

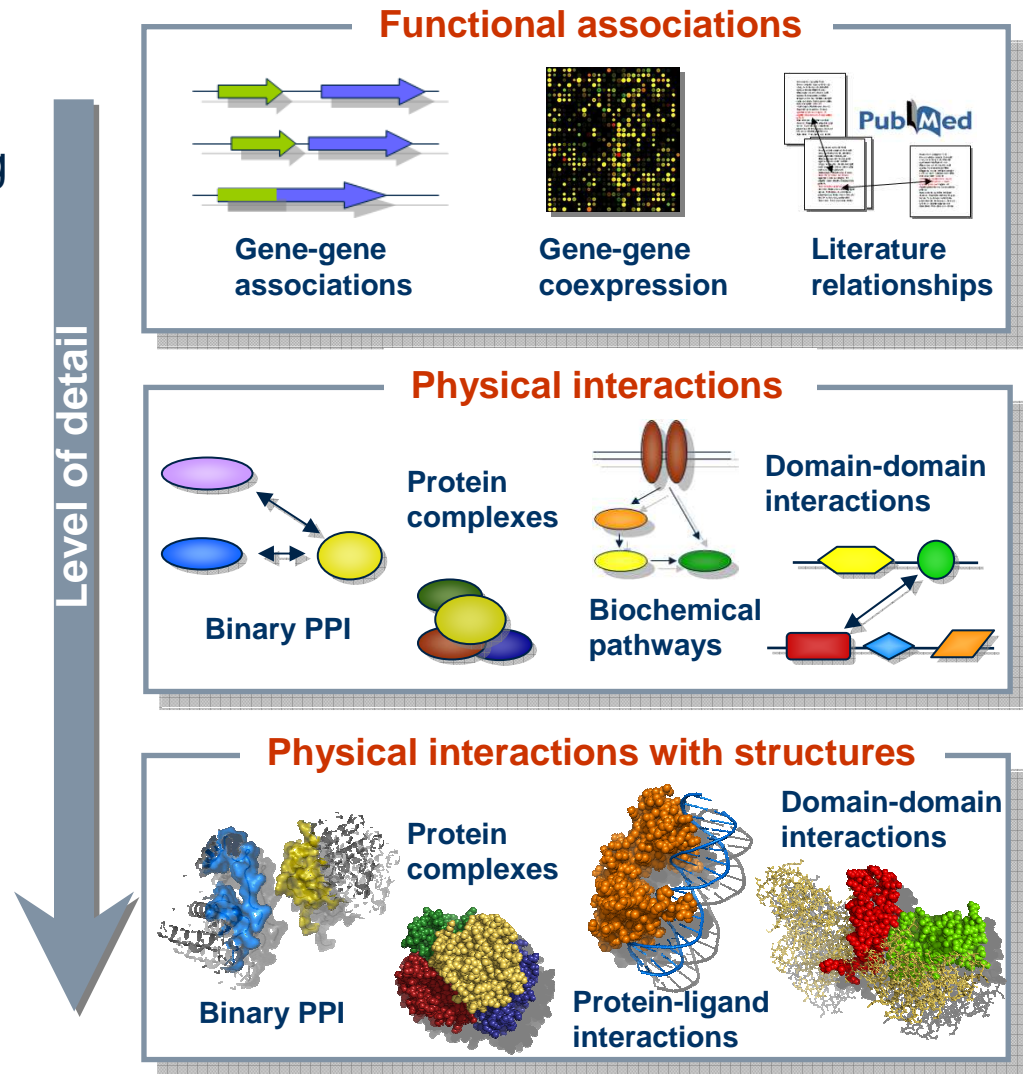


DAS for Molecular Interactions

Hagen Blankenburg

Importance of molecular interactions

- Fundamental for understanding of cellular processes
 - Prediction of protein function
 - Importance in certain diseases
 - Essentiality of hub proteins?
- The next big thing?!
 - „Interactomics“, „network medicine“, ...



