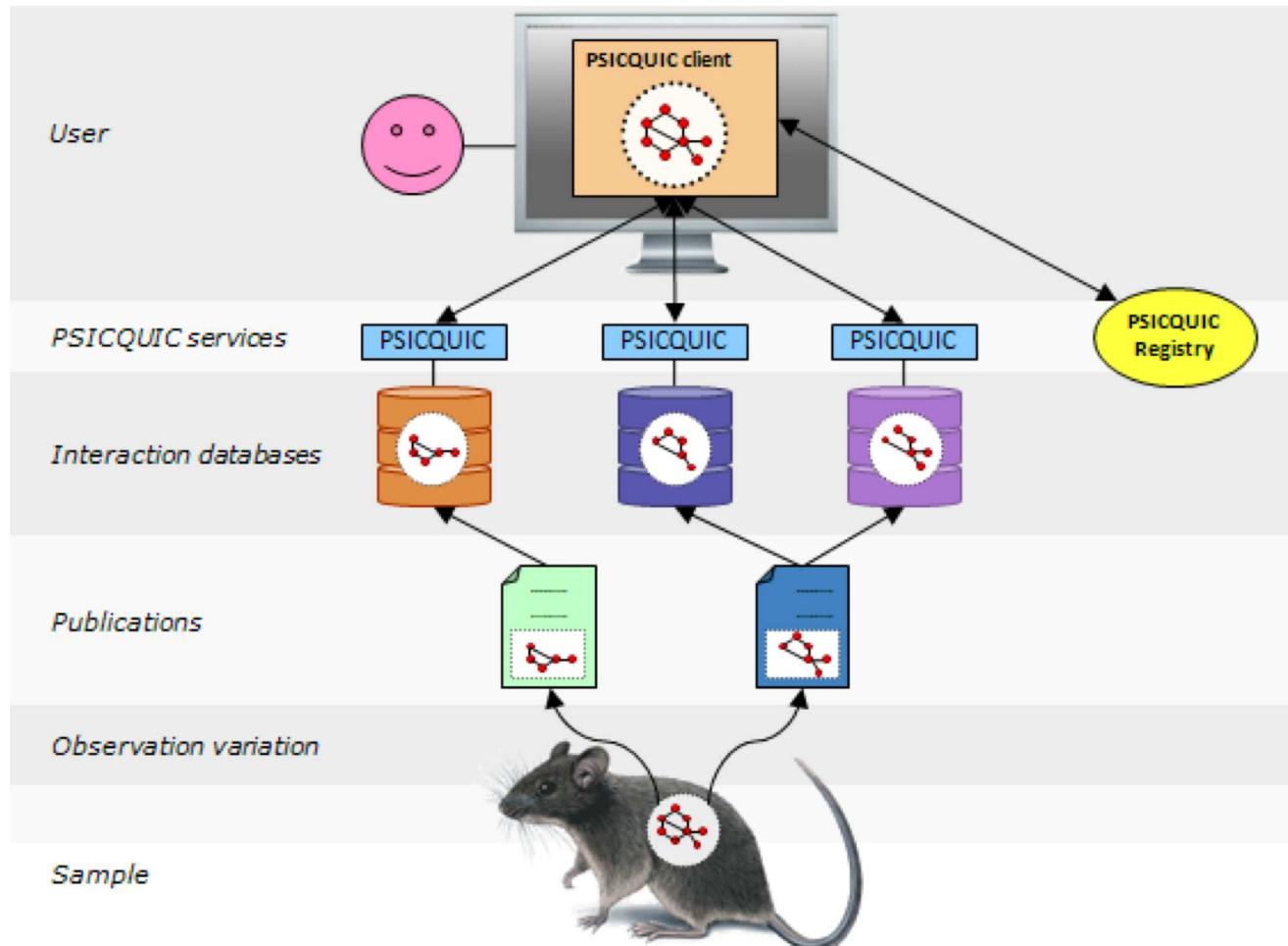








PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe



Web resources describing results of
PPI experiments,
design of such databases,
minimal information to describe PPIs

Web resources describing results of
PPI experiments,
design of such databases,
minimal information to describe PPIs

Web resources

The mission of [UniProt](#) is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

UniProtKB
UniProt Knowledgebase
Swiss-Prot (558,590)
Manually annotated and reviewed.
TrEMBL (126,780,198)
Automatically annotated and not reviewed.

UniRef
Sequence clusters

UniParc
Sequence archive

Proteomes

Supporting data

Literature citations

Cross-ref. databases

Taxonomy

Diseases

Subcellular locations

Keywords

News

Forthcoming changes
Planned changes for UniProt

UniProt release 2018_09
Tubulin code: a long sought-after player identified

UniProt release 2018_08
Human brain development: slow and steady wins the race | 'Enzyme regulation' becomes 'Activity regulation' | New advanced search interfac...

News archive

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Web resources

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News archive

Advanced ▾ Search

BLAST Align Retrieve/ID mapping Peptide search Help Contact

Web resources

Protein-protein
interaction databases
(8)

<input type="checkbox"/>	Cross-reference
<input type="checkbox"/>	BioGrid The Biological General Repository for Interaction Datasets (BioGrid) · UniProtKB (50,375) Category: Protein-protein interaction databases
<input type="checkbox"/>	ComplexPortal ComplexPortal: manually curated resource of macromolecular complexes · UniProtKB (4,546) Category: Protein-protein interaction databases
<input type="checkbox"/>	CORUM CORUM comprehensive resource of mammalian protein complexes · UniProtKB (5,282) Category: Protein-protein interaction databases
<input type="checkbox"/>	DIP Database of interacting proteins · UniProtKB (20,525) Category: Protein-protein interaction databases
<input type="checkbox"/>	ELM The Eukaryotic Linear Motif resource for Functional Sites in Proteins · UniProtKB (1,912) Category: Protein-protein interaction databases
<input type="checkbox"/>	IntAct Protein interaction database and analysis system · UniProtKB (78,315) Category: Protein-protein interaction databases
<input type="checkbox"/>	MINT Molecular INTeraction database · UniProtKB (24,448) Category: Protein-protein interaction databases
<input type="checkbox"/>	STRING STRING: functional protein association networks · UniProtKB (6,761,003) Category: Protein-protein interaction databases

