

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

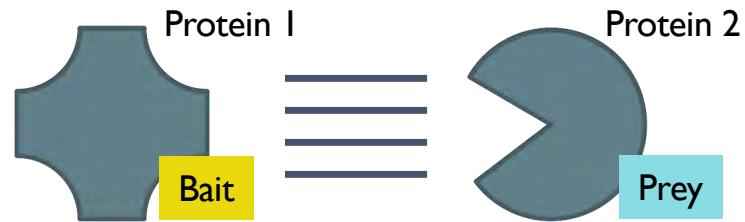
**EMBO PPI November 2018**  
Natasha Wood

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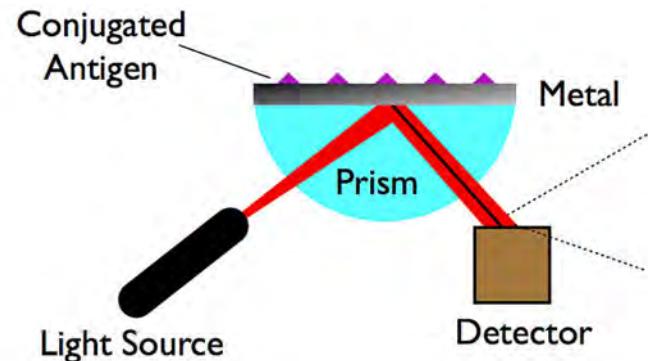
Web resources describing results of  
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# PPI Experiments

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

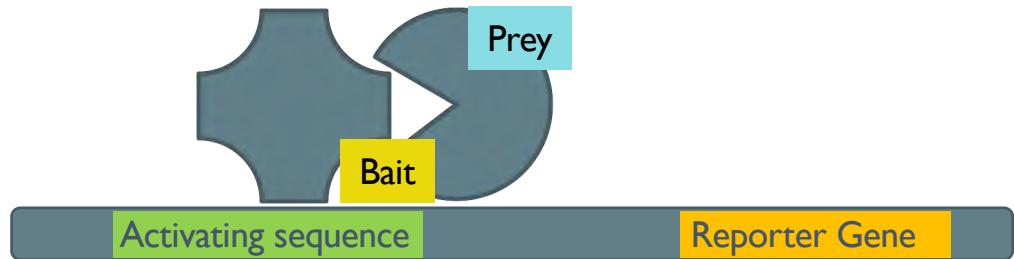


- Biophysical / Theoretical
  - Surface plasmon resonance (SPR)

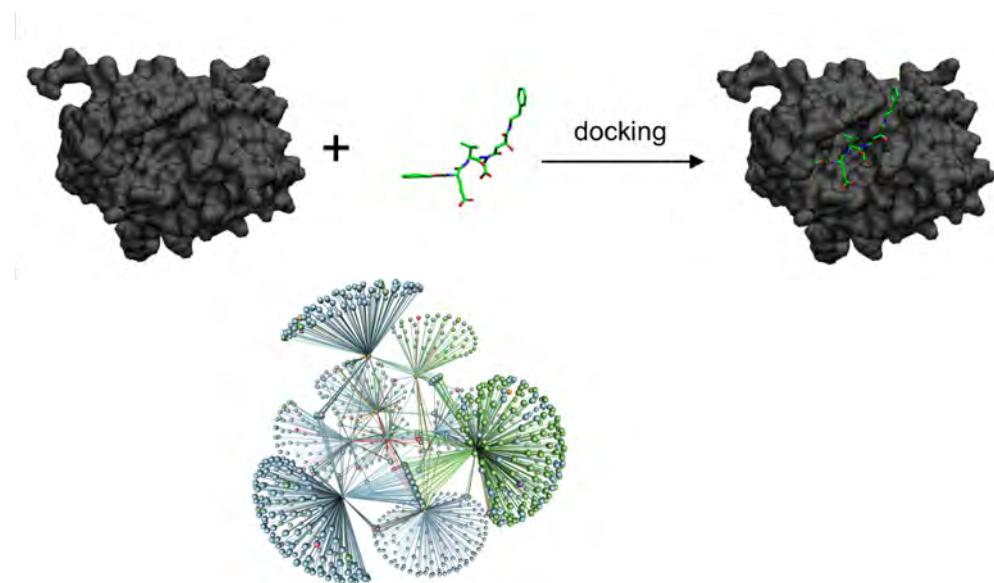


# PPI Experiments

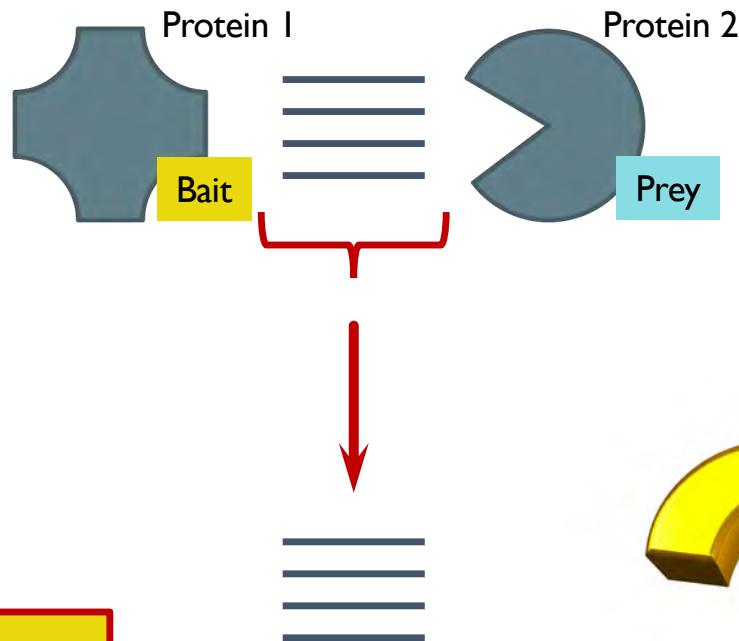
- Genetic
  - Yeast two-hybrid



- Computational
  - Docking
  - Network analysis



# PPI Experiments



Different  
interaction  
types



# PPI Types

- Weak or strong



- Direction



- Directional or Symmetrical



- Causality



- Permanent or Transient



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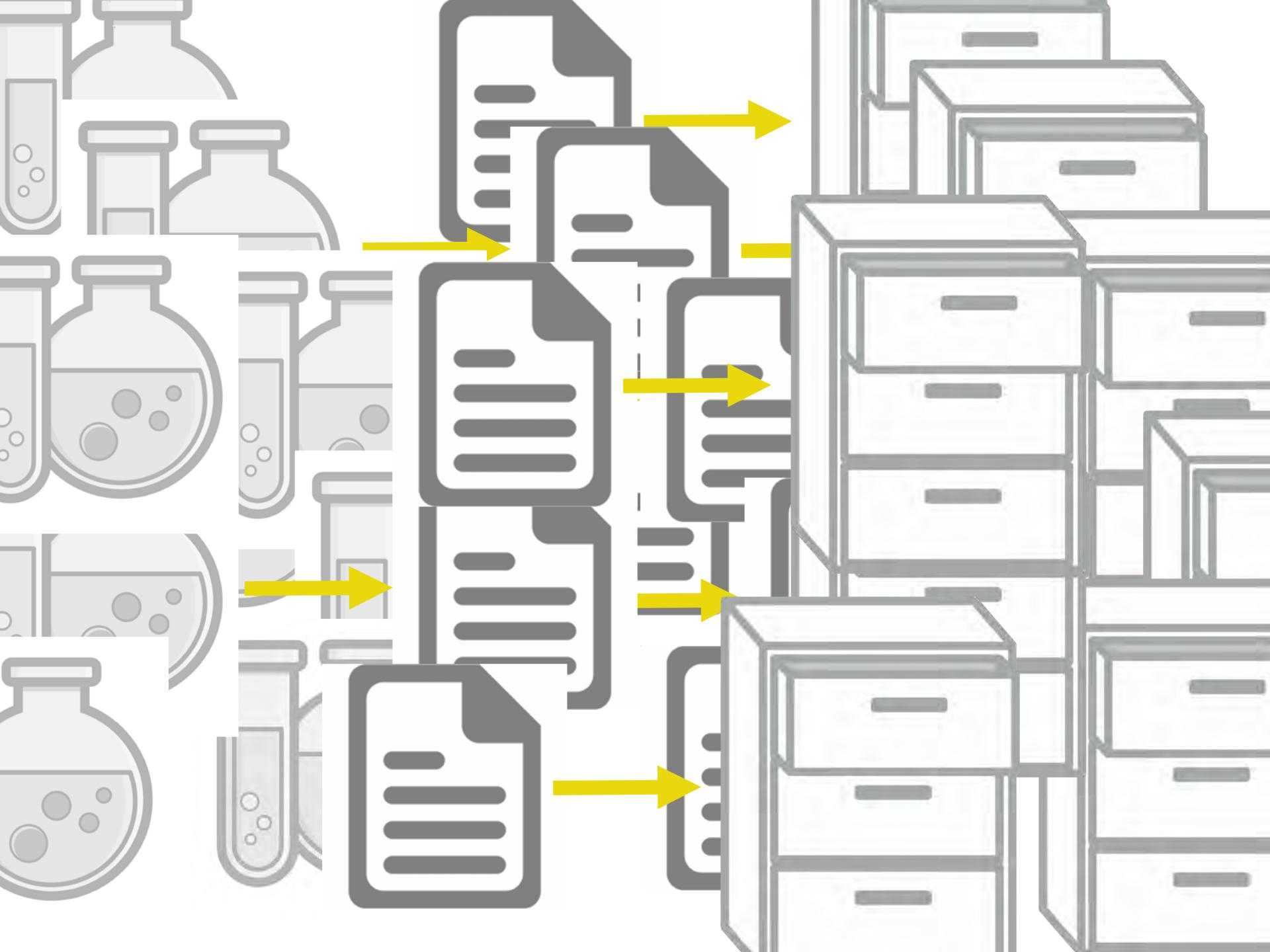
ppi





*Website of  
Protein-Protein  
Interactions*





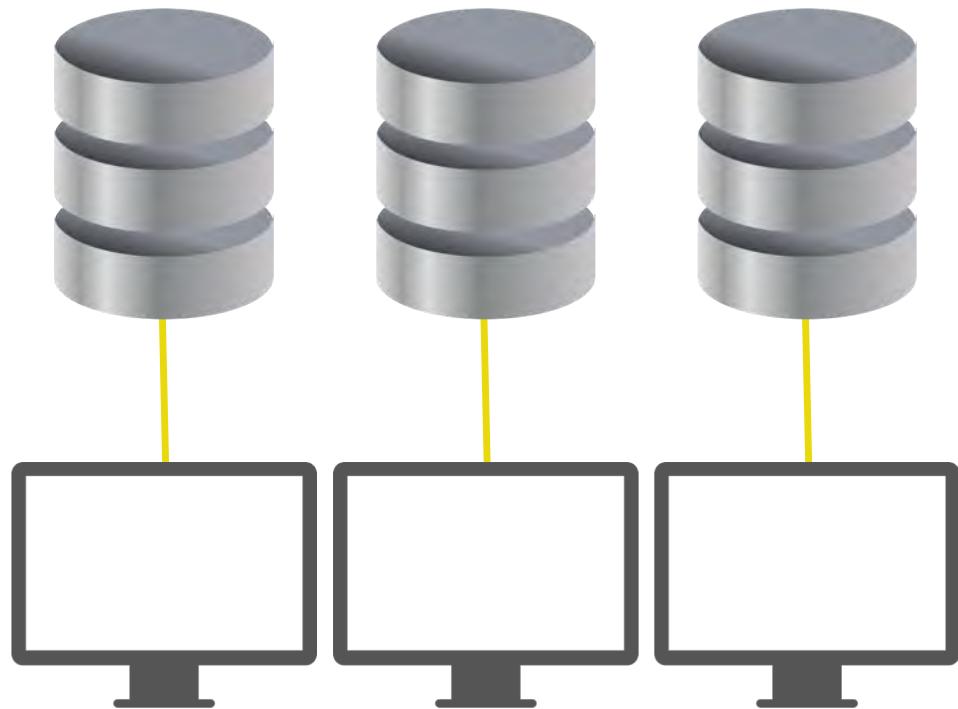
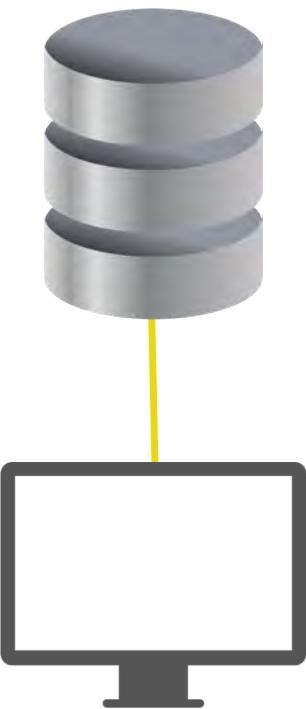
# Protein features (in PPIs)