Problem I: Data abundance and distribution

Proteins Interacting in the Nucleus

3DID - 3D interacting domains



max planck institut
informatik

PIN Database



Protein-Protein Interaction Database

PSI BASE



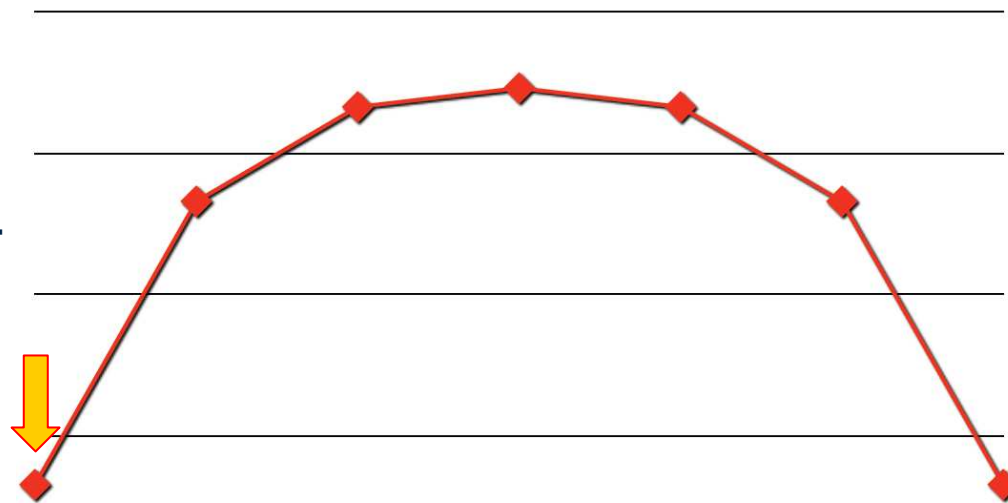
PIPs

Human Protein-Protein Interaction Prediction

predictome



Scientific impact



Domino
domain peptide
interactions database



(Credit: Tim Hubbard)

Too little bioinformatics

Too many databases

Too diverse interfaces



MINT a Molecular INTERactions database

DIMA

HomoMINT: an inferred human network
domain interaction map

Human Annotated and Predicted Protein Interaction (HAPPI)