Welcome to the Biological General Repository for Interaction Datasets

BioGRID is an interaction repository with data compiled through comprehensive curation efforts. Our current index is version **3.5.166** and searches **67,477** publications for **1,623,645** protein and genetic interactions, **28,093** chemical associations and **726,378** post translational modifications from major model organism species. All data are **freely** provided via our search index and available for download in standardized formats.

[INTERACTION STATISTICS](#)[LATEST DOWNLOADS](#)

AREAS OF INTEREST TO HELP YOU GET STARTED



Build and Download Interaction Datasets

Create custom interaction datasets by protein or by publication. You can also download our entire dataset in a wide variety of standard formats.



Link To Us or Submit Interactions

Send us your datasets or link to the BioGRID directly from your own website or database. Full details on how to contribute are available [here](#).



Online Tools and Resources

We've developed tools that make use of BioGRID data. Check out the list of tools to see if we can help you work with our data.



View Our Interaction Statistics

Find out how many organisms, proteins, publications, and interactions are available in the current release of the BioGRID.

Search the BioGRID

Search by identifiers, keywords, and gene names...

All Organisms

SUBMIT GENE SEARCH Q



Advanced
Search



Search
Tips



Featured
Datasets

By Gene

By Publication

BIOGRID FUNDING AND PARTNERS



more partners



Complex Portal

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Feedback

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Explore the Complex Portal

The Complex Portal is a manually curated, encyclopaedic resource of macromolecular complexes from a number of key model organisms. The majority of complexes are made up of proteins but may also include nucleic acids or small molecules. All data is freely available for search and download. To perform a search for macromolecular complexes use the search box below. Read more [here >](#).



Examples:

- GO term(s): [GO:0016491](#)
- Gene name(s): [Ndc80](#)
- UniProt AC(s): [Q05471](#)
- Protein name(s): [PCNA](#)
- Complex AC: [CPX-2158](#)
- Complex Name: [nuclear pore](#)
- List of ACs: [Q15554, P54274, Q96AP0](#)

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News

Complex Portal
@complexportal



Read our latest paper describing the content of the @complexportal.
[europemc.org/abstract/MED/3...](#)

Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes [↗](#)

Břízgit H M Medval [↗](#), Hema Bye-A-Jee, Lukáš Gajdoš, Zuzana Hammerová, Areta Horáčková, Filip Melicher, Livia Perfetto, Daniel Pokorný, Milagros Rodríguez López, Alžbeta Túrková, ... [Show more](#)

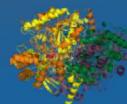
Nucleic Acids Research, gky1001, <https://doi.org/10.1093/nar/gky1001>

Published: 24 October 2018 Article history ↗

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HelmholtzZentrum münchen

German Research Center for Environmental Health



CORUM

The comprehensive resource of mammalian protein complexes

Welcome to CORUM

Search for...

Search

Advanced search

All complexes Core set



Database of Interacting Proteins



Search by:[protein] [sequence] [motif] [article] [IMEx] [pathBLAST]

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[Articles](#)

[Links](#)

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[MIF](#)

THE DIP DATABASE

The DIP™ database catalogs experimentally determined interactions between proteins. It combines information from a variety of sources to create a single, consistent set of protein-protein interactions. The data stored within the DIP database were curated, both, manually by expert curators and also automatically using computational approaches that utilize the knowledge about the protein-protein interaction networks extracted from the most reliable, core subset of the DIP data. Please, check the [reference](#) page to find articles describing the DIP database in greater detail.

This page serves also as an access point to other projects related to DIP, such as The Database of Ligand-Receptor Partners ([DLRP](#)) and JDIP.

DIP PAGES

NEWS	Announcements about the most recent additions and changes to the database.
REGISTRATION/ ACCOUNT	Registration and account maintenance. Registration is required to gain access to most of the DIP features. Registration is free to the members of the academic community. Trial accounts for the commercial users are also available. Please, consult Terms of Use for further details.
STATISTICS	Detailed information about the current state of the database as well as some statistics on server usage.
SATELLITES	DIP-related projects, such as DLRP and JDIP .
SERVICES	DIP-derived services.
ARTICLES	DIP in press. Both, papers published on DIP as well as a list of publications referring to DIP.
SEARCH	Database search. This is the starting point of the database exploration. Once the initial protein is found through keyword or sequence searches the interaction network can be explored by interactively following the interaction links.
LINKS	Links to other protein interaction databases and related sites.
FILES	Download the complete DIP dataset as well as specialized DIP subsets and additional data (<i>registration required</i>).