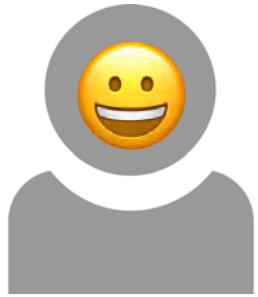
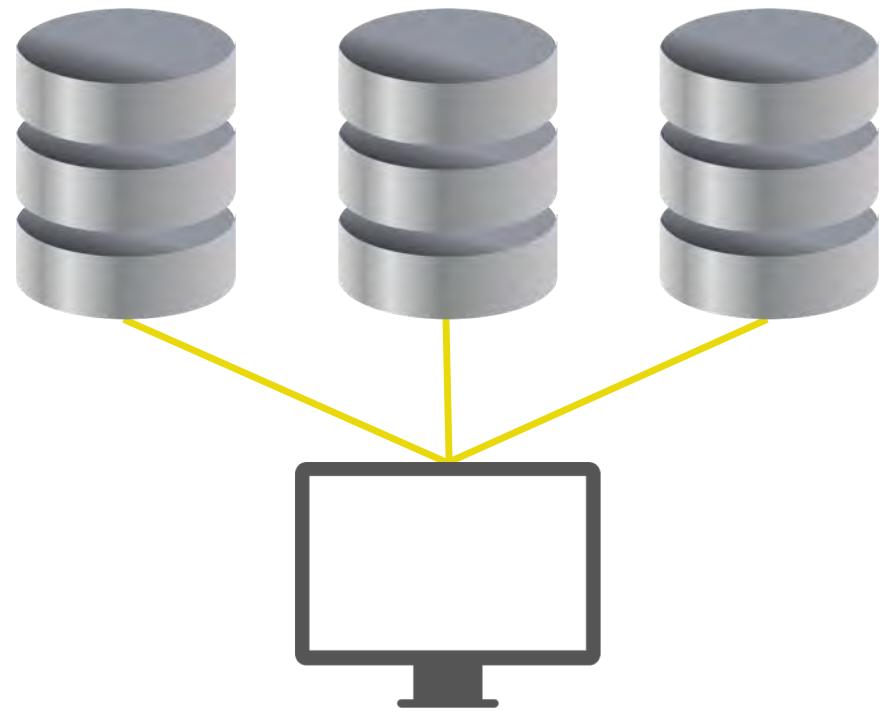
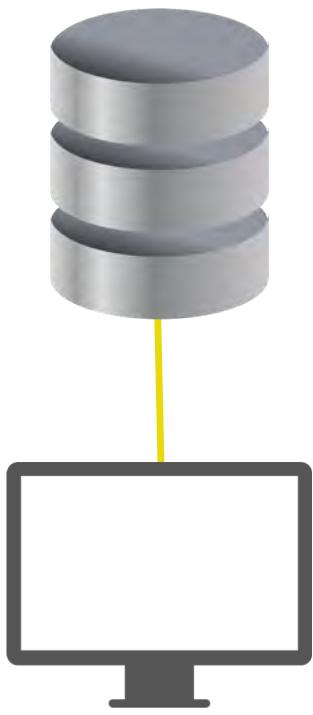


- Protein sequence and structure
  - Discover motifs that predict protein function
- Conserved sequences / evolutionary history
  - Identify key regulatory residues
- Expression profile
  - Regulation of expression and cell-type specificity
- Intracellular localisation
  - Implies certain protein function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

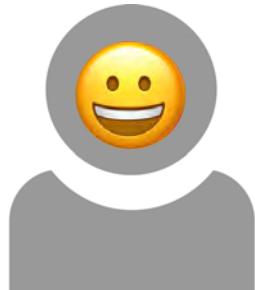
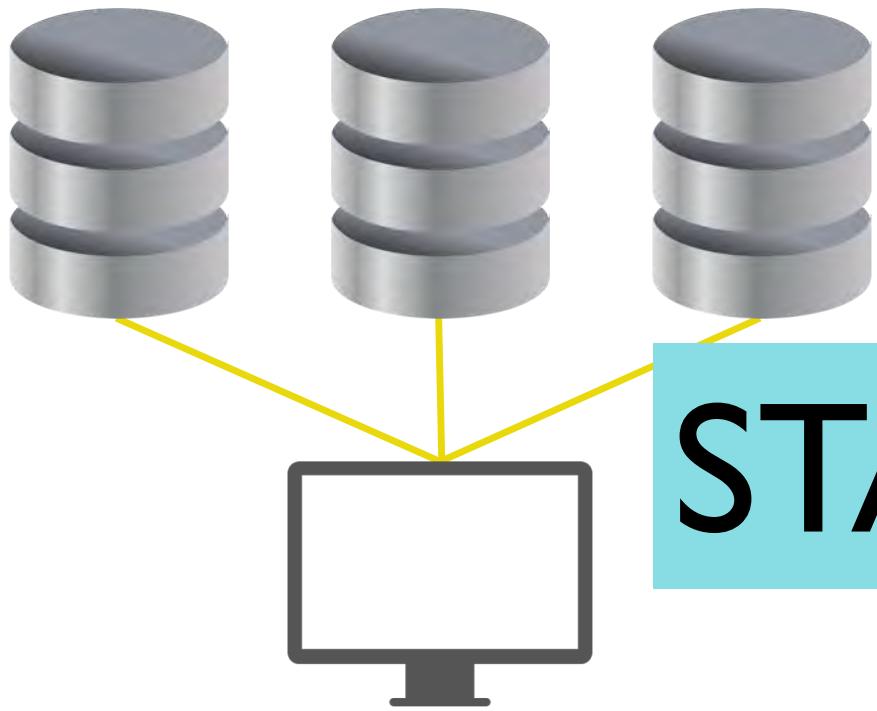
# PPIs: what the researcher wants

- 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



US



AU

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

EMBL-EBI

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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. 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 01 Nov 2018 09:07

- 216 ontologies
- 5,526,032 terms
- 19,119 properties
- 479,516 individuals

### Tweets by @EBIOLS

EBISPORT OLS Retweeted

Simon Jupp @simonjupp We're looking to hire a senior developer to join us at @emblebi working on @EBIOLS and our full stack of #ontology services. DM me for more info embl.de/jobs/searchjob...

Aug 13, 2018

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

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Tweets by @EBIOLS

EBISPORT OLS Retweeted

Simon Jupp @simonjupp

We're looking to hire a senior developer to join us at @emblebi working on @EBIOLS and our full stack of #ontology services. DM me for more info embl.de/jobs/searchjob...

Aug 13, 2018

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

# Controlled Vocabularies

OLS > Molecular Interactions Controlled Vocabulary  > MI:0000 

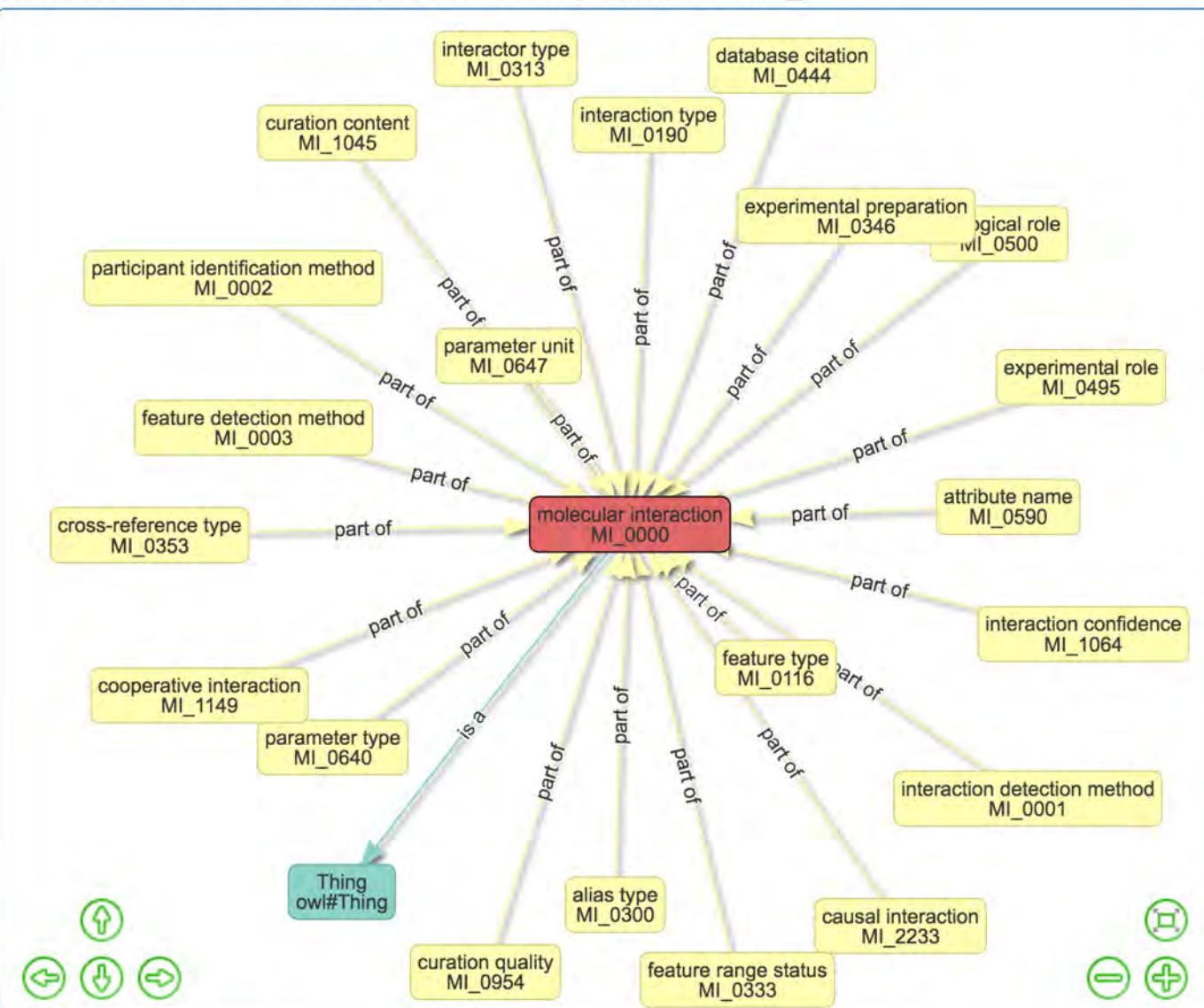
## molecular interaction

 [http://purl.obolibrary.org/obo/MI\\_0000](http://purl.obolibrary.org/obo/MI_0000) 