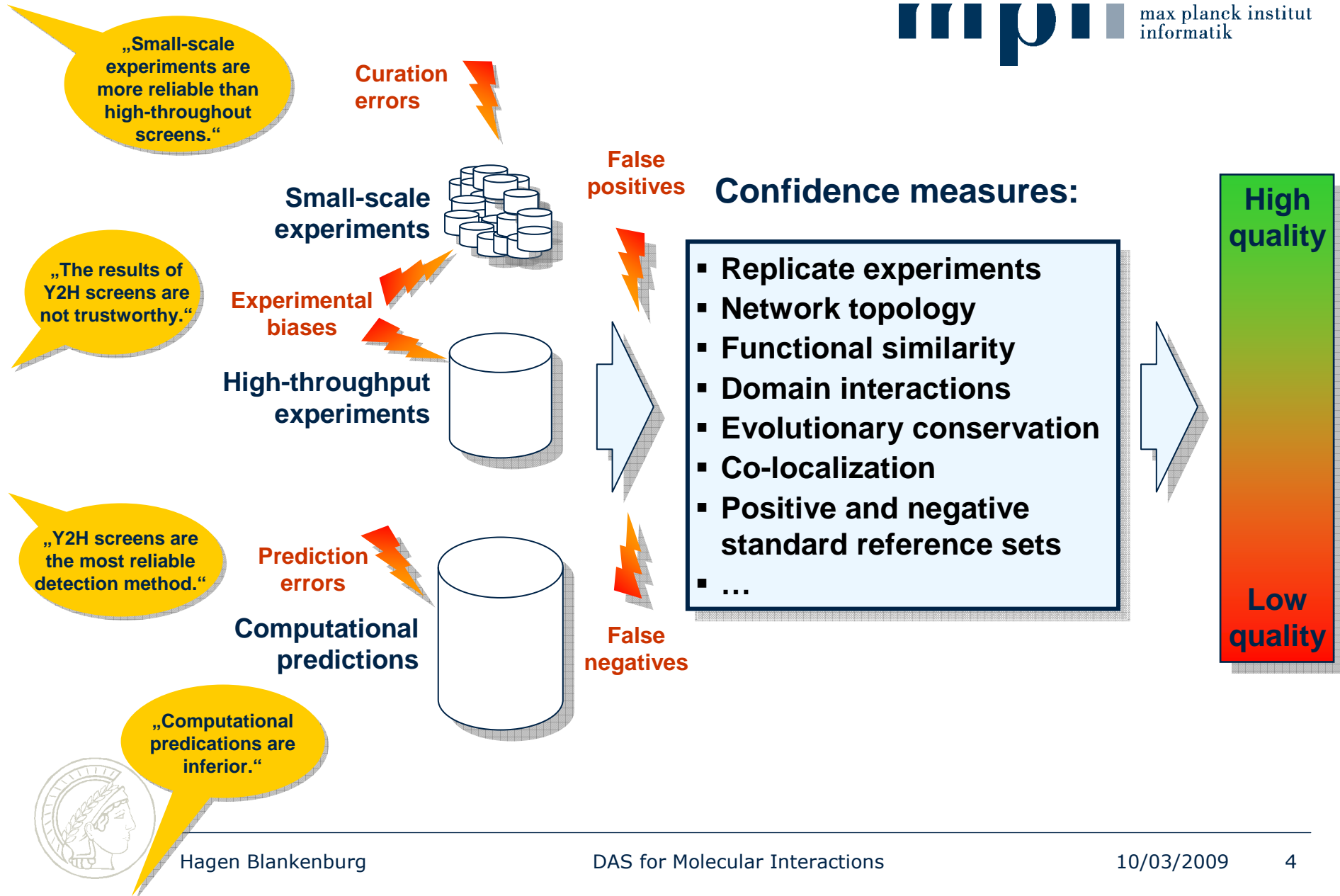
InterDom

Human protein-protein interaction network database search

Database of Interacting Domains



Problem II: Data quality



Problem II: Data quality

STRING

Your Input:

- ATXN1 Ataxin-1 (Spinocerebellar ataxia type 1 protein) (815 aa) (*Homo sapiens*)

Predicted Functional Partners:

Protein	Description	Neighborhood	Gene Fusion	Cooccurrence	Coexpression	Experiments	Databases	Textmining	[Homology]	Score
UBQLN4	Ubiquilin-4 (Ataxin-1 ubiquitin-like interacting protein A1U) (601 aa)									0.978
ANP32A	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Potent heat-stable)									0.969
PQBP1	polyglutamine binding protein 1 isoform 1 (265 aa)									0.950
COIL	Coilin (p80) (576 aa)									0.928
ATXN7	Ataxin-7 (Spinocerebellar ataxia type 7 protein) (945 aa)									0.928

PIPS

Protein 1	Protein 2	Name of Protein 2	Module Scores				Scores	Evidence	Database
			Expression	Orthology	Combined	Transitive			
RFC4	RFC3	RFC3: Replication factor C subunit 3					2.41E6	Evidence	o
RFC4	RFC5	RFC5: Replication factor C subunit 5					1.58E5	Evidence	o
RFC4	RFC2	RFC2: Replication factor C subunit 2					1.43E4	Evidence	o
RFC4	PCNA	PCNA: Proliferating cell nuclear antigen					1.25E4	Evidence	o

MINT

● APTX: Aprataxin (Q7Z2E3)
found to interact with 14 partner(s):

protein	interactions	score
x ● XRCC1 Homo sapiens (P18887)	10	0.95
● PARP1 Homo sapiens (P09874)	2	0.52
x ● XRCC4 Homo sapiens (Q13426)	2	0.43
● CEP350 Homo sapiens (Q5VT06)	1	0.24
● CNTROB Homo sapiens (Q8N137)	1	0.24
x ● HIVEP1 Homo sapiens (P15822)	1	0.24
● HRIHFB2216 Homo sapiens (O94799)	2	0.24
● KIAA0596 Homo sapiens (O60336)	1	0.24
● P02686 Homo sapiens (P02686)	1	0.24
x ● PICK1 Homo sapiens (Q9NRD5)	1	0.24
● q53hd4_human Homo sapiens (Q53HD4)	1	0.24
● SYT17 Homo sapiens (Q9BSW7)	1	0.24
x ● TRIM37 Homo sapiens (O94972)	2	0.24
● ZNF639 Homo sapiens (Q9UID6)	2	0.24

x proteins linked to a disease.




APID

PROTEIN INTERACTