

HUPO Proteomics Standards Initiative

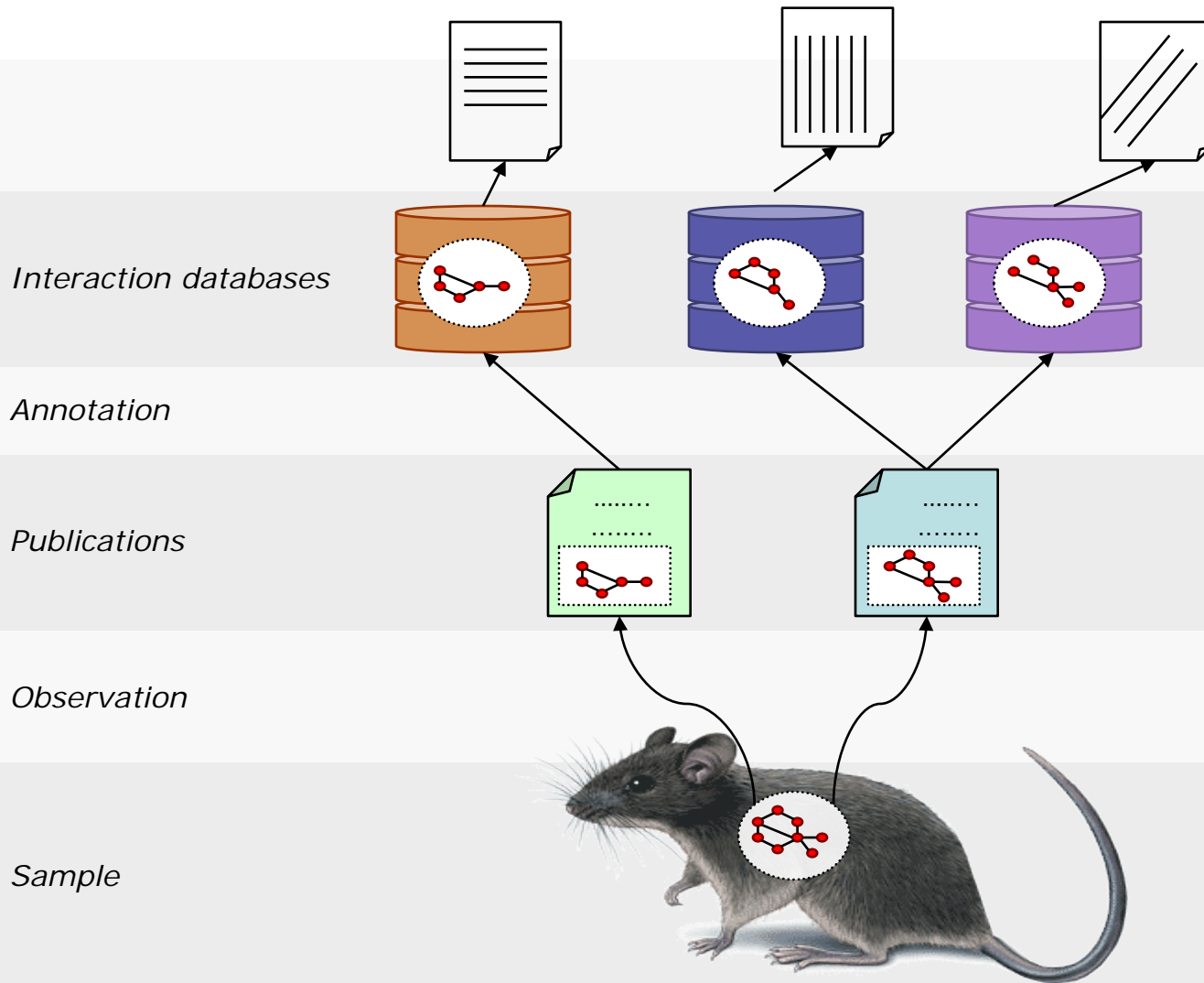
PSICQUIC, the
PSI Common Query Interface