News:

<https://dip.doe-mbi.ucla.edu/dip/News.cgi>

<https://dip.doe-mbi.ucla.edu/dip/Main.cgi>



The Eukaryotic Linear Motif resource for Functional Sites in Proteins

search ELM Database

[ELM Home](#) [ELM Prediction](#) [ELM DB](#) [ELM Candidates](#) [ELM Information](#) [ELM downloads](#)

Help

Welcome to the Eukaryotic Linear Motif (ELM) resource

This computational biology resource mainly focuses on annotation and detection of eukaryotic linear motifs (ELMs) by providing both a repository of annotated motif data and an exploratory tool for motif prediction. ELMs, or short linear motifs (SLiMs), are compact protein interaction sites composed of short stretches of adjacent amino acids. They are enriched in intrinsically disordered regions of the proteome and provide a wide range of functionality to proteins ([Davey,2011](#), [Van Roey,2014](#)) They play crucial roles in cell regulation and are also of clinical importance, as aberrant SLiM function has been associated with several diseases and SLiM mimics are often used by pathogens to manipulate their hosts' cellular machinery ([Davey,2011](#), [Uyar,2014](#))

ELM Prediction

The **ELM prediction** tool scans user-submitted protein sequences for matches to the regular expressions defined in ELM. Distinction is made between matches that correspond to experimentally validated motif instances already curated in the ELM database and matches that correspond to putative motifs based on the sequence. Since SLiMs are short and degenerate, overprediction is likely and many putative SLiMs will be false positives. However, predictive power is improved by using additional filters based on contextual information, including taxonomy, cellular compartment, evolutionary conservation and structural features.

Protein sequence

Enter Uniprot identifier or accession number: (auto-completion)
e.g. **EPN1_HUMAN, P04637, TAU_HUMAN, [RANDOM]**



PDB-Structure 2O8G showing a peptide from ELM class **DOC_PP1_SILK_1**

- ELM database update
Added 9 new instances for **DOC_CYCLIN_RxL_1**
- ELM database update
Updated the motif **DOC_CYCLIN_RxL_1** and 19 motif instances
- ELM database update
Added a new motif: **LIG_PROFILIN_1**, and news instances for **MOD_CAAbox** and **MOD_CDK_SPxK_1**
- ELM database update
22 New Fungal instances added for **MOD_Plk_1**



The Molecular INTeraction Database

An ELIXIR Core Resource

[Home](#) [Stats](#) [Download](#) [API](#) [Advanced Search](#) [Contacts](#) [About](#)

Proteins, genes, public

Search

Welcome to MINT, the Molecular INTeraction database

MINT focuses on experimentally verified protein-protein interactions mined from the scientific literature by expert curators.

Protein interaction databases represent unique tools to store, in a computer readable form, the protein interaction information disseminated in the scientific literature. Well organized and easily accessible databases permit the easy retrieval and analysis of large interaction data sets. Here we present MINT, a database designed to store data on functional interactions between proteins. Beyond cataloguing binary complexes, MINT was conceived to store other types of functional interactions, including enzymatic modifications of one of the partners.

Do you need more interactions?

[mentha](#) integrates 5 different resources without redundancy

[SIGNOR](#) collects causal interactions

DATA CONTENT

Publications:	6024
Interactions:	131695
Interactors:	26344
Organisms:	647



MINT database

[Follow](#)

MINT is a public database developed at the University of Tor Vergata in Rome and it focuses on experimentally verified protein-protein interactions.

 [MINT database Retweeted](#)

 [ELIXIR Europe](#) 27 Nov



The Molecular INTeraction Database

An ELIXIR Core Resource

[Home](#) [Stats](#) [Download](#) [API](#) [Advanced Search](#) [Contacts](#) [About](#)

Proteins, genes, public

Search

MINT has signed the [IMEx agreement](#) to share curation efforts and supports the Protein Standard Initiative (PSI) recommendation.

Starting September 2013, MINT uses the IntAct database infrastructure to limit the duplication of efforts and to optimise future software development. Data maintenance and release, [MINT PSICQUIC](#) and [IMEx services](#) are under the responsibility of the IntAct team, while curation effort will be carried by both groups.

Data manually curated by the MINT curators can now also be accessed from the [IntAct homepage](#) at the EBI.

Other resources:

MENTHA: <http://mentha.uniroma2.it/>

VirusMENTHA: <http://virusmentha.uniroma2.it/>

SIGNOR: <http://signor.uniroma2.it/>

Version: 11.0

[LOGIN](#) | [REGISTER](#)



[Search](#)

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[Help](#)

[My Data](#)

Welcome to STRING

Protein-Protein Interaction Networks
Functional Enrichment Analysis

ORGANISMS | PROTEINS | INTERACTIONS
5090 | **24.6 mio** | **>2000 mio**

[SEARCH](#)

IntAct Molecular Interaction Database

IntAct provides a freely available, open source database system and analysis tools for molecular interaction data. All interactions are derived from literature curation or direct user submissions and are freely available. The IntAct Team also produce the [Complex Portal](#).

Search in IntAct

Enter search term(s)...

Search

 Search Tips

Examples

- Gene, Protein, RNA or Chemical name:
[BRCA2](#), [Staurosporine](#)
- UniProtKB or ChEBI AC: [Q06609](#),
[CHEBI:15996](#)
- UniProtKB ID: [LCK_HUMAN](#)
- RNACentral ID: [URS00004C95F4_559292](#)
- PMID: [25416956](#)
- IMEx ID: [IM-23318](#)

Featured Dataset

Proteome-wide analysis of phospho-regulated PDZ domain interactions.

- Sundell et al.  [PSI-MI 2.5](#)

 PSI-MI TAB

- Go to Archive

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News

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 IntAct at EBI Retweeted

 Complex Portal
@complexportal

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 and tabular formats.

Web resources describing results of
PPI experiments,
design of such databases,
minimal information to describe PPIs

In summary...

In summary...

- Language/standards are important
- Many web resources
 - PPIs are important
- Databases evolve, don't panic.

Practical example

“You are a researcher working on the structure of the human proteasome, the main protein degradation machinery of the cell.

You are specially interested in knowing if the subunits B5 (UniProtKB id PSB5_HUMAN) and A7 (UniProtKB id PSA7_HUMAN) of the proteasome have been reported to be directly linked or if they are linked through a third protein.

You also want to know if the interactions found are proven to be binary interactions.”