Search MI



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



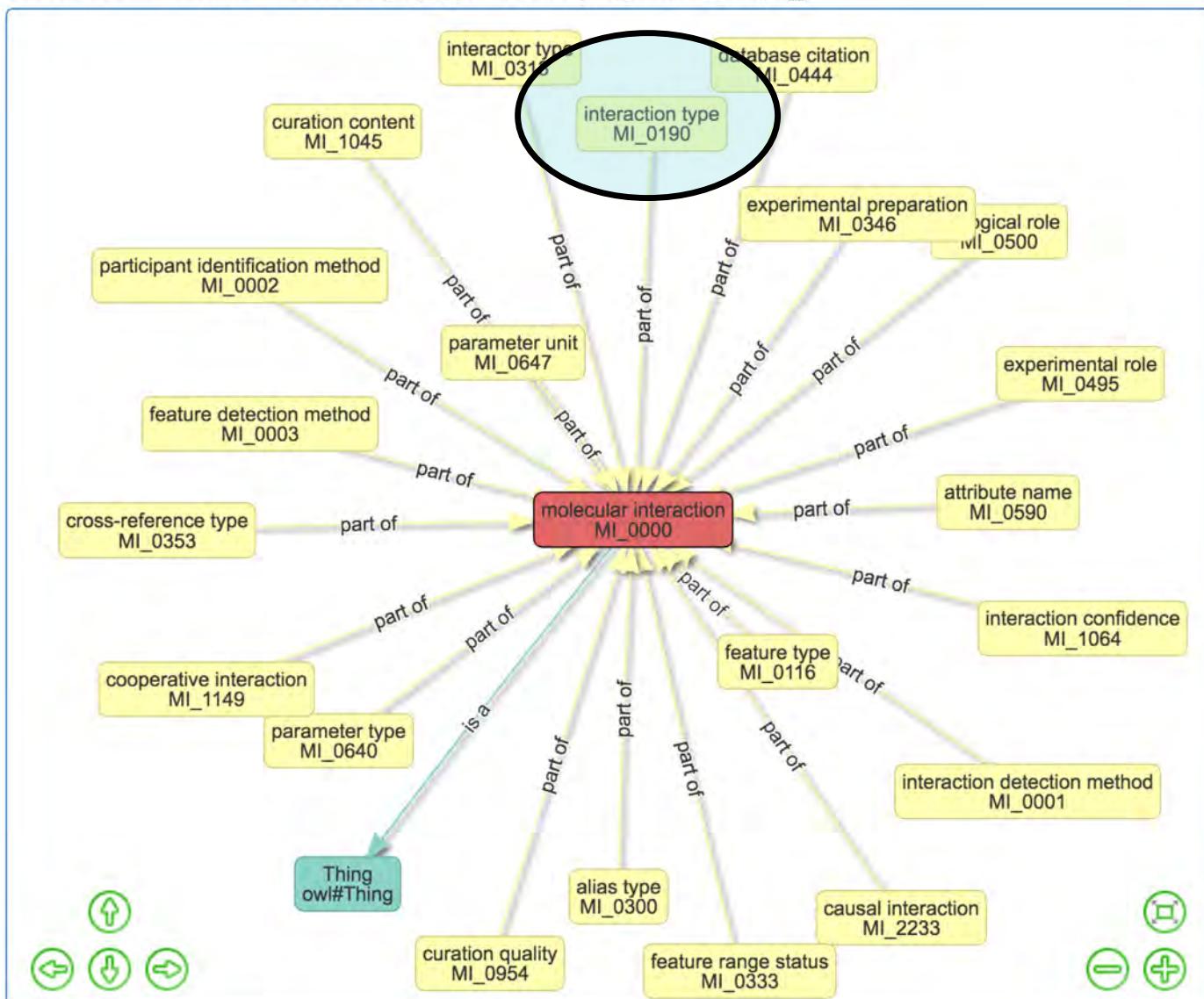
## LEGEND

Relationship	Color	Visibility
Extended nodes (*)	<span style="background-color: red;">■</span>	-
is a	<span style="background-color: teal;">■</span>	<input checked="" type="checkbox"/>
part of	<span style="background-color: yellow;">■</span>	<input checked="" type="checkbox"/>
Select/Deselect all	<span style="background-color: lightgray;">■</span>	<input type="checkbox"/>

## List of extended nodes (\*):

- molecular interaction (MI\_0000)





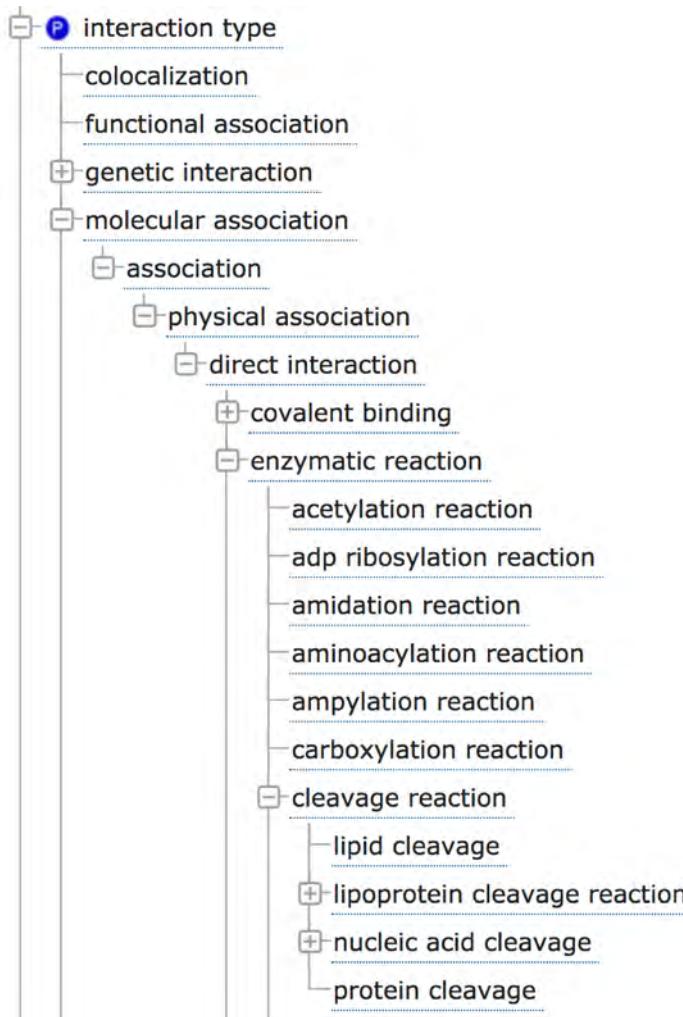
## LEGEND

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"/>

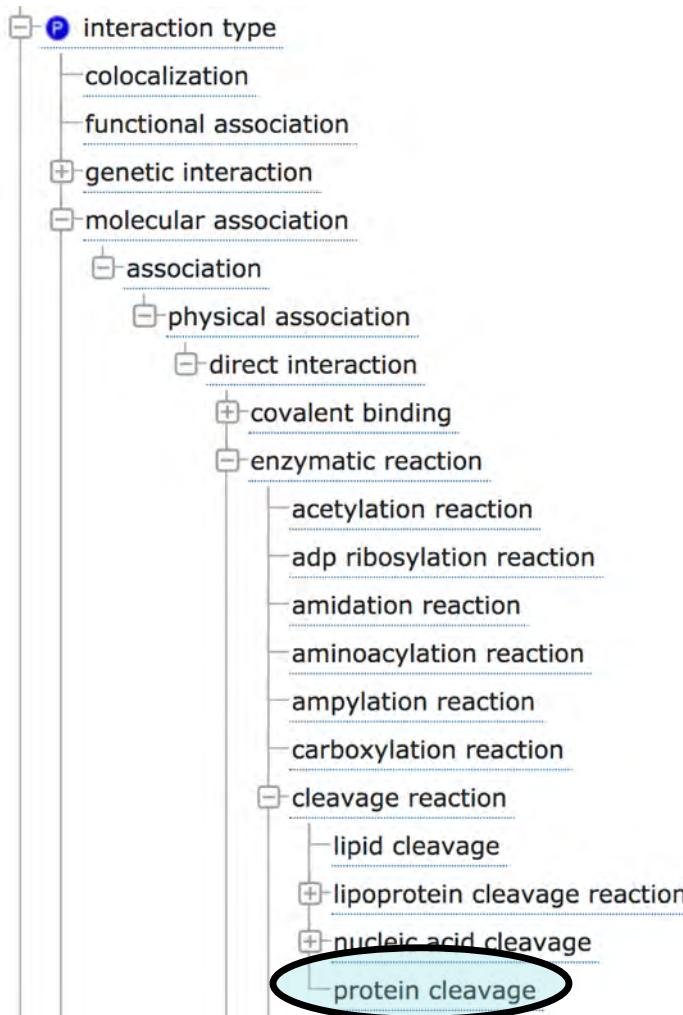
## List of extended nodes (\*):

- molecular interaction (MI\_0000)

# 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

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- Support for implementation of the standard in publicly available tools

# PSI

## 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 Mass Spectrometry	MIAPAR	1.0.0	MITAB	2.7	PAR CV	n/a
	Mass spectrometry (MIAPE-MS)	2.98	mzML	1.1.0		
Group charter Proteomics Informatics	Identification (MIAPE-MSI)	1.1	TraML	1.0.0	PSI-MS	4.0.15
	Mass spectrometry Quantification (MIAPE-Quant)	1.0	mzData (deprecated)	1.05		
Group charter Quality Control			mzIdentML	1.2.0	XLMOD	1.1.0
			mzQuantML	1.0.1		
Group charter Protein separations			mzTab	1.0.0	sepCV	1.0.0
	Gel electrophoresis (MIAPE-GE)	1.4	proBed	1.0.0		
(inactive)	Gel informatics (MIAPE-GI)	1.0	proBAM	1.0.0		
	Column chromatography (MIAPE-CC)	1.1	PEFF (under review)			
	Capillary electrophoresis (MIAPE-CE)	0.9.3	qcML			
	Phosphoproteomics (MIASSPE)	0.9.	(PSI spec. under construction)			

# PSI

## HUPO-PSI Working groups and Outputs

Working Groups	Guidelines	v.	Formats	v.	Controlled Vocabularies	v.
Molecular Interactions	MIMIx	1.1.1	PSI-MI XML	2.5.4	PSI-MI CV	2.5.0
	MIABE	1.0.0	PSI-MI XML	3.0.0		
Group charter Mass Spectrometry	MIAPAR	1.0.0	MIAB	2.7	PAR CV	n/a
	Mass spectrometry (MIAPE-MS)	2.98	mzML	1.1.0		
Group charter Proteomics Informatics	Identification (MIAPE-MSI)	1.1	TraML	1.0.0	PSI-MS	4.0.15
	Mass spectrometry Quantification (MIAPE-Quant)	1.0	mzData (deprecated)	1.05		
Group charter Quality Control			mzIdentML	1.2.0	XLMOD	1.1.0
			mzQuantML	1.0.1		
Group charter Protein separations			mzTab	1.0.0	sepCV	1.0.0
			proBed	1.0.0		
(inactive)			proBAM	1.0.0		
			PEFF (under review)			
			qcML			
			(PSI spec. under construction)			
	Gel electrophoresis (MIAPE-GE)	1.4	GelML	1.1.0		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**

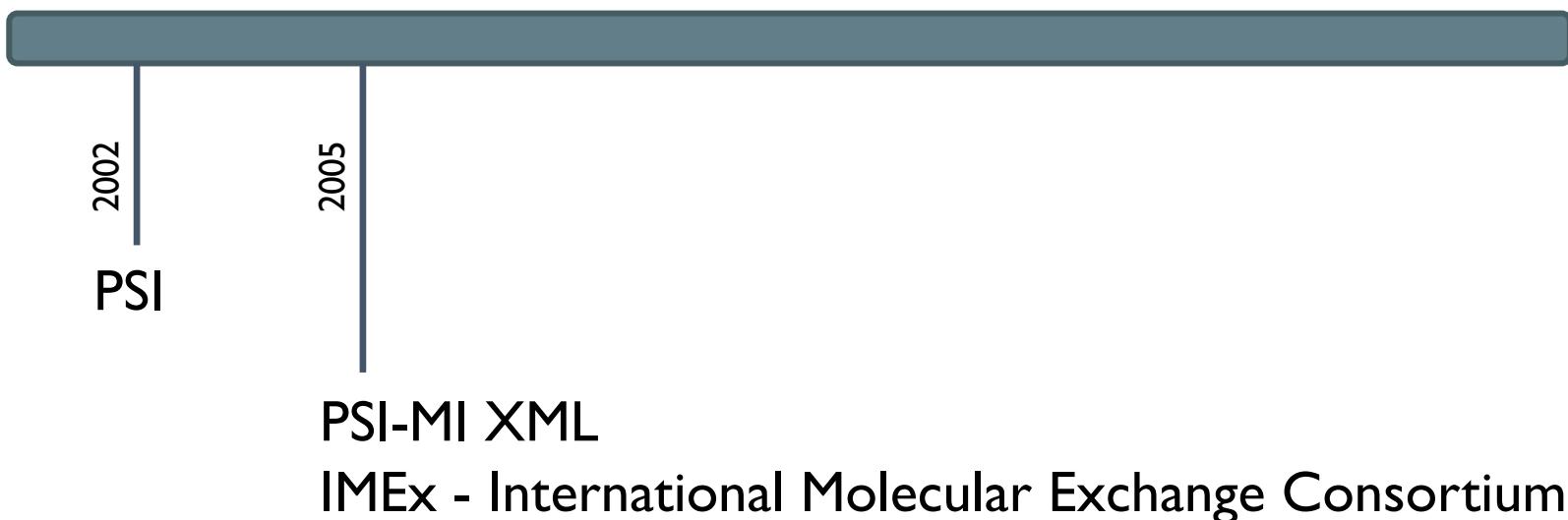
Available for use now, estimated formal release - Spring 2016

# 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-I...

Software

Open Access

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

Samuel Kerrien<sup>\*1</sup>, Sandra Orchard<sup>1</sup>, Luisa Montecchi-Palazzi<sup>1</sup>,  
Bruno Aranda<sup>1</sup>, Antony F Quinn<sup>1</sup>, Nisha Vinod<sup>1</sup>, Gary D Bader<sup>2,3</sup>,  
Ioannis Xenarios<sup>4</sup>, Jérôme Wojcik<sup>4</sup>, David Sherman<sup>5</sup>, Mike Tyers<sup>3</sup>,  
John J Salama<sup>6</sup>, Susan Moore<sup>6,7</sup>, Arnaud Ceol<sup>8</sup>, Andrew Chatr-aryamontri<sup>8</sup>,  
Matthias Oesterheld<sup>9</sup>, Volker Stümpflen<sup>9</sup>, Lukasz Salwinski<sup>10</sup>,  
Jason Nerothin<sup>10</sup>, Ethan Cerami<sup>11</sup>, Michael E Cusick<sup>12</sup>, Marc Vidal<sup>12</sup>,  
Michael Gilson<sup>13</sup>, John Armstrong<sup>14</sup>, Peter Woollard<sup>14</sup>, Christopher Hogue<sup>15</sup>,  
David Eisenberg<sup>10</sup>, Gianni Cesareni<sup>8</sup>, Rolf Apweiler<sup>1</sup> and  
Henning Hermjakob<sup>1</sup>

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

Email: Samuel Kerrien - [skerrien@ebi.ac.uk](mailto:skerrien@ebi.ac.uk); Sandra Orchard - [orchard@ebi.ac.uk](mailto:orchard@ebi.ac.uk); Luisa Montecchi-Palazzi - [luisa@ebi.ac.uk](mailto:luisa@ebi.ac.uk); Bruno Aranda - [baranda@ebi.ac.uk](mailto:baranda@ebi.ac.uk); Antony F Quinn - [quinn@ebi.ac.uk](mailto:quinn@ebi.ac.uk); Nisha Vinod - [nvind@ebi.ac.uk](mailto:nvind@ebi.ac.uk); Gary D Bader - [bader@cbio.mskcc.org](mailto:bader@cbio.mskcc.org); Ioannis Xenarios - [ioannis.xenarios@isb-sib.ch](mailto:ioannis.xenarios@isb-sib.ch); Jérôme Wojcik - [Jerome.Wojcik@serono.com](mailto:Jerome.Wojcik@serono.com); David Sherman - [david.sherman@enseirb.fr](mailto:david.sherman@enseirb.fr); Mike Tyers - [tyers@mshri.on.ca](mailto:tyers@mshri.on.ca); John J Salama - [jj.salama@gmail.com](mailto:jj.salama@gmail.com); Susan Moore - [susanmoore197@hotmail.com](mailto:susanmoore197@hotmail.com); Arnaud Ceol - [arnaud.ceol@uniroma2.it](mailto:arnaud.ceol@uniroma2.it); Andrew Chatr-aryamontri - [aryamontri@hotmail.com](mailto:aryamontri@hotmail.com); Matthias Oesterheld - [m.oesterheld@gsf.de](mailto:m.oesterheld@gsf.de); Volker Stümpflen - [v.stuempflen@gsf.de](mailto:v.stuempflen@gsf.de); Lukasz Salwinski - [lukasz@mbl.ucla.edu](mailto:lukasz@mbl.ucla.edu); Jason Nerothin - [jason@mbl.ucla.edu](mailto:jason@mbl.ucla.edu); Ethan Cerami - [cerami@cbio.mskcc.org](mailto:cerami@cbio.mskcc.org); Michael E Cusick - [Michael\\_cusick@dfci.harvard.edu](mailto:Michael_cusick@dfci.harvard.edu); Marc Vidal - [marc\\_vidal@dfci.harvard.edu](mailto:marc_vidal@dfci.harvard.edu); Michael Gilson - [gilson@umbi.umd.edu](mailto:gilson@umbi.umd.edu); John Armstrong - [john.armstrong@gsk.com](mailto:john.armstrong@gsk.com); Peter Woollard - [peter.m.woollard@gsk.com](mailto:peter.m.woollard@gsk.com); Christopher Hogue - [cwhogue@gmail.com](mailto:cwhogue@gmail.com); David Eisenberg - [david@mbl.ucla.edu](mailto:david@mbl.ucla.edu); Gianni Cesareni - [cesareni@uniroma2.it](mailto:cesareni@uniroma2.it); Rolf Apweiler - [apweiler@ebi.ac.uk](mailto:apweiler@ebi.ac.uk); Henning Hermjakob - [hhe@ebi.ac.uk](mailto:hhe@ebi.ac.uk)

\* Corresponding author

Published: 9 October 2007

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

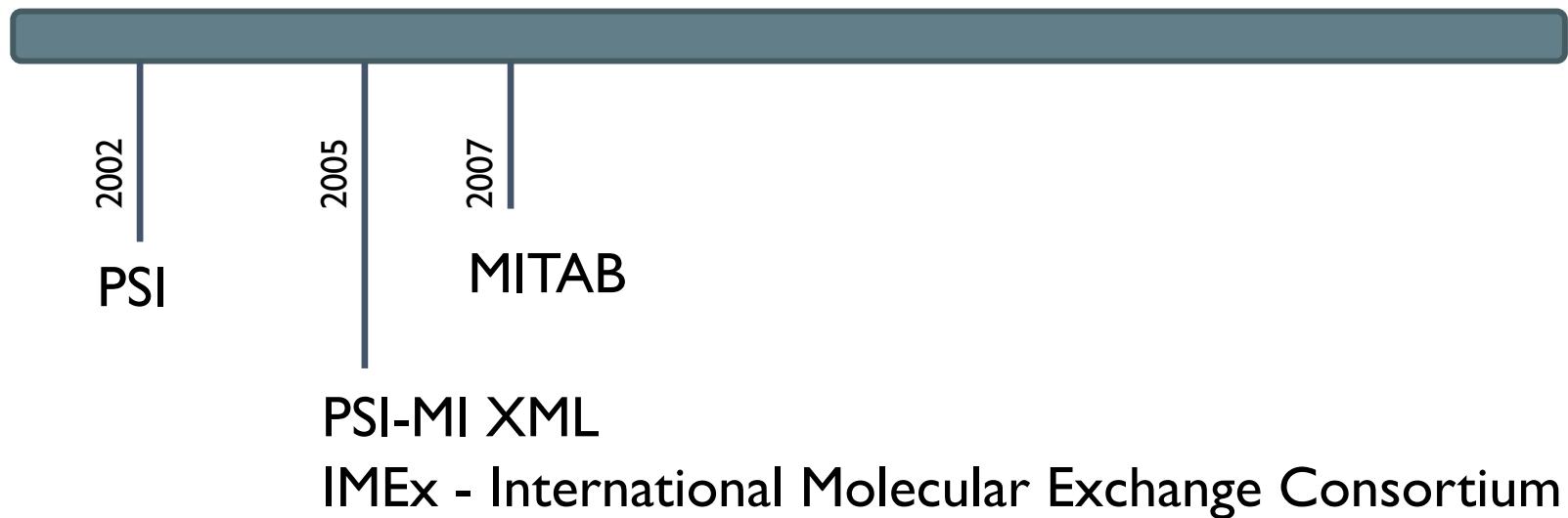
Received: 19 February 2007

Accepted: 9 October 2007

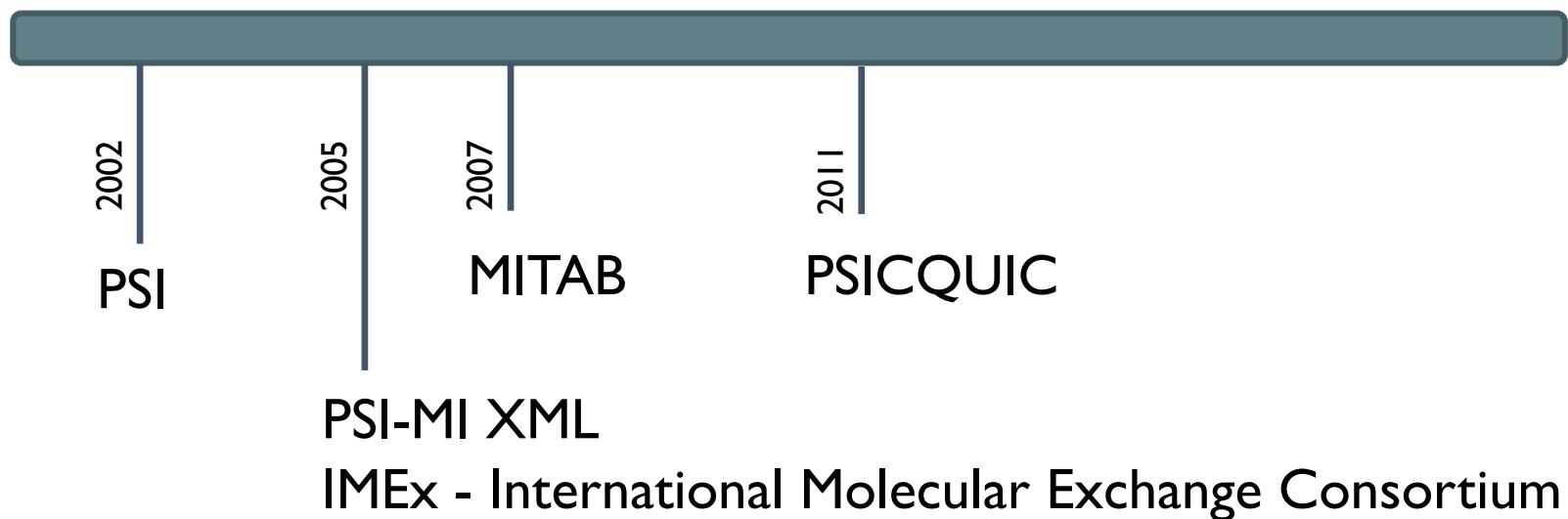
# P-Standards-I...

- 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: **10,398,970** Interactions from **33** PSICQUIC Services, of which **9** are currently down.

Filter:

Name	Status	Interactions	Version	URLs
iRefIndex	<span>●</span>	2,338,337	1.3.14	SOAP: <a href="http://irefindex.vib.be/webservices/psicquic">http://irefindex.vib.be/webservices/psicquic</a> REST: <a href="http://irefindex.vib.be/webservices/current/search/">http://irefindex.vib.be/webservices/current/search/</a>  <a href="#">REST example</a>
BioGrid	<span>●</span>	1,513,281	1.3.14	SOAP: <a href="http://tyersrest.tyerslab.com:8805/psicquic/webservices/psicquic">http://tyersrest.tyerslab.com:8805/psicquic/webservices/psicquic</a> REST: <a href="http://tyersrest.tyerslab.com:8805/psicquic/webservices/current/search/">http://tyersrest.tyerslab.com:8805/psicquic/webservices/current/search/</a>  <a href="#">REST example</a>
mentha	<span>●</span>	1,272,096	1.3.13	SOAP: <a href="http://mentha.uniroma2.it:9090/psicquic/webservices/psicquic">http://mentha.uniroma2.it:9090/psicquic/webservices/psicquic</a> REST: <a href="http://mentha.uniroma2.it:9090/psicquic/webservices/current/search/">http://mentha.uniroma2.it:9090/psicquic/webservices/current/search/</a>  <a href="#">REST example</a>
BindingDB	<span>●</span>	1,011,029	v1.3	SOAP: <a href="http://bindingdb.org/psicquic-ws">http://bindingdb.org/psicquic-ws</a> REST: <a href="http://bindingdb.org/psicquic-ws/webservices/psicquic/current/search/">http://bindingdb.org/psicquic-ws/webservices/psicquic/current/search/</a>  <a href="#">REST example</a>
I2D	<span>●</span>	817,915	1.1.6	SOAP: <a href="http://ophid.utoronto.ca/psicquic-ws/webservices/psicquic">http://ophid.utoronto.ca/psicquic-ws/webservices/psicquic</a> REST: <a href="http://ophid.utoronto.ca/psicquic-ws/webservices/current/search/">http://ophid.utoronto.ca/psicquic-ws/webservices/current/search/</a>  <a href="#">REST example</a>
IMEx	<span>●</span>	686,747	1.3.14	SOAP: <a href="http://www.ebi.ac.uk/Tools/webservices/psicquic/imex/webservices/psicquic">http://www.ebi.ac.uk/Tools/webservices/psicquic/imex/webservices/psicquic</a> REST: <a href="http://www.ebi.ac.uk/Tools/webservices/psicquic/imex/webservices/current/search/">http://www.ebi.ac.uk/Tools/webservices/psicquic/imex/webservices/current/search/</a>  <a href="#">REST example</a>
IntAct	<span>●</span>	661,649	1.3.14	SOAP: <a href="http://www.ebi.ac.uk/Tools/webservices/psicquic/intact/webservices/psicquic">http://www.ebi.ac.uk/Tools/webservices/psicquic/intact/webservices/psicquic</a> REST: <a href="http://www.ebi.ac.uk/Tools/webservices/psicquic/intact/webservices/current/search/">http://www.ebi.ac.uk/Tools/webservices/psicquic/intact/webservices/current/search/</a>

# PSICQUIC View

[Input Form](#) [Browse](#) [Help](#)

[Search](#)

[Feedback](#)

[Input Form > Browse](#)

## 10,398,970 binary interactions found for search term \*

<a href="#"> APID Interactomes</a>	<a href="#"> BAR - 115,325</a>	<a href="#"> bhf-ucl - 4,019</a>	<a href="#"> BIND</a>
<a href="#"> BindingDB - 1,011,029</a>	<a href="#"> BioGrid - 1,513,281</a>	<a href="#"> ChEMBL - 628,504</a>	<a href="#"> DIP</a>
<a href="#"> DIP-IMEx</a>	<a href="#"> DrugBank</a>	<a href="#"> EBI-GOA-miRNA - 2,852</a>	<a href="#"> EBI-GOAnonIntAct - 69,134</a>
<a href="#"> GeneMANIA</a>	<a href="#"> HPIDb - 5,046</a>	<a href="#"> I2D - 817,915</a>	<a href="#"> IMEx - 686,747</a>
<a href="#"> InnateDB - 33,295</a>	<a href="#"> InnateDB-All - 578,350</a>	<a href="#"> IntAct - 661,649</a>	<a href="#"> Interoporc</a>
<a href="#"> iRefIndex - 2,338,337</a>	<a href="#"> MatrixDB - 128,545</a>	<a href="#"> MBInfo - 638</a>	<a href="#"> mentha - 1,272,096</a>
<a href="#"> MINT - 123,906</a>	<a href="#"> MPIDB - 1,751</a>	<a href="#"> Reactome - 141,996</a>	<a href="#"> Reactome-Fls - 209,988</a>
<a href="#"> Spike</a>	<a href="#"> TopFind</a>	<a href="#"> UniProt - 17,256</a>	<a href="#"> VirHostNet - 28,814</a>
<a href="#"> ZINC - 8,497</a>			

### Status of the service

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

**10,398,970 selected interactions**

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

# PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe



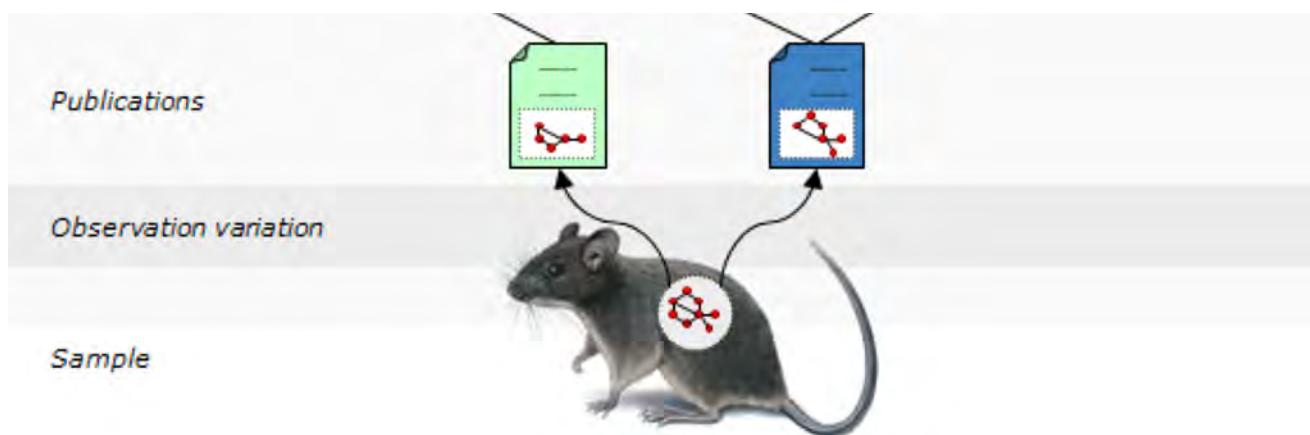
# PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe



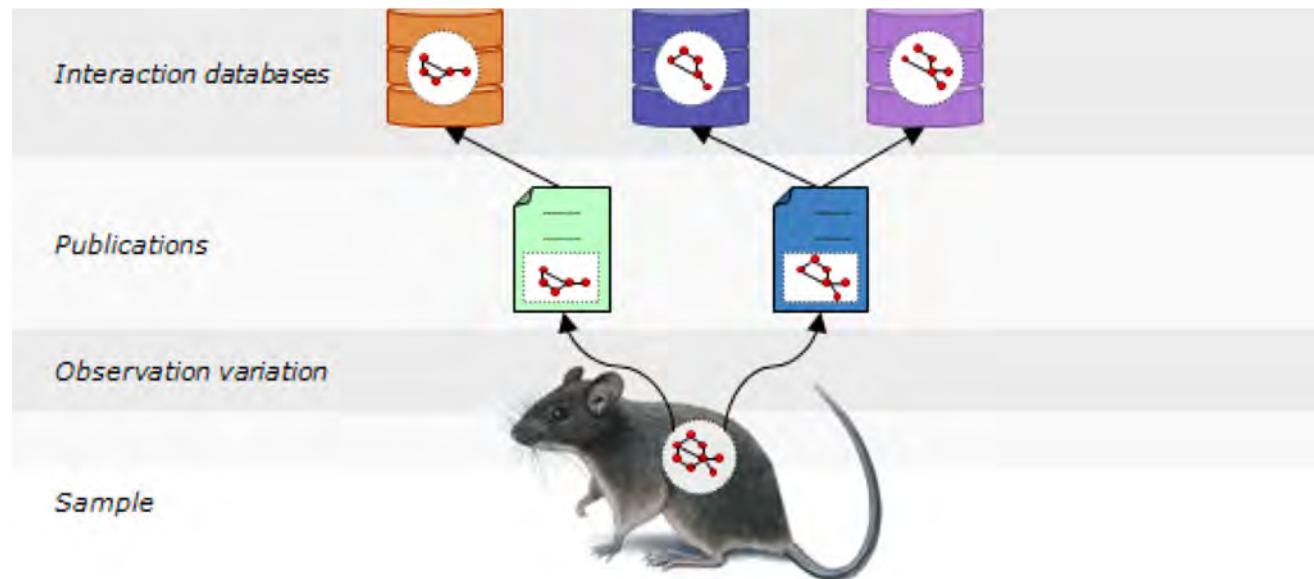
*Observation variation*

*Sample*

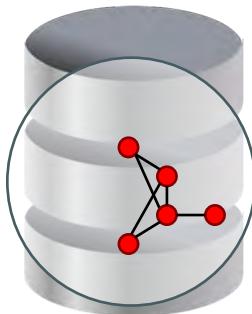
# PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe



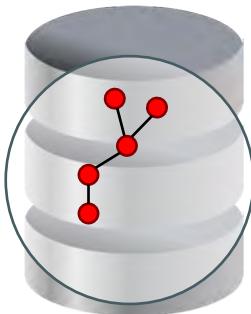
# PSICQUIC: The Proteomics Standard Initiative Common QUery InterfaCe



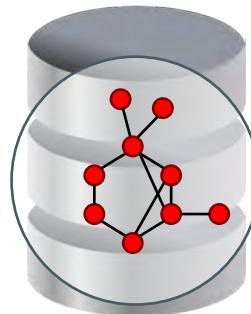
Interaction  
Databases

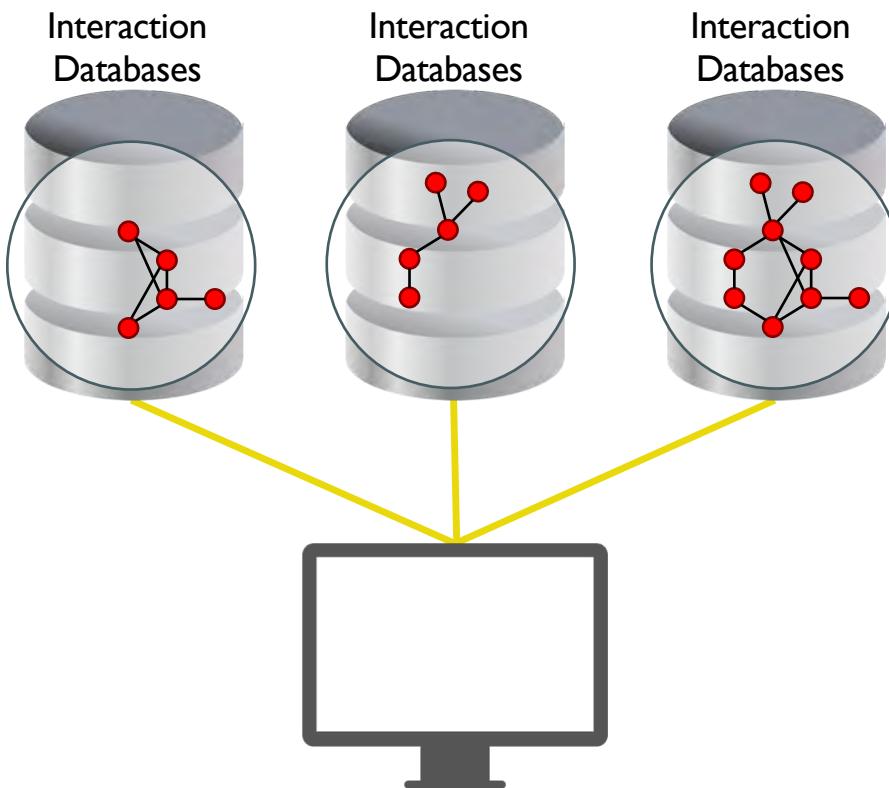


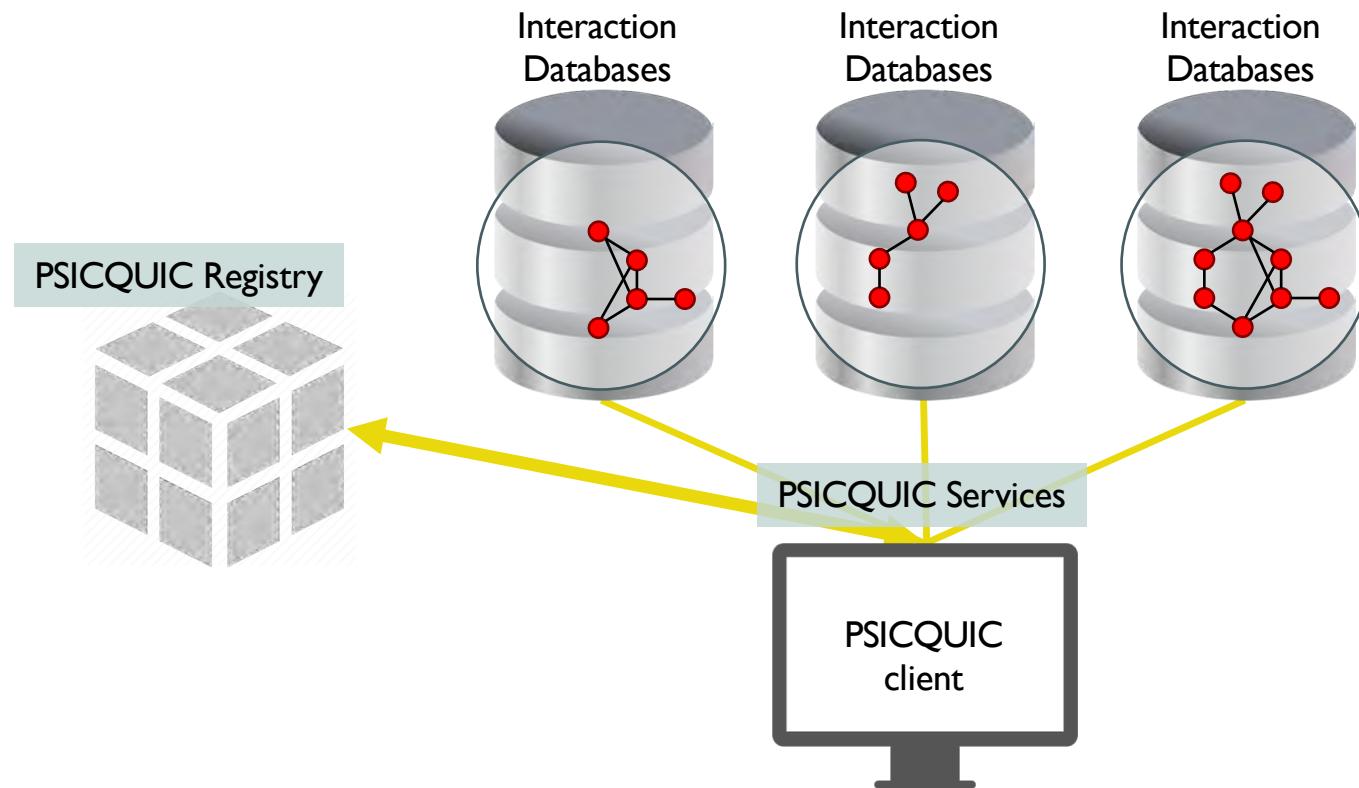
Interaction  
Databases

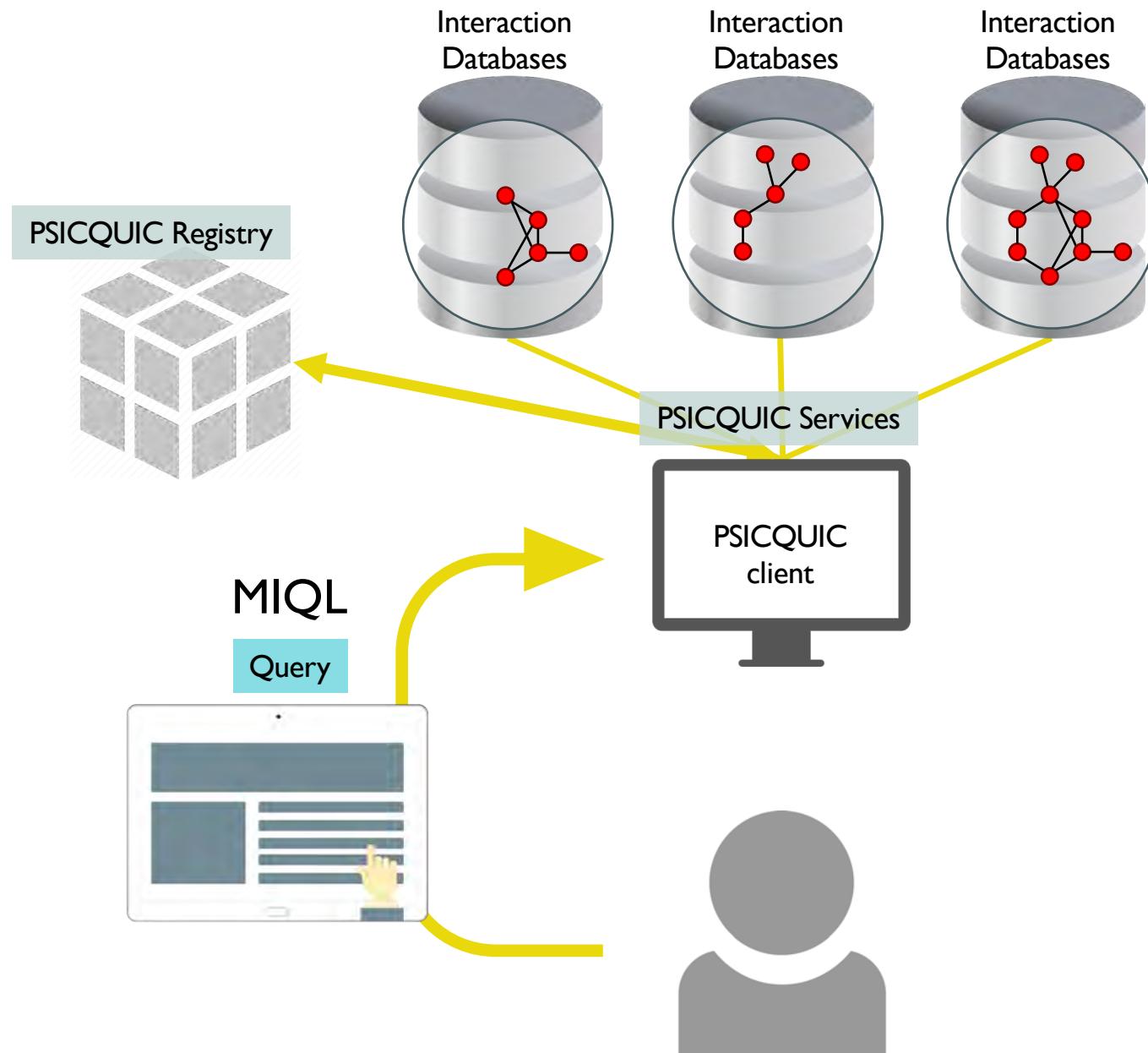


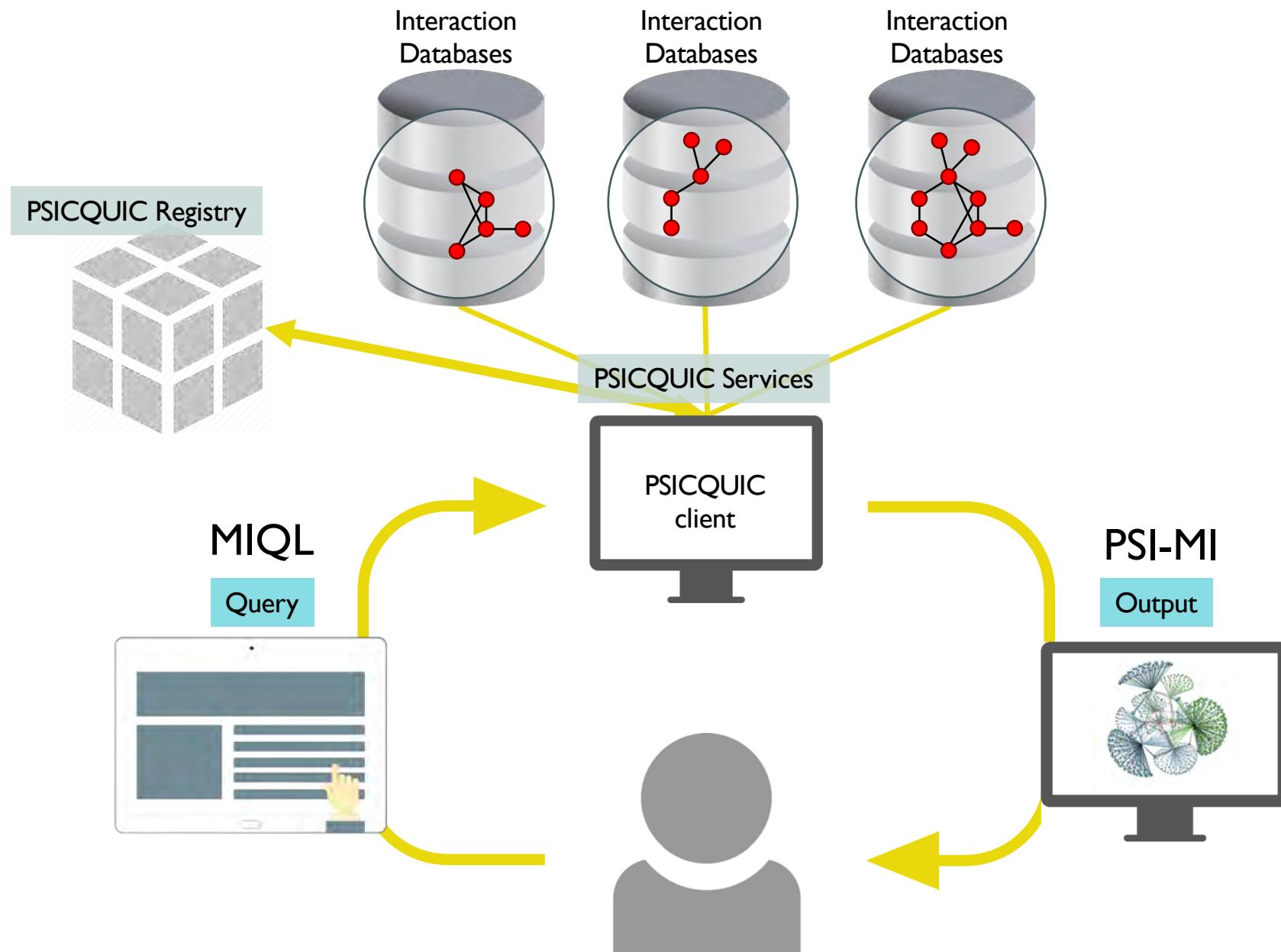
Interaction  
Databases

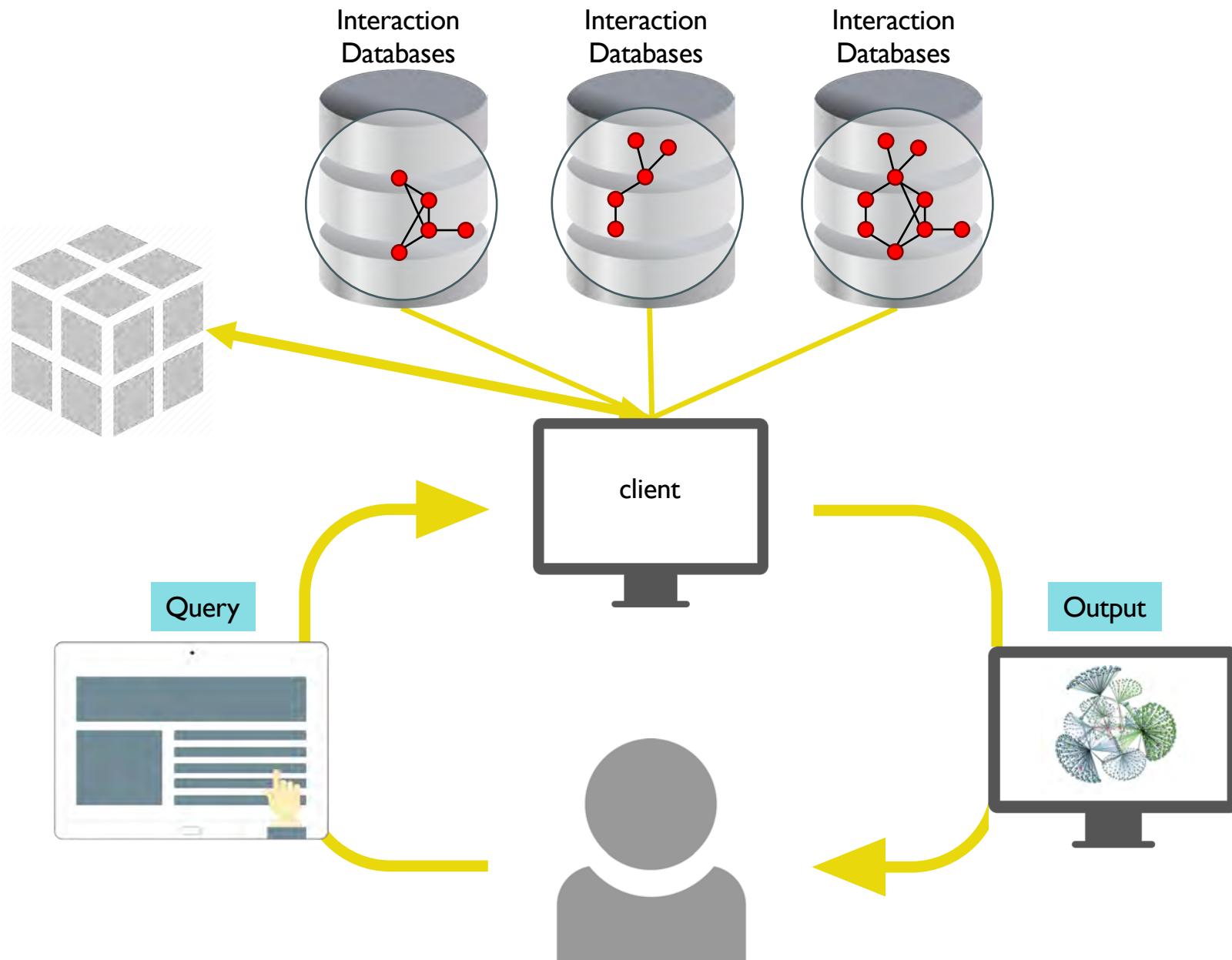












Web resources describing results of  
PPI experiments,  
design of such databases,  
minimal information to describe PPIs

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

News archive

# Web resources

## Protein-protein interaction databases (8)

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



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Search



Search  
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Featured  
Datasets

By Gene

By Publication

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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

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@complexportal

Read our latest paper describing the content of the @complexportal.  
[europepmc.org/abstract/MED/3...](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6370003/)

Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes

Hérgi H M Miklósi , Hanna Bye Al-Jarbi, László Györgyi, Zsuzsanna Hammann, Ágota Horváthová, Flávio Meloche, Luisa Perletti, Daniel Wiklund, Miquel Rodríguez López, Alibéba Törökne, ... [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]

[Help][LOGIN]

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[SEARCH](#)

[SUBMIT](#)

[Software](#)

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## 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

<a href="#">NEWS</a>	Announcements about the most recent additions and changes to the database.
<a href="#">REGISTRATION/ ACCOUNT</a>	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 <a href="#">Terms of Use</a> for further details.
<a href="#">STATISTICS</a>	Detailed information about the current state of the database as well as some statistics on server usage.
<a href="#">SATELLITES</a>	DIP-related projects, such as <a href="#">DLRP</a> and <a href="#">JDIP</a> .
<a href="#">SERVICES</a>	DIP-derived services.
<a href="#">ARTICLES</a>	DIP in press. Both, papers published on DIP as well as a list of publications referring to DIP.
<a href="#">SEARCH</a>	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.
<a href="#">LINKS</a>	Links to other protein interaction databases and related sites.
<a href="#">FILES</a>	Download the complete DIP dataset as well as specialized DIP subsets and additional data ( <i>registration required</i> ).



# 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

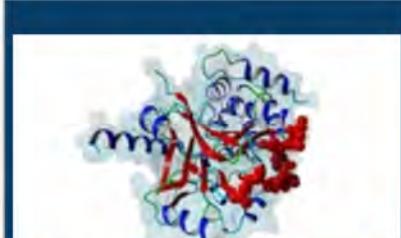
This computational biology resource mainly focuses on annotation and detection of eukaryotic linear motifs (ELMs) by providing both a repository of annotated motif data and an exploratory tool for motif prediction. ELMs, or short linear motifs (SLiMs), are compact protein interaction sites composed of 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](#)



# MINT

## The Molecular INTeraction Database

An ELIXIR Core Resource

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### 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.

### DATA CONTENT

Publications:	5395
Interactions:	117001
Interactors:	24421
Organisms:	607



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# Welcome to STRING

Protein-Protein Interaction Networks

ORGANISMS

2031

PROTEINS

9.6 mio

INTERACTIONS

1380 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. [IntAct](#) [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

# Practical example

The screenshot shows the IntAct homepage. At the top left is the EMBL-EBI logo. The main header features the IntAct logo, which includes the word "IntAct" in a stylized font with a yellow swoosh, and a small green molecular structure icon above the "t". Below the header is a navigation bar with links for Home, Advanced Search, About, Resources, and Download. The "Home" link is currently selected, indicated by a thicker border.

## 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 [\[1\]](#).

The screenshot shows the search interface of the IntAct database. On the left, there is a search bar with the placeholder text "Enter search term(s)...". Below the search bar are two buttons: "Search" and "Search Tips". To the right, under the heading "Examples", 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](#)

# 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.

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

<https://mint.bio.uniroma2.it/>

 **MINT** The Molecular INTeraction Database  
*An ELIXIR Core Resource*

---

Welcome Statistics Download Developers Contacts About PSB5\_HUMAN | PSA7\_HU Search

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Interactions:	117001
Interactors:	24421
Organisms:	607



**MINT database**

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<https://mint.bio.uniroma2.it/>

 MINT The Molecular INTeraction Database  
*An ELIXIR Core Resource*

PSB5\_HUMAN PSA7\_HUMAN

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Interactors:	24421
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MINT database

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# The Molecular INTeraction Database

An ELIXIR Core Resource

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Proteins, genes, public

Search

You searched for: PSB5\_HUMAN PSA7\_HUMAN

48 results for your query

Evidence List | Interaction Network

SHOW 10 ↑ ENTRIES

FILTER RESULTS:

Gene A	Gene B	Interaction Type	Detection Method	PubMed	Details
ABRAXAS2 Homo sapiens	PSMA7 Homo sapiens	Association	Biochemical	19214193	
BCRF1 Murid herpesvirus 4	PSMB5 Homo sapiens	Physical association	Two hybrid array	22028648	



# The Molecular INTeraction Database

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Gene A	Gene B	Interaction Type	Detection Method	PubMed	Details
ABRAXAS2 Homo sapiens	PSMA7 Homo sapiens	Association	Biochemical	19214193	
BCRF1 Murid herpesvirus 4	PSMB5 Homo sapiens	Physical association	Two hybrid array	22028648	

Gene A	Gene B	Interaction Type	Detection Method	PubMed	Details
PSMA4 Homo sapiens	PSMA7 Homo sapiens	Physical association	Two hybrid	17948026	
PSMA6 Homo sapiens	PSMA7 Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	
PSMA6 Homo sapiens	PSMA7 Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	
PSMA6 Homo sapiens	PSMB5 Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	
PSMA7 Homo sapiens	PSMA6 Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	
PSMA7 Homo sapiens	PSMA6 Homo sapiens	Physical association	Two hybrid	17948026	
PSMA7 Homo sapiens	PSMA6 Homo sapiens	Physical association	Two hybrid	17948026	
PSMA7 Homo sapiens	POMP Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	

Gene A	Gene B	Interaction Type	Detection Method	PubMed	Details
PSMA4 Homo sapiens	PSMA7 Homo sapiens	Physical association	Two hybrid	17948026	
PSMA6 Homo sapiens	PSMA7 Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	
PSMA6 Homo sapiens	PSMA7 Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	
PSMA6 Homo sapiens	PSMB5 Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	
PSMA7 Homo sapiens	PSMA6 Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	
PSMA7 Homo sapiens	PSMA6 Homo sapiens	Physical association	Two hybrid	17948026	
PSMA7 Homo sapiens	PSMA6 Homo sapiens	Physical association	Two hybrid	17948026	
PSMA7 Homo sapiens	POMP Homo sapiens	Association	Anti bait coimmunoprecipitation	17948026	

Format: Abstract ▾

Send to ▾

EMBO Rep. 2007 Dec;8(12):1170-5. Epub 2007 Oct 19.

## The proteasome maturation protein POMP facilitates major steps of 20S proteasome formation at the endoplasmic reticulum.

Fricke B<sup>1</sup>, Heink S, Steffen J, Kloetzel PM, Krüger E.

### Author information

#### Abstract

The quality control of proteins mediated by the plasticity of the proteasome system is regulated by the timely and flexible formation of this multisubunit proteolytic enzyme complex. Adaptable biogenesis of the 20S proteasome core complex is therefore of vital importance for adjusting to changing proteolytic requirements. However, the molecular mechanism and the cellular sites of mammalian proteasome formation are still unresolved. By using precursor complex-specific antibodies, we now show that the main steps in 20S core complex formation take place at the endoplasmic reticulum (ER). Thereby, the proteasome maturation protein (POMP)--an essential factor of mammalian proteasome biogenesis--interacts with ER membranes, binds to alpha1-7 rings, recruits beta-subunits stepwise and mediates the association of mammalian precursor complexes with the ER. Thus, POMP facilitates the main steps in 20S core complex formation at the ER to coordinate the assembly process and to provide cells with freshly formed proteasomes at their site of function.

PMID: 17948026 PMCID: [PMC2267243](#) DOI: [10.1038/sj.embor.7401091](https://doi.org/10.1038/sj.embor.7401091)

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# 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.”

# 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](#).

PSB5\_HUMAN PSA7\_HUMAN

Search in IntAct

PSB5\_HUMAN  
PSA7\_HUMAN

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](#)

# 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. 

Customize view   Select format to Download  Download								
(1 of 10)   1 2 3 4 5 6 7 8 9 10  								
Dts	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Interaction Detection Method	Interaction AC	Source Database	
  PSMA7	O14818	PSMA1	P25786	proximity-dependent biotin identification	EBI-16797733 imex : IM-26301-55	IntAct		
 				proximity-dependent biotin identification	EBI-16797676 imex : IM-26301-153	IntAct		
 				proximity-dependent biotin identification	EBI-16797556 imex : IM-26301-191	IntAct		

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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)

Your query also matches 1,549 interaction evidences from 6 other databases.

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

Customize view | Select format to Download ▾ Download

(1 of 10) 1 2 3 4 5 6 7 8 9 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

# Practical example

188 binary interactions  
PSB5\_HUMAN PSA

Interactions (188) Interactors Interactants

- Filter out the spoke expanded co-complexes

Customize view Select for download

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 Interacting

- Filter out the spoke expanded co-complexes

Customize view Select f...

Dts	Molecule 'A'	Links 'A'
1	PSMA7	O14818 EBI-603272
2		
3		
4		
5		
6		
7		
8		
9		
10		

Complex Expansion

Spoke expansion: Links the bait molecule to all prey molecules. If N is the count of molecule in the complex, it generated  $N-1$  binary interactions.

Matrix expansion: Links all molecule to all other molecule present in the complex. If N is the count of molecule in the complex, it generated  $(N*(N-1))/2$  binary interactions.

Now the issue (as illustrated at the bottom right of the diagram above) with these two models lies in the fact that the real complex might not be articulated around the experimental bait but instead, this bait might be linked to a smaller complex, hence most binary interaction generated by spoke and matrix expansion result in false positive.

# 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? [?](#)

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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
<a href="#">1</a>	PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	two hybrid	EBI-696762	IntAct
<a href="#">2</a>					two hybrid	EBI-696846	IntAct
<a href="#">3</a>					two hybrid	EBI-1388227	IntAct
<a href="#">4</a>					pull down	EBI-1388238	IntAct
<a href="#">5</a>					pull down	EBI-1388404	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. [?](#)

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

# 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? [?](#)

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
<a href="#">1</a>	PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	two hybrid	EBI-696762	IntAct
<a href="#">2</a>					two hybrid	EBI-696846	IntAct
<a href="#">3</a>					two hybrid	EBI-1388227	IntAct
<a href="#">4</a>					pull down	EBI-1388238	IntAct
<a href="#">5</a>					pull down	EBI-1388404	IntAct

**112** binary interactions found for search term  
***PSB5\_HUMAN PSA7\_HUMAN***

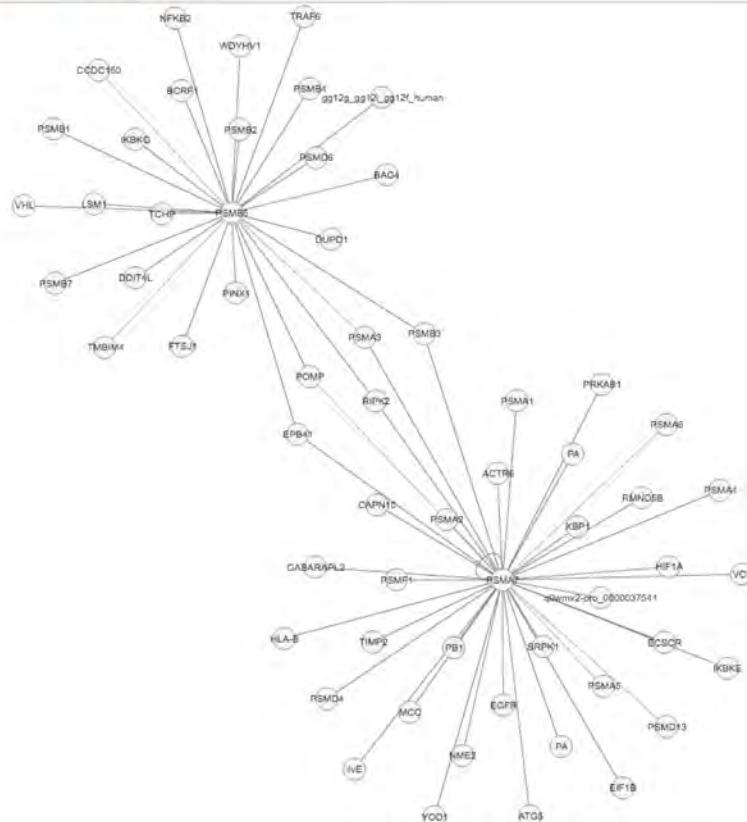
## Interactions (112)