Henning Hermjakob
Edinburgh, October 2010

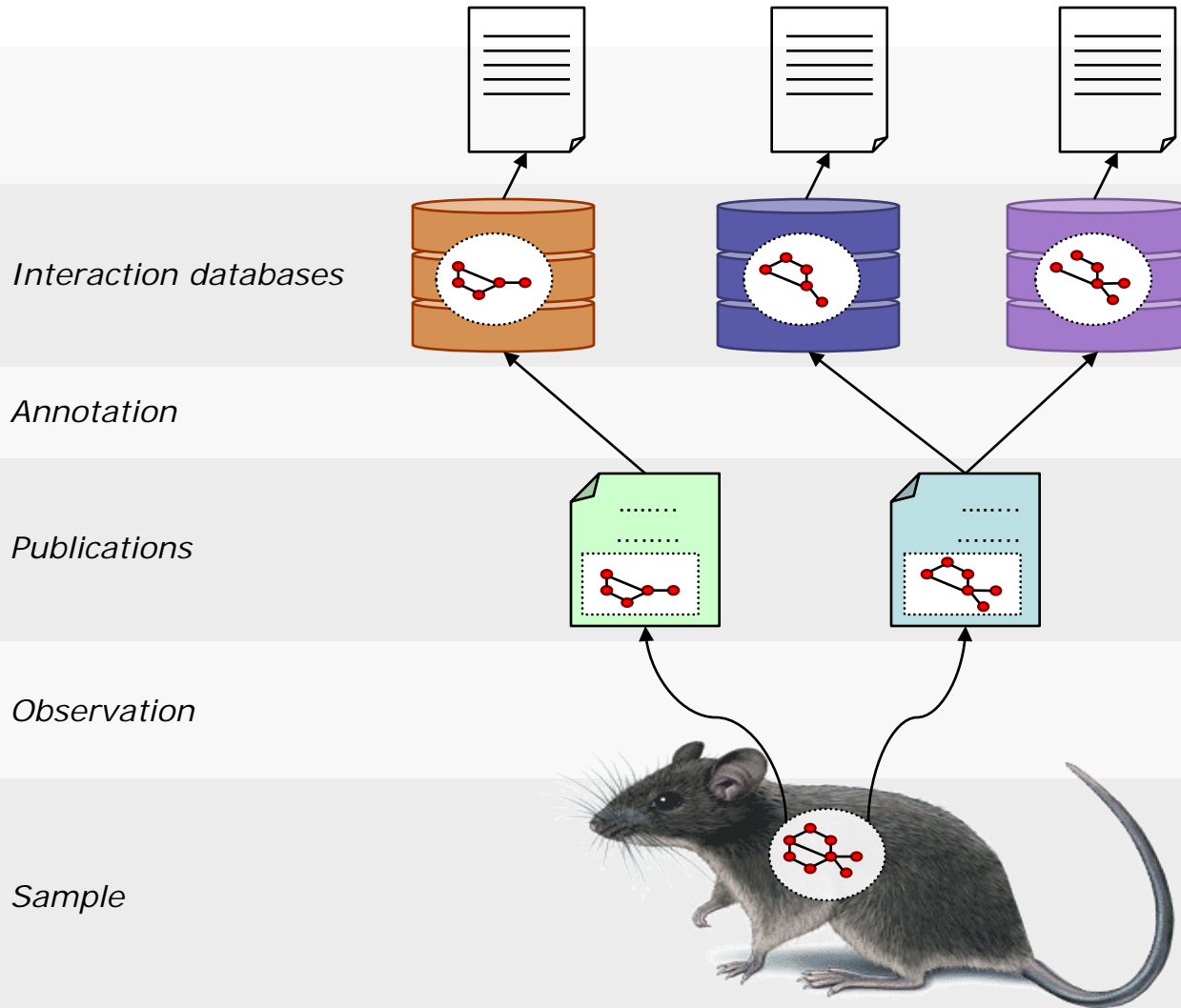
EMBL-EBI

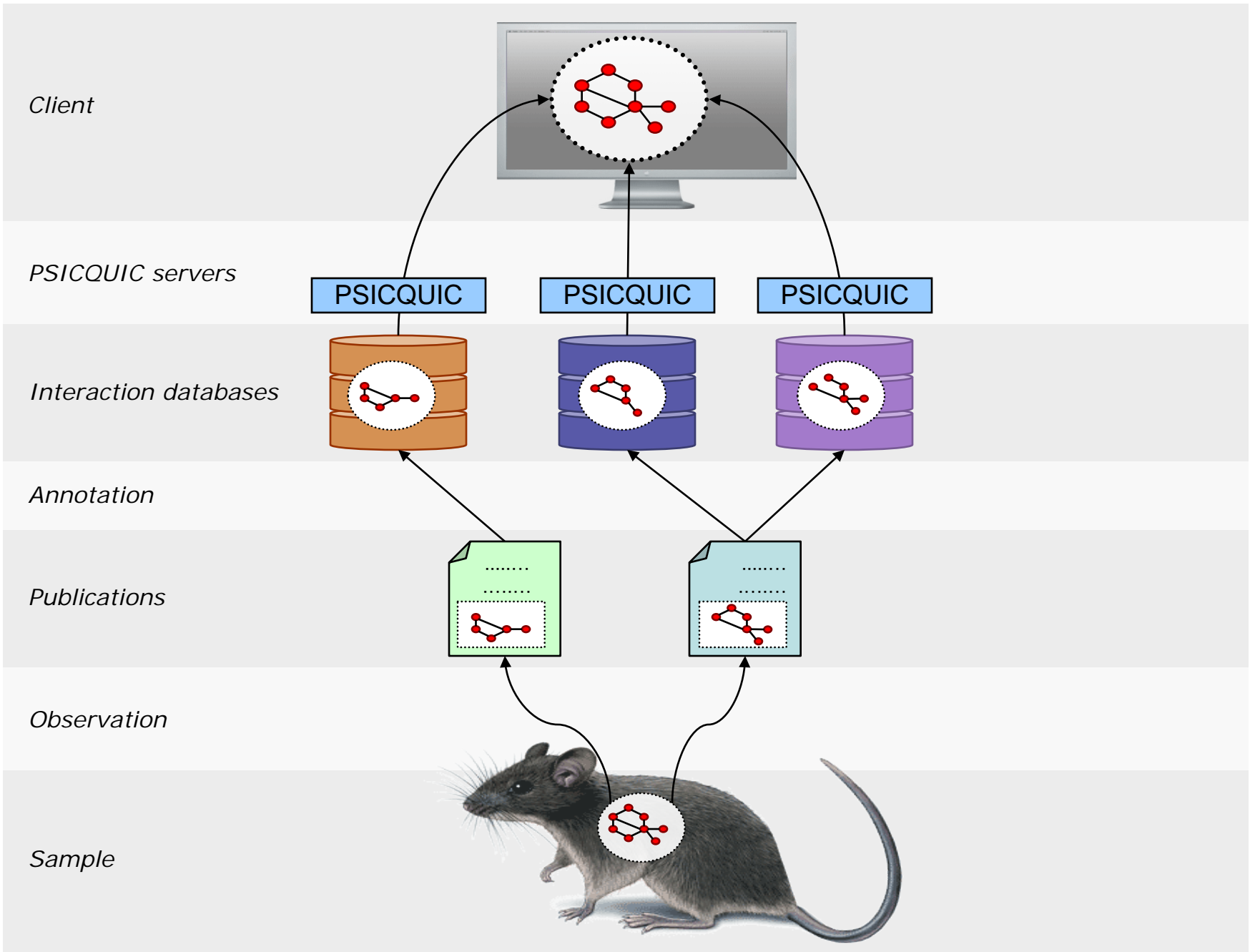


PSI MI XML: Consistent format



PSI MI XML: Consistent format





- Common computational interface for querying molecular interaction databases
 - Simple interface, open source server implementation exists, can be “fed” from a tab-delimited file => easy to provide data
 - Not limited to protein-protein interactions, also e.g.
 - Drug-target interactions
 - Simplified pathway data

Total: **14,665,530** binary interactions

Click on the links below to display the results for each service ([refresh](#))

● [APID](#) - 416,124

● [BioGrid](#) - 337,957

● [ChEMBL](#) - 581,858

● [DIP](#) - 20,769

● [InnateDB](#) - 9,909

● [IntAct](#) - 228,262

● [iRefIndex](#) - 404,453

● [MatrixDB](#) - 845

● [MINT](#) - 124,473

● [MPIDB](#) - 24,268

● [Reactome](#) - 74,861

● [Reactome-Fls](#) - 209,988

● [STRING](#) - 12,231,763



PSICQUIC: Simple PSICQUIC viewer



PSICQUIC View

Search:

[Fields »](#)

[MIQL syntax](#)

Total: 1,648 bins

Click on the links below to display the results for each service ([refresh](#))

- [APID](#) - 0
- [BioGrid](#) - 438
- [ChEMBL](#) - 0
- [DIP](#) - 0
- [InnateDB](#) - 5
- [IntAct](#) - 205
- [iRefIndex](#) - 230
- [MatrixDB](#) - 0
- [MINT](#) - 80
- [MPIDB](#) - 0
- [Reactome](#) - 0
- [Reactome-FIs](#) - 126
- [STRING](#) - 564

EBI > Databases > Pathways & Networks > IntAct > View



Search: [Show Advanced Fields »](#)

[Home](#) |
 [Search](#) |
 [Interactions \(89\)](#) |
 [Browse](#) |
 [Lists](#) |
 [Interaction Details](#) |