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PSB5_HUMAN PSA7_HUMAN

Search in IntAct

PSB5_HUMAN
PSA7_HUMAN

[Search](#) [Search Tips](#)

The screenshot shows the IntAct search interface. At the top, there are two search results: "PSB5_HUMAN" and "PSA7_HUMAN". Below the search bar, there are two buttons: "Search" and "Search Tips". To the right, under the heading "Examples", there is a list of search terms with their corresponding links:

- Gene, Protein, RNA or Chemical name: [BRCA2](#), [Staurosporine](#)
- UniProtKB or ChEBI AC: [Q06609](#), [CHEBI:15996](#)
- UniProtKB ID: [LCK_HUMAN](#)
- RNACentral ID: [URS00004C95F4_559292](#)
- PMID: [25416956](#)
- IMEx ID: [IM-23318](#)

Practical example

188 binary interactions found for search term
PSB5_HUMAN PSA7_HUMAN

Interactions (188)

Interactors

Interaction Details

Graph

- Filter out the spoke expanded co-complexes [?](#) (76)

Your query also matches 1,549 interaction evidences from 6 other databases. [?](#)

[What is this view? ?](#)

Your query also matches 117 interaction evidences from 1 other IMEx databases. [?](#)

(1 of 10)								
Dts	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Interaction Detection Method	Interaction AC	Source Database	
1	 PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	proximity-dependent biotin identification	EBI-16797733 imex : IM-26301-55	IntAct	
2					proximity-dependent biotin identification	EBI-16797676 imex : IM-26301-153	IntAct	
3					proximity-dependent biotin identification	EBI-16797556 imex : IM-26301-191	IntAct	

When did you do the search?
Which version of the database?

Practical example

“You are a researcher working on the structure of the human proteasome, the main protein degradation machinery of the cell.

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Practical example

188 binary interactions found for search term
PSB5_HUMAN PSA7_HUMAN

Interactions (188)

Interactors

Interaction Details

Graph

- Filter out the spoke expanded co-complexes [?](#) (76)

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(1 of 10)								Customize view	Select format to Download	Download
Dts	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Interaction Detection Method			Interaction AC	Source Database	
1	  PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	proximity-dependent biotin identification	EBI-16797733 imex : IM-26301-55		IntAct		
2	 				proximity-dependent biotin identification	EBI-16797676 imex : IM-26301-153		IntAct		
3	 				proximity-dependent biotin identification	EBI-16797556 imex : IM-26301-191		IntAct		

Practical example

188 binary interactions
PSB5_HUMAN PSA

Interactions (188)

Interactors

Interactants

- Filter out the spoke expanded co-complexes

Customize view

Select f

Dts	Molecule 'A'	Links 'A'
●	PSMA7	O14818
		EBI-603272
●		
●		
●		
●		
●		

Complex Expansion

Binary interactions generated by co-complex expansion

Why should you care about complex expansion ?

Some experimental methods such as Tandem Affinity Purification do generate molecular interactions that can involve more than 2 molecules. Despite the fact that IntAct curation team do capture the molecular interaction as they were reported in the corresponding experiment, when you search using the intact web site, the results of your query is always shown as set of binary interactions (i.e. 2 molecules). We would like to draw your attention on the fact that whenever the reported interaction was a co-complex we do apply an expansion algorithm that transform this n-ary interaction into a set of binary interactions. While none of these algorithms is perfect and will very likely generate some false positive interactions, it is useful to present the data in a consistent manner. Bear in mind that we will strive to differentiate in the search results which interactions are a real experimental binary from expanded ones.

Existing expansion algorithm

There are several known algorithm allowing to transform an n-ary interaction into a set of binaries. The illustration below present the two well known expansion model and illustrates why they can be incorrect.