## 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.

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# 112 binary interactions found for search term *PSB5\_HUMAN PSA7\_HUMAN*

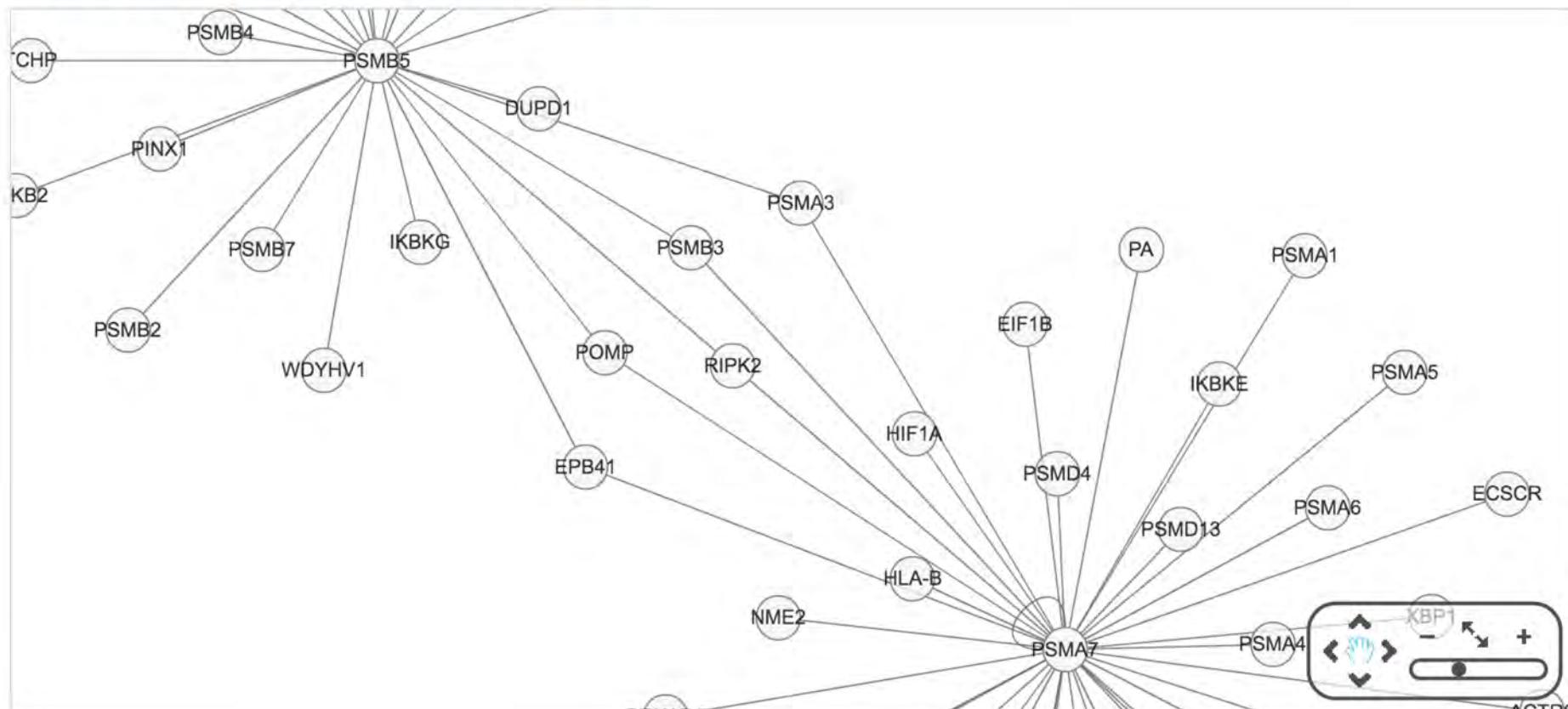
Interactions (112)

Interactors

Interaction Details

Graph

## Network visualisation



# 112 binary interactions found for search term *PSB5\_HUMAN PSA7\_HUMAN*

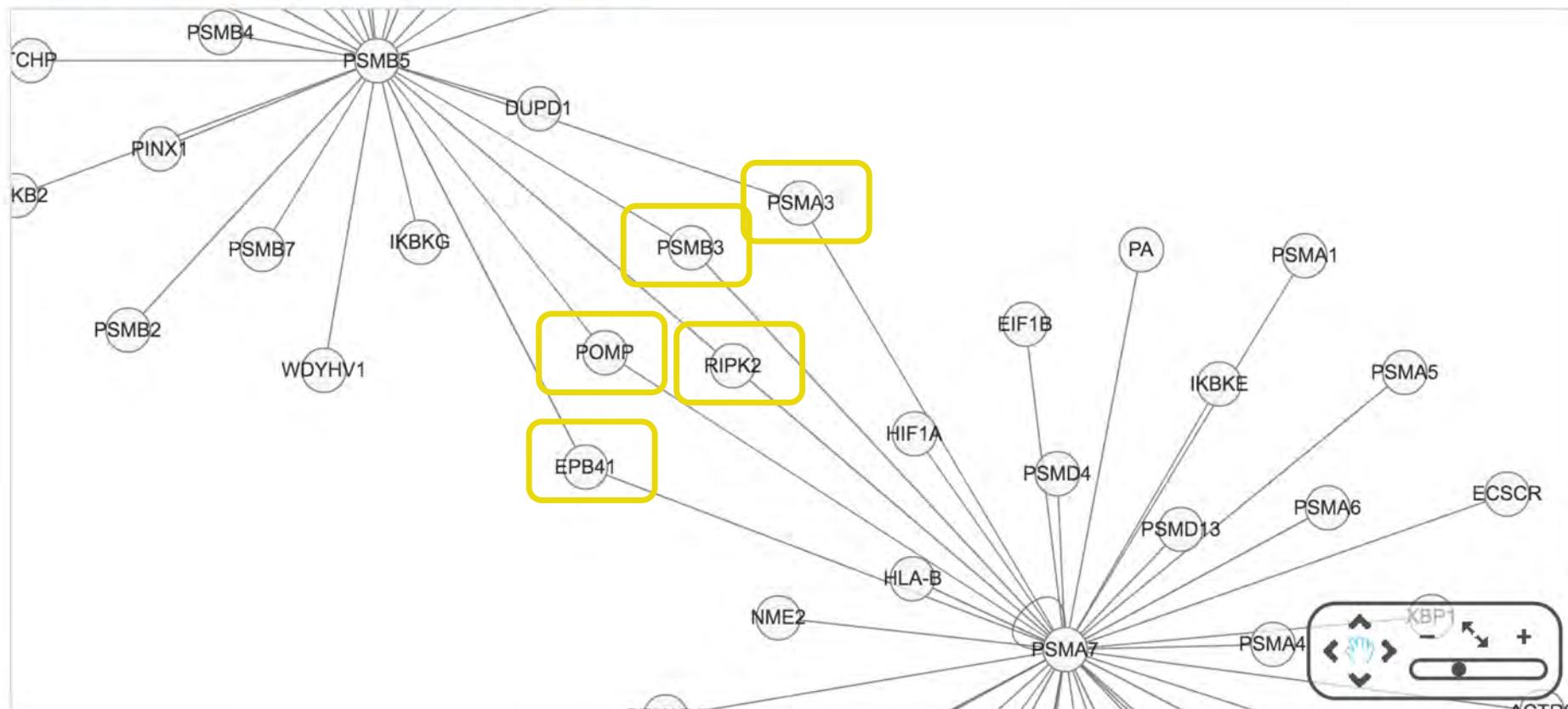
Interactions (112)

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**.”

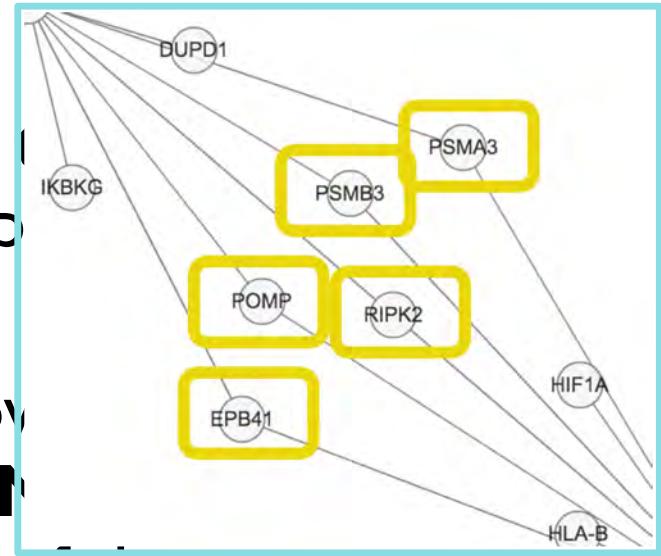
# Practical example

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

You are specially interested in knowing more about the protein PSB5 (UniProtKB id **PSB5\_HUMAN**)

(UniProtKB id **PSB5\_HUMAN**). You have found that 5 other proteins 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 [?](#)

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



# The Molecular INTeraction Database

An ELIXIR Core Resource

Welcome Statistics Download Developers Contacts About

Proteins, genes, public

Search

You searched for: PSB5\_HUMAN PSA7\_HUMAN

48 results for your query

Evidence List | Interaction Network

SHOW 10 ↑ ENTRIES

FILTER RESULTS:

Gene A	Gene B	Interaction Type	Detection Method	PubMed	Details
ABRAXAS2 Homo sapiens	PSMA7 Homo sapiens	Association	Biochemical	19214193	
BCRF1 Murid herpesvirus 4	PSMB5 Homo sapiens	Physical association	Two hybrid array	22028648	

# 112 binary interactions found for search term PSB5\_HUMAN PSA7\_HUMAN

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

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

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Dts	Molecule 'A'	Links 'A'	Molecule 'B'	Links 'B'	Interaction Detection Method	Interaction AC	Source Database
<a href="#"></a>	PSMA7	O14818 EBI-603272	PSMA1	P25786 EBI-359352	two hybrid	EBI-696762	IntAct
<a href="#"></a>					two hybrid	EBI-696846	IntAct
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<a href="#"></a>					two hybrid	EBI-7660417 MINT-6176430 <b>imex : IM-11502-35</b>	MINT
<a href="#"></a>	PSMA7	O14818 EBI-603272	PSMA4	P25789 EBI-359310	two hybrid array	EBI-19768999 <b>imex : IM-25472-46189</b>	IntAct
<a href="#"></a>					two hybrid	EBI-696834	IntAct

# 112 binary interactions found for search term *PSB5 HUMAN PSA7 HUMAN*

Interactions (112) Interactors Interaction Details [Glossary](#)

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

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(1)

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

Columns displayed [X](#)

Select: Minimal | Standard | Complete

Interaction Detection Method

First Author

Publication Identifier

Species 'A'

Species 'B'

Interaction Type (1)

Source Database

Interaction AC

Confidence Value

[Update](#)

Action evidences from **6** other IMEx entries [What is this view?](#)

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

**112 binary interactions found for search term  
*PSB5\_HUMAN PSA7\_HUMAN***

# 112 binary interactions found for search term PSB5\_HUMAN PSA7\_HUMAN

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

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

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[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](#) [Next](#) [Last](#)

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	EBI-696762	IntAct
2					two hybrid	physical association	EBI-696846	IntAct
3					two hybrid	physical association	EBI-1388227	IntAct
4					pull down	physical association	EBI-1388238	IntAct
5					pull down	physical association	EBI-1388404	IntAct
6					two hybrid	physical association	EBI-7660417 MINT-6176430 <b>imex : IM-11502-35</b>	MINT

# 112 binary interactions found for search term PSB5\_HUMAN PSA7\_HUMAN

Interactions (112)

Interactors

Interaction Details

Graph

- Include the spoke expanded co-complexes

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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	PSA7	two hybrid	physical association	EBI-696846	IntAct
		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	MINT imex : IM-11502-35

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.