 [Molecule View](#) |
 [Graph](#)

Browse by [taxonomy](#), [gene ontology](#), [ChEBI ontology](#)

> **89** binary interactions were found in IntAct. 23 of them are originated from [spoke expanded co-complexes](#) and you may want to [filter](#) them.
 > [Counting results in other databases...]

Previous | Export to: Previous

	Name molecule A	Links molecule A	Name molecule B	Links molecule B	Aliases molecule A	Aliases molecule B	Species molecule A	Species molecule B	Publication Identifier	Interaction Detection Method	In
1	FANCD1 <small>PR: NE: IN:</small>		atp <small>SM: NE: EN:</small>		FANCD1; FACD; Fanconi anemia group D1 protein; [+]	atp	9606		19303847	atpase assay	EE
2	<small>PR: NE: IN:</small>		<small>SM: NE: EN:</small>						19303847	atpase assay	EE
3	<small>PR: NE: IN:</small>		<small>SM: NE: EN:</small>						19303847	atpase assay	EE
4	<small>PR: NE: IN:</small>		<small>SM: NE: EN:</small>						19303847	atpase assay	EE
5	<small>PR: NE: IN:</small>		<small>SM: NE: EN:</small>						19303847	atpase assay	EE

<http://www.ebi.ac.uk/intact>

EBI > Databases > Pathways & Networks > IntAct > View



Search: [Show Advanced Fields »](#)

[Home](#) |
 [Search](#) |
 [Interactions \(89\)](#) |
 [Browse](#) |
 [Lists](#) |
 [Interaction Details](#) |
 [Molecule View](#) |
 [Graph](#)

Browse by [taxonomy](#), [gene ontology](#), [ChEBI ontology](#)

> 89 binary interactions were found in IntAct. 23 of them are originated from [spoke expanded co-complexes](#) and you may want to [filter](#) them.
 > Your query also matches [82](#) interaction evidences from [3](#) other databases.