Practical example

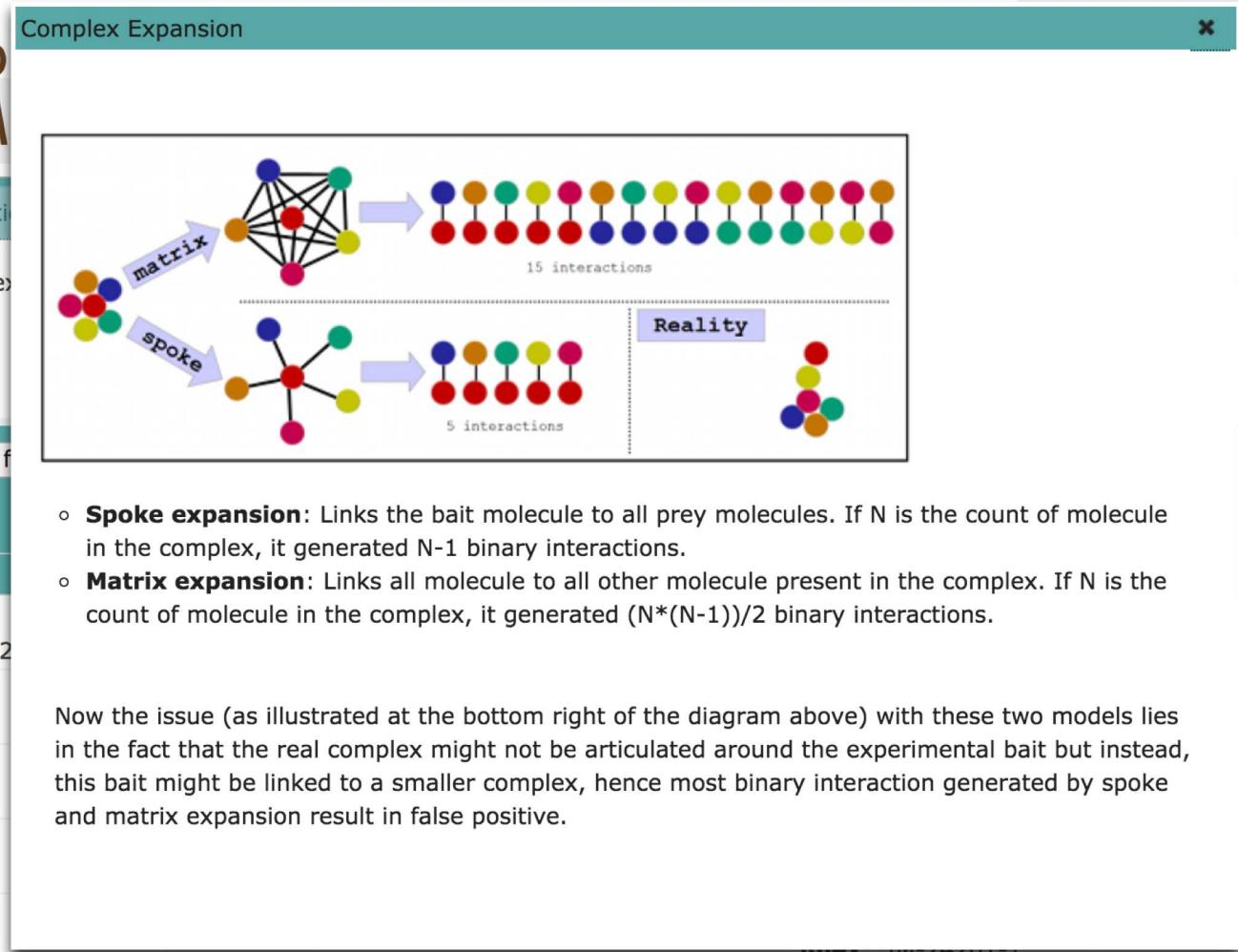
188 binary interactions
PSB5_HUMAN PSA

Interactions (188) Interactors Interactions

- Filter out the spoke expanded co-complexes

Customize view Select filters

Dts	Molecule 'A'	Links 'A'
●	PSMA7	O14818 EBI-603272
●		
●		
●		
●		



Practical example

112 binary interactions found for search term
PSB5_HUMAN PSA7_HUMAN

Interactions (112) Interactors Interaction Details Graph

Include the spoke expanded co-complexes ?

Your query also matches 1,549 interaction evidences from 6 other databases. (1 database(s) non responding) ?

What is this view? ?

Your query also matches 117 interaction evidences from 1 other IMEx databases. ?

Customize view Select format to Download ▾ Download

(1 of 6) 1 2 3 4 5 6

Dts	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Interaction Detection Method	Interaction AC	Source Database
1	PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	two hybrid	EBI-696762	IntAct
2					two hybrid	EBI-696846	IntAct
3					two hybrid	EBI-1388227	IntAct
4					pull down	EBI-1388238	IntAct
5					pull down	EBI-1388404	IntAct

Practical example

112 binary interactions found for search term
PSB5_HUMAN PSA7_HUMAN

Interactions (112) Interactors Interaction Details **Graph** Graph

o Include the spoke expanded co-complexes [?](#) Your query also matches **1,549** interaction evidences from **6** other databases. (1 database(s) non responding) [?](#) What is this view? [?](#)

Customize view Select format to Download [Download](#) (1 of 6) [|<](#) [<<](#) [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [>>](#) [|>](#)

	Dts	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Interaction Detection Method	Interaction AC	Source Database
1		PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	two hybrid	EBI-696762	IntAct
2						two hybrid	EBI-696846	IntAct
3						two hybrid	EBI-1388227	IntAct
4						pull down	EBI-1388238	IntAct
5						pull down	EBI-1388404	IntAct

112 binary interactions found for search term *PSB5_HUMAN PSA7_HUMAN*

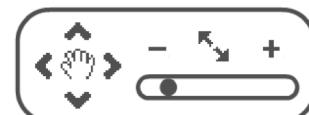
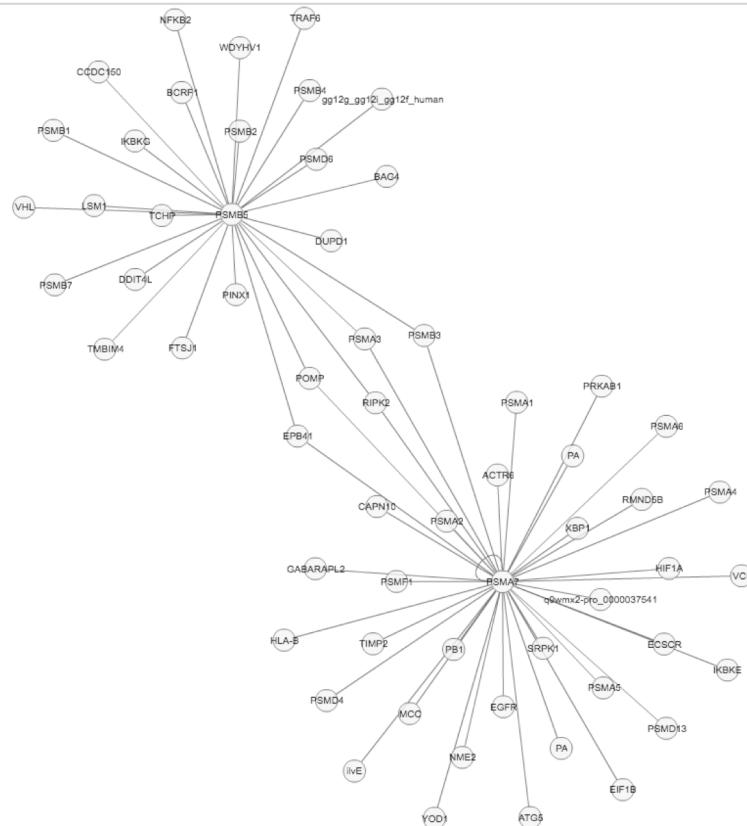
Interactions (112)

Interactors

Interaction Details

Graph

Network visualisation



Practical example

“You are a researcher working on the structure of the human proteasome, the main protein degradation machinery of the cell.

You are specially interested in knowing if the subunits B5 (UniProtKB id **PSB5_HUMAN**) and A7 (UniProtKB id **PSA7_HUMAN**) of the proteasome have been reported to be directly linked or if they are linked through a third protein.

You also want to know if the interactions found are **proven to be binary interactions**.”

112 binary interactions found for search term *PSB5_HUMAN PSA7_HUMAN*

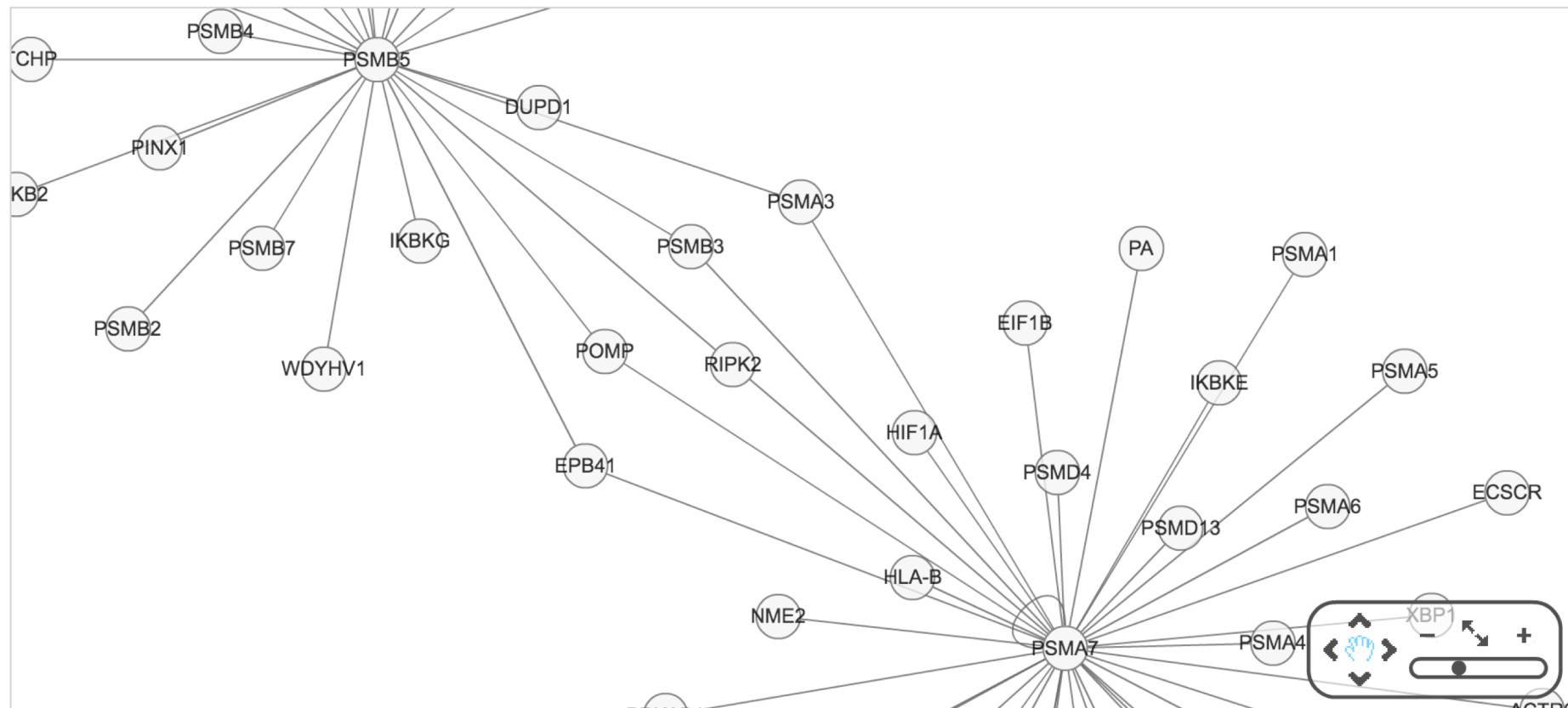
Interactions (112)

Interactors

Interaction Details

Graph

Network visualisation



112 binary interactions found for search term *PSB5_HUMAN PSA7_HUMAN*

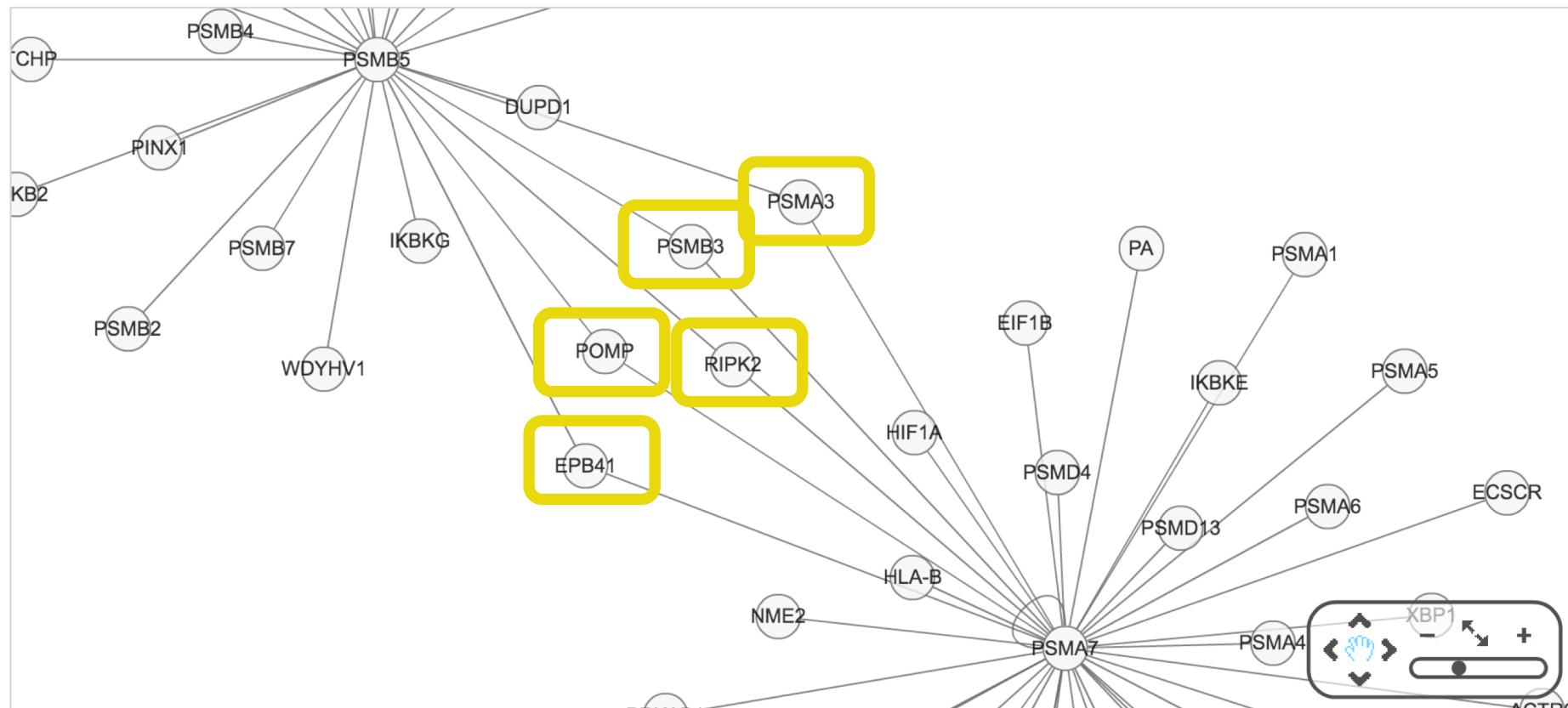
Interactions (112)

Interactors

Interaction Details

Graph

Network visualisation



Practical example

“You are a researcher working on the structure of the human proteasome, the main protein degradation machinery of the cell.

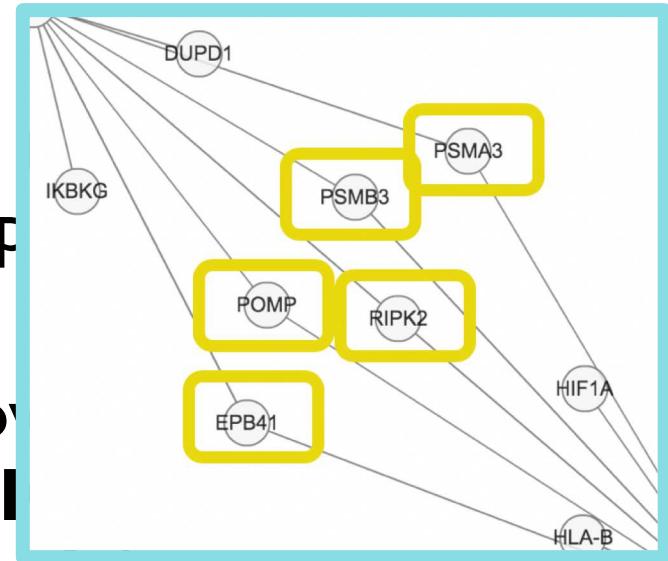
You are specially interested in knowing if the subunits B5 (UniProtKB id **PSB5_HUMAN**) and A7 (UniProtKB id **PSA7_HUMAN**) of the proteasome have been reported to be directly linked or if they are linked through a third protein.

You also want to know if the interactions found are **proven to be binary interactions**.”

Practical example

“You are a researcher working on the human proteasome, the main protein machinery of the cell.

You are specially interested in knowing which proteins interact with PSB5 (UniProtKB id **PSB5_HUMAN**) (UniProtKB id **PSB5AT_HUMAN**). You have been told that they are linked through 5 other proteins. They are linked through a third protein.



You also want to know if the interactions found are proven to be binary interactions.”

112 binary interactions found for search term PSB5_HUMAN PSA7_HUMAN

[Interactions \(112\)](#)[Interactors](#)[Interaction Details](#)[Graph](#)

- Include the spoke expanded co-complexes [?](#)

Your query also matches **1,549** interaction evidences from **6** other databases. [?](#)

[What is this view? ?](#)

Your query also matches **117** interaction evidences from **1** other IMEx databases. [?](#)

Customize view Select format to Download Download								
(1 of 6) 1 2 3 4 5 6 >> >>>								
Dts	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Interaction Detection Method	Interaction AC	Source Database	
	PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	two hybrid	EBI-696762	IntAct	
					two hybrid	EBI-696846	IntAct	
					two hybrid	EBI-1388227	IntAct	
					pull down	EBI-1388238	IntAct	
					pull down	EBI-1388404	IntAct	
					two hybrid	EBI-7660417 MINT-6176430 imex : IM-11502-35	MINT	
	PSMA7	O14818 EBI-603272	PSMA4	P25789 EBI-359310	two hybrid array	EBI-19768999 imex : IM-25472-46189	IntAct	
					two hybrid	EBI-696834	IntAct	

112 binary interactions found for search term PSB5_HUMAN PSA7_HUMAN

[Interactions \(112\)](#)[Interactors](#)[Interaction Details](#)[Graph](#)

- Include the spoke expanded co-complexes [?](#)

Your query also matches **1,549** interaction evidences from **6** other databases. [?](#)

[What is this view? ?](#)

Your query also matches **117** interaction evidences from **1** other IMEx databases. [?](#)

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(1 of 6) [|<](#) [<<](#) [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [>](#) [|>](#)

	Dts	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Interaction Detection Method	Interaction AC	Source Database
		PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	two hybrid	EBI-696762	IntAct
						two hybrid	EBI-696846	IntAct
						two hybrid	EBI-1388227	IntAct
						pull down	EBI-1388238	IntAct
						pull down	EBI-1388404	IntAct
						two hybrid	EBI-7660417 MINT-6176430 imex : IM-11502-35	MINT
		PSMA7	O14818 EBI-603272	PSMA4	P25789 EBI-359310	two hybrid array	EBI-19768999 imex : IM-25472-46189	IntAct
						two hybrid	EBI-696834	IntAct

112 binary interactions found for search term PSB5_HUMAN PSA7_HUMAN

Interactions (112) Interactors Interaction Details G

Include the spoke expanded co-complexes ?

Customize view Select format to Download

Dts	Molecule 'A'	Links 'A'	Molecule 'B'
1	PSMA7	O14818 EBI-603272	PSMA1
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Select: Minimal | Standard | Complete

Interaction Detection Method

First Author

Publication Identifier

Species 'A'

Species 'B'

Interaction Type

Source Database

Interaction AC

Confidence Value

Update

Action evidences from 6 other IMEx What is this view? ?

Action evidences from 1 other IMEx

Interaction AC	Source Database
EBI-696762	IntAct
EBI-696846	IntAct
EBI-1388227	IntAct
EBI-1388238	IntAct
EBI-1388404	IntAct
EBI-7660417	MINT
MINT-6176430	
imex : IM-11502-35	
FRT-10768000	IntAct

112 binary interactions found for search term PSB5_HUMAN PSA7_HUMAN

Interactions (112) Interactors Interaction Details G

Include the spoke expanded co-complexes ?

Customize view Select format to Download

Dts	Molecule 'A'	Links 'A'	Molecule 'B'
1	PSMA7	O14818 EBI-603272	PSMA1
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112			

Columns displayed

Select: Minimal | Standard | Complete

Interaction Detection Method

First Author

Publication Identifier

Species 'A'

Species 'B'

Interaction Type

Source Database

Interaction AC

Confidence Value

Update

Interaction evidences from 6 other IMEx sources

What is this view? ?

Interaction AC Source Database

Interaction AC	Source Database
EBI-696762	IntAct
EBI-696846	IntAct
EBI-1388227	IntAct
EBI-1388238	IntAct
EBI-1388404	IntAct
EBI-7660417	MINT
MINT-6176430	
imex : IM-11502-35	
EBI-10760000	

112 binary interactions found for search term PSB5_HUMAN PSA7_HUMAN

[Interactions \(112\)](#)[Interactors](#)[Interaction Details](#)[Graph](#)

- Include the spoke expanded co-complexes [?](#)

Your query also matches **1,549** interaction evidences from **6** other databases. [?](#)

[What is this view? ?](#)

Your query also matches **117** interaction evidences from **1** other IMEx databases. [?](#)

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(1 of 6) [1](#) [2](#) [3](#) [4](#) [5](#) [6](#) [>](#) [>>](#)

Dts	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Interaction Detection Method	Interaction Type	Interaction AC	Source Database
1	PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	two hybrid	physical association	E-I-696762	IntAct
2					two hybrid	physical association	E-I-696846	IntAct
3					two hybrid	physical association	E-I-1388227	IntAct
4					pull down	physical association	E-I-1388238	IntAct
5					pull down	physical association	E-I-1388404	IntAct
6					two hybrid	physical association	E-I-7660417 INT-6176430 imex : IM-11502-35	MINT

112 binary interactions found for search term PSB5_HUMAN PSA7_HUMAN

Interactions (112) Interactors Interaction Details Graph

- Include the spoke expanded co-complexes [?](#)

Your query also matches **1,549** interaction evidences from **6** other databases. [?](#)

[What is this view? ?](#)

Your query also matches **117** interaction evidences from **1** other IMEx databases. [?](#)

Customize view

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- MI-TAB 2.5
- MI-TAB 2.6
- MI-TAB 2.7
- MI-XML 2.5.3
- MI-XML 2.5.4
- MI-XML 2.5(HTML view)
- BioPAX (Level 3)
- BioPAX (Level 2)
- RDF/XML
- RDF/XML (Abbrev)
- RDF (N3)
- RDF (N-Triples)
- RDF (Turtle)
- XGMML (Cytoscape)

Download

(1 of 6) | < > | 1 2 3 4 5 6 | >> | > |

Dts	Molecule A	Interaction Detection Method	Interaction Type	Interaction AC	Source Database
16	PSMA7	two hybrid	physical association	EBI-696762	IntAct
593		two hybrid	physical association	EBI-696846	IntAct
2		two hybrid	physical association	EBI-1388227	IntAct
		pull down	physical association	EBI-1388238	IntAct
		pull down	physical association	EBI-1388404	IntAct
		two hybrid	physical association	EBI-7660417 MINT-6176430 imex : IM-11502-35	MINT

Example 2

- <https://www.ebi.ac.uk/training/online/course/intact-molecular-interactions-ebi/exercises/human-valosin-containing-protein-or-vcp>