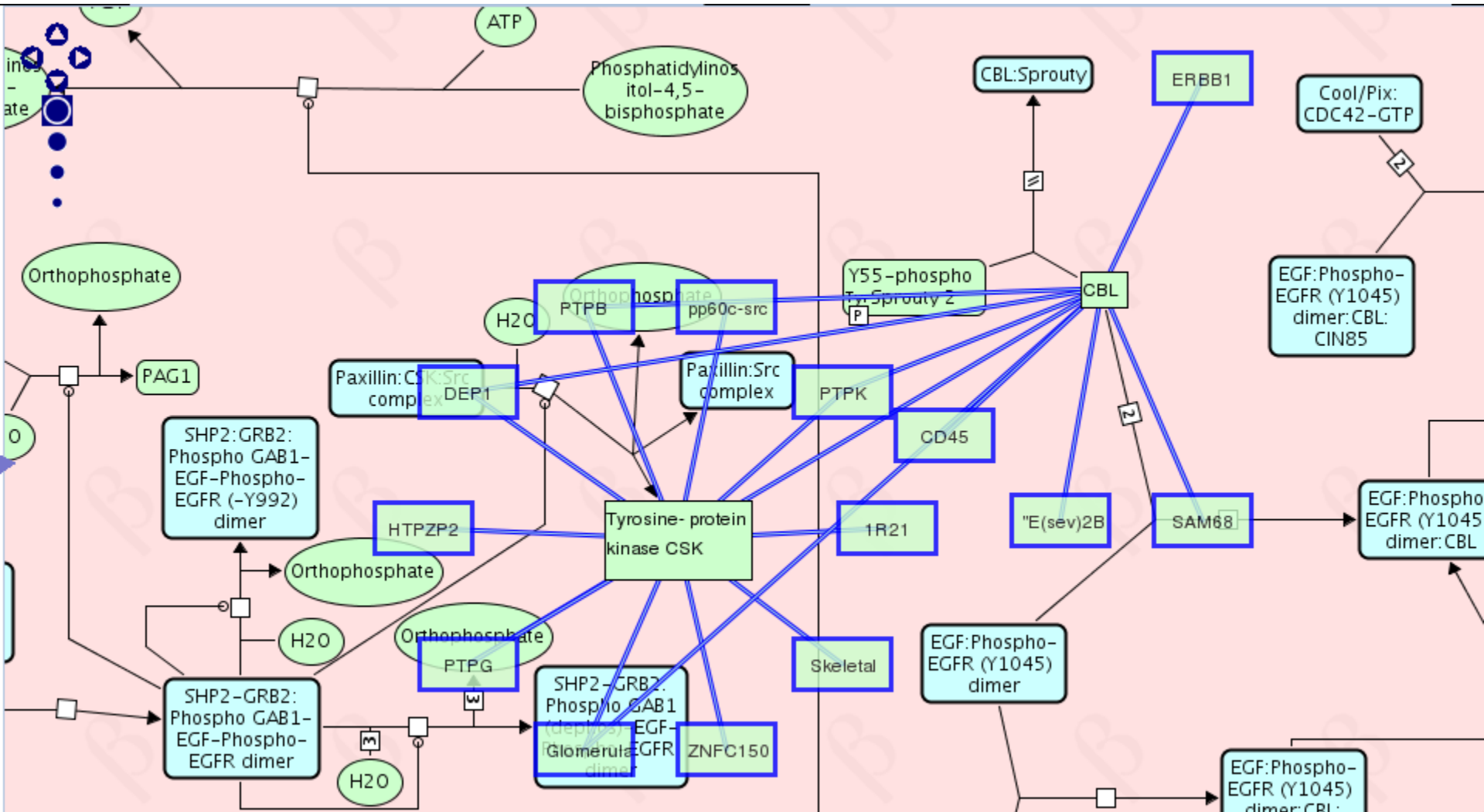
Previous | 1-30 of 89 | [Next 30](#) |
 Export to: |
 Export |
 |
 Previous

	Name molecule A	Links molecule A	Name molecule B	Links molecule B	Aliases molecule A	Aliases molecule B	Species molecule A	Species molecule B	Publication Identifier	Interaction Detection Method	In
1	FANCD1 <small>PR: NE: IN:</small>		atp <small>SM: NE: EN:</small>		FANCD1; FACD; Fanconi anemia group D1 protein; +	atp	9606		19303847	atpase assay	EE
2	<small>PR: NE: IN:</small>		<small>SM: NE: EN:</small>						19303847	atpase assay	EE
3	<small>PR: NE: IN:</small>		<small>SM: NE: EN:</small>						19303847	atpase assay	EE
4	<small>PR: NE: IN:</small>		<small>SM: NE: EN:</small>						19303847	atpase assay	EE
5	<small>PR: NE: IN:</small>		<small>SM: NE: EN:</small>						19303847	atpase assay	EE

<http://www.ebi.ac.uk/intact>



PSICQUIC: Overlay of molecular interactions on Reactome pathways (beta)



- Based on Lucene, with specific field names
- Example: `ppx AND species:"Escherichia coli"`

Field Name	Searches on	Implicit*	Example
<code>idA</code>	IdentifierA	No	idA:P74565
<code>id</code>	Identifiers (A or B)	No	id:P74565
<code>alias</code>	Aliases (A or B)	No	alias:(KHDRBS1 HCK)
<code>identifiers</code>	Identifiers and Aliases undistinctively	Yes	identifier:P74565
<code>pubauth</code>	Publication 1st author(s)	Yes	pubauth:scott
<code>pubid</code>	Publication Identifier(s) OR	Yes	pubid:(10837477 12029088)
<code>taxidA</code>	Tax ID interactor A: be it the tax ID or the species name	No	taxidA:mouse
<code>taxidB</code>	Tax ID interactor B: be it the tax ID or species name	No	taxidB:9606
<code>species</code>	Species. Tax ID A and Tax ID B	Yes	species:human
<code>type</code>	Interaction type(s)	Yes	type:"physical interaction"
<code>detmethod</code>	Interaction Detection method(s)	Yes	detmethod:"two hybrid"
<code>interaction_id</code>	Interaction identifier(s)	Yes	interaction_id:EBI- 761050
<code>annotation</code>	Annotations Interactor A or B	No	annotation:experimental
<code>properties</code>	Properties of Interactor A or B (note that this field also contains parent terms of ontology terms of GO, InterPro and PSI-MI)	Yes	properties:"1GQ5"
<code>expansion</code>	Expansion method(s)	Yes	expansion:spoke
<code>dataset</code>	Dataset name(s)	Yes	dataset:Apoptosis
<code>experimentalRole</code>	Experimental role(s) interactor A or interactor B	No	experimentalRole:prev
<code>biologicalRole</code>	Biological role(s) interactor A or interactor B	No	biologicalRole:enzyme
<code>hostOrganism</code>	Host organism in which the interaction was detected	Yes	hostOrganism:human




PSICQUIC: The challenge

FROM:










Search: [Fields »](#)

- [BioGrid \(0\)](#)
[ChEMBL \(0\)](#)
[DIP \(0\)](#)
[InnateDB \(2\)](#)
[IntAct \(89\)](#)
[MINT \(22\)](#)
[MPIDB \(0\)](#)
[MatrixDB \(0\)](#)
[Reactome \(0\)](#)
[Reactome-Functional-Interactions \(29\)](#)
[iRefIndex \(31\)](#)

Export: [MITAB 2.5](#) [PSI-XML 2.5.4](#)

	Name molecule A	Links molecule A	Name molecule B	Links molecule B	Alt. identifiers molecule A	Alt. identifiers molecule B	Aliases molecule A	Aliases molecule B	Species molecule A	Species molecule B	First Author	PubMed Identifier	Interaction Type	Interaction Detected
1	P51587 ; EBI-79792		EBI-539895		FANCD1 ; FACD ; Fanconi anemia group D1 protein ; brca2_human		BRCA2		Human (9606)	-1	Pellegrini et al. (2002)	12442171	physical association	x-ray
2	P51587 ; EBI-79792		Q9BXW9-2 ; EBI-596878		FANCD1 ; FACD ; Fanconi	Q9BXW9-2	BRCA2		Human (9606)	Human (9606)	Wilson et al. (2008)	18212739	physical association	anti body coimmunoprecipitation

TO:

PR PY UN		PR BA UN					Marston et al. (1999)	10373512	coimmunoprecipitation		EBI-79852
At4g00020 PR BA UN	 	DMC1 PR PY UN	 	3702	3702		Siaud et al. (2004)	15014444	two hybrid		EBI-307726
PR BA UN		PR PY UN					Dray et al. (2006)	16415210	two hybrid		EBI-930902
PR BA UN		PR PY UN					Siaud et al. (2004)	15014444	two hybrid		EBI-930747
PR BA UN		PR PY UN					Dray et al. (2006)	16415210	anti tag coimmunoprecipitation		EBI-930779



PSICQUIC View

Search: BRCA1 AND species:9606 AND NOT cofactor

Search

Clear

[Fields »](#)

[MIQL syntax reference](#)

Total: **1,600** binary interactions

Click on the links below to display the results for each service ([refresh](#))

- [APID](#) - 0
- [BioGrid](#) - 438
- [ChEMBL](#) - 0
- [DIP](#) - 0
- [InnateDB](#) - 5
- [IntAct](#) - 173
- [iRefindex](#) - 230
- [MatrixDB](#) - 0
- [MINT](#) - 64
- [MPIDB](#) - 0
- [Reactome](#) - 0
- [Reactome-FIs](#) - 126
- [STRING](#) - 564

• Status of your cluster queries

BRCA1 AND species:9606	COMPLETED	view remove
BRCA1 AND species:9606 AND NOT cofactor	QUEUED	view remove

Cluster this query





Search:

[Fields »](#)

[← Back to all services](#)

Clustered query: 'BRCA1 AND species:9606 AND NOT cofactor' from BioGrid, InnateDB, IntAct, MINT, Reactome-FIs, STRING, iRefIndex

	Name molecule A	Links molecule A	Name molecule B	Links molecule B	First Author	PubMed Identifier	Interaction Detection Method
151	P46736		P38398		Dong et al. (2003) Wu et al.(2010)	14636569 20482850 PMID019615732 omim:00113705 omim:00300617 omim:00609433	experimental interaction detection arti tag coimmunoprecipitation predictive text mining experimental knowledge based
152	entrez gene/focuslink:672		entrez gene/focuslink:4800		Fan W (2002)	11777930	affinity chromatography technology
153	entrez gene/focuslink:15951		entrez gene/focuslink:672		Aglipay JA (2003)	14654789	imaging technique affinity chromatography technology
154	entrez gene/focuslink:672		entrez gene/focuslink:851212		Bennett CB (2008)	18197258	genetic interference
155	entrez gene/focuslink:672		entrez gene/focuslink:851212		Bennett CB (2008)	18197258	genetic interference

Molecular Interactions - Dataset: set3

It provides molecular interaction data from different molecular interactions databases. It makes use of PSICQUIC.

[Table view](#) [Network view](#)

Pubmed ID selection

Database selection

chembl intact mint

Experiment selection

Filter by number

Associated databases

- none
- 1 or more
- 2 or more
- 3 or more
- 4 or more

Associated pubmeds

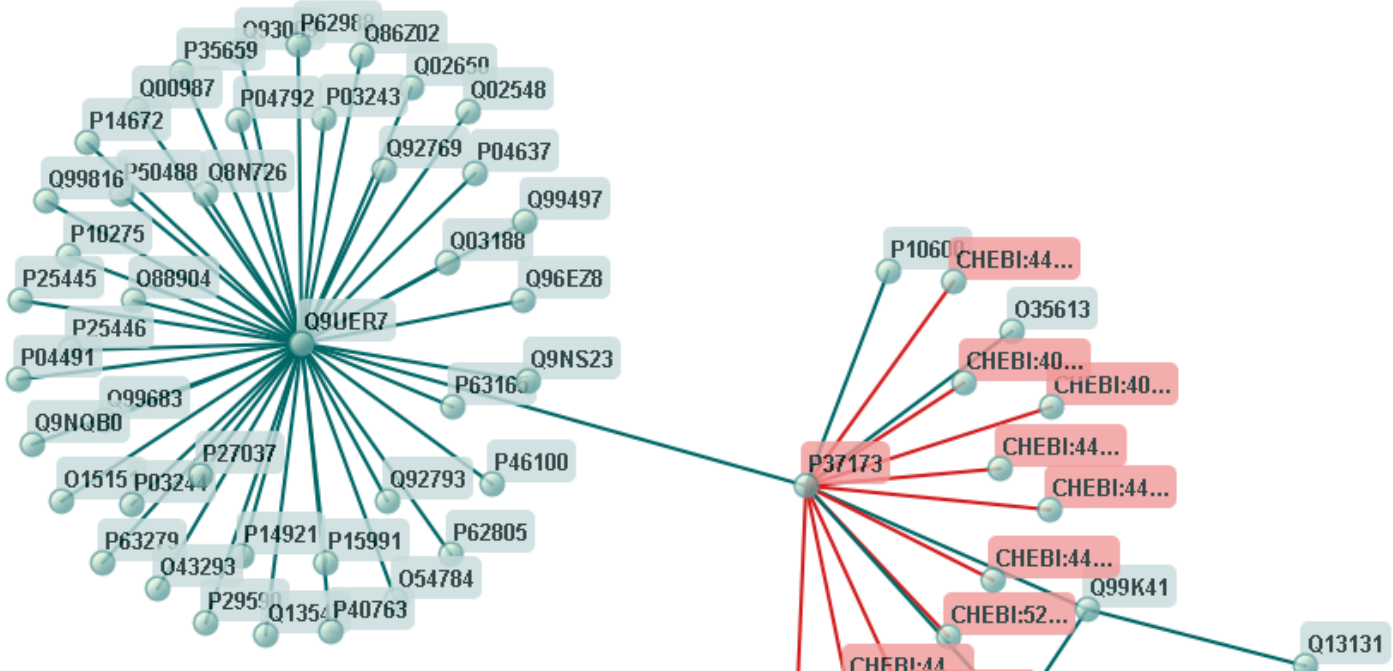
- none
- 1 or more
- 2 or more
- 3 or more
- 4 or more

Associated experiments

- none
- 1 or more
- 2 or more
- 3 or more
- 4 or more

10 interactions with 20 interactors for the "chembl" database

[Download ALL the interactions](#)
[Download SELECTED interactions](#)



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 - set2
 - set3
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- Protein identifications
- Biological pathways
- Molecular interactions
- Protein localization
- Biological models
- Protein length
- Dataset history
- Download results
- Dataset Manager
- Contact

DASMIweb - dynamic online integration and annotation of molecular interaction data

Query

e.g. [Entrez Gene](#), [GI](#), [Pfam](#), [RefSeq](#) [UniProtKB](#)

Batch retrieval

Interactor Information

Identifier: [961 \(Entrez Gene\)](#) (Leukocyte surface antigen CD47 precursor (Integrin-associated protein)(IAP) (Antigenic surface determinant protein OA3) (Protein MER6).) (CD47 molecule)

UniProtKB [CD47_HUMAN, A8K198_HUMAN, Q71A41_HUMAN,](#)

UniGene [Hs.446414,](#)

Entrez Gene [961,](#)

30 interactions (showing 11 to 20) Export as ... Select confidence measure ... Query Confidence Sources

Scoring algorithms offered by PSISCORE servers

- Select confidence measure ...
- Bioverse (originalConfidenceScore)
- Domain support (crystal-structure)
- Domain support (predicted)
- FunSimMat2.1 (BPscore)
- FunSimMat2.1 (CCscore)
- FunSimMat2.1 (MFscore)
- HiMAP (originalConfidenceScore)

	0	6	17	0	0	0
HiMAP-CORE						
POINT						
OPHID						
MPIDB						
MDC						
DIP						

Name	ID	Description																
ITGB3 UBQLN1 ITGAV	3690 29979 3685	Integrin beta-3 precursor (Platelet membrane glycoprotein IIIa)(GPIIIa) (CD61 antigen). Ubiquilin-1 (Protein linking IAP with cytoskeleton 1) (PLIC-1) (hPLIC-1). Ubiquilin 1 isoform 1 variant (Fragment). Integrin alpha-V precursor (Vitronectin receptor subunit alpha) (CD51antigen) [Contains: Integrin alpha-V heavy chain; Integrin alpha-Vlight chain].																
EPB42	2038	Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)(P4.2).																
THBS1	7057	Thrombospondin-1p180 (Fragment).																
SIRPA	140885 , 23755	signal-regulatory protein alpha																
UBQLN1	29979	Ubiquilin 1 isoform 1 variant (Fragment).																
P2RY2	5029	P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)(Purinergic receptor).																
RHAG	6005	Rhesus blood group-associated glycoprotein (Rhesus blood group-associated ammonia channel) (Erythrocyte plasma membrane 50 kDaglycoprotein) (Rh50A) (CD241 antigen).																
ITGA6	3655	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrinalpha-6 heavy chain; Integrin alpha-6 light chain].																
sirpg_human	55423	Signal-regulatory protein gamma precursor (Signal-regulatory proteinbeta-2) (SIRP-beta-2) (SIRP-b2) (CD172g antigen).																
PAK1	5058	p21/Cdc42/Rac1-activated kinase 1 (STE20 homolog, yeast)																
COMP	1311	Cartilage oligomeric matrix protein variant (Fragment).																

DASMIweb - dynamic online integration and annotation of molecular interaction data

Query

e.g. [Entrez Gene](#), [GI](#), [Pfam](#), [RefSeq](#) [UniProtKB](#)

[Batch retrieval](#)

Interactor Information

Identifier: [961 \(Entrez Gene\)](#) (Leukocyte surface antigen CD47 precursor (Integrin-associated protein)(IAP) (Antigenic surface determinant protein OA3) (Protein MER6).) (CD47 molecule)

UniProtKB [CD47_HUMAN](#), [A8K198_HUMAN](#), [Q71A41_HUMAN](#),

UniGene [Hs.446414](#),

Entrez Gene [961](#),

30 interactions (showing 11 to 20) Export as ... FunSimMat2.1 (BPscore) Query Confidence Sources

Name	ID	Description	SANGER-CORE	CCSB-HII	HPRD	BIOVERSE	SANGER	MINT	INTACT	HOMOMINT	HIMAP	HIMAP-CORE	POINT	OPHID	MPIDB	MDC	DIP
ITGB3 UBQLN1 ITGAV	3690 29979 3685	Integrin beta-3 precursor (Platelet membrane glycoprotein IIIa)(GPIIIa) (CD61 antigen). Ubiquilin-1 (Protein linking IAP with cytoskeleton 1) (PLIC-1) (hPLIC-1). Ubiquilin 1 isoform 1 variant (Fragment). Integrin alpha-V precursor (Vitronectin receptor subunit alpha) (CD51antigen) [Contains: Integrin alpha-V heavy chain; Integrin alpha-Vlight chain].															
EPB42	2038	Erythrocyte memb 4.2)(P4.2).			0.31												0.31
THBS1	7057	Thrombospondin-1			0.47	0.47											0.47
SIRPA	140885 , 23755	signal-regulatory p			0.55								0.55	0.55			
UBQLN1	29979	Ubiquilin 1 isoform 1 variant (Fragment).			0.26												0.26
P2RY2	5029	P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)(Purinergic receptor).			0.66												0.66
RHAG	6005	Rhesus blood group-associated glycoprotein (Rhesus blood group-associated ammonia channel) (Erythrocyte plasma membrane 50 kDaglycoprotein) (Rh50A) (CD241 antigen).			0.16												0.16
ITGA6	3655	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrinalpha-6 heavy chain; In									0.91						
sirpg_human	55423	Signal-regulatory protein gamma proteinbeta-2) (SIRP-beta-2) (S															
PAK1	5058	p21/Cdc42/Rac1-activated kina															0.52
COMP	1311	Cartilage oligomeric matrix pro															

Scoring algorithms offered by PSISCORE servers

Exemplary visualization of a scoring algorithm with a 0-1 range

Scoring algorithm description, provided by scoring server / registry

Details for FunSimMat2.1 (BPscore)

The BPscore is based on biological process annotation of the Gene Ontology.
Range: 0-1
<http://funsimmat.bioinf.mpg-inf.mpg.de/help.php>

- **PSICQUIC**

- Samuel Kerrien
- Bruno Aranda
- Sandra Orchard

- **PSISCORE**

- Hagen Blankenburg
- Mario Albrecht

- **Editors**

- Mike Dunn, Proteomics
- Kathy Aschheim, NBT

- **Funding**

- EU FW6 Felics
- EU FW6 Enfin
- EU FW7 PSIMEx

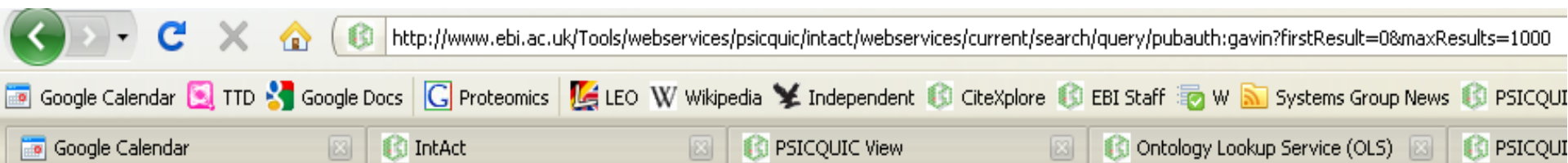
- **All participants** of the HUPO Proteomics Standards Initiative, IMEx, and ProteomeXchange

- **All authors** who make their interaction data publicly accessible, preferably through deposition to <http://www.imexconsortium.org>





PSICQUIC: SOAP and REST interfaces



```
uniprotkb:P53859|intact:EBI-1731      uniprotkb:Q02821|intact:EBI-1797      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:P40579|intact:EBI-1804      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:P53859|intact:EBI-1731      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:Q08162|intact:EBI-1740      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:P48240|intact:EBI-1749      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:P38792|intact:EBI-1757      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:Q12277|intact:EBI-1765      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:P25359|intact:EBI-1773      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:Q12149|intact:EBI-1782      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:P46948|intact:EBI-1788      uniprotkb:YNL232W(locus name)|uni
uniprotkb:P53859|intact:EBI-1731      uniprotkb:Q08491|intact:EBI-1389      uniprotkb:YNL232W(locus name)|uni
uniprotkb:Q05636|intact:EBI-1810      uniprotkb:Q05636|intact:EBI-1810      uniprotkb:YDR280W(locus name)|uni
uniprotkb:Q05636|intact:EBI-1810      uniprotkb:P53859|intact:EBI-1731      uniprotkb:YDR280W(locus name)|uni
uniprotkb:Q05636|intact:EBI-1810      uniprotkb:Q08162|intact:EBI-1740      uniprotkb:YDR280W(locus name)|uni
uniprotkb:Q05636|intact:EBI-1810      uniprotkb:Q04217|intact:EBI-1820      uniprotkb:YDR280W(locus name)|uni
uniprotkb:Q05636|intact:EBI-1810      uniprotkb:P48240|intact:EBI-1749      uniprotkb:YDR280W(locus name)|uni
uniprotkb:Q05636|intact:EBI-1810      uniprotkb:P38792|intact:EBI-1757      uniprotkb:YDR280W(locus name)|uni
uniprotkb:Q05636|intact:EBI-1810      uniprotkb:Q08285|intact:EBI-1831      uniprotkb:YDR280W(locus name)|uni
uniprotkb:Q05636|intact:EBI-1810      uniprotkb:P25359|intact:EBI-1773      uniprotkb:YDR280W(locus name)|uni
```

<http://code.google.com/p/psicquic/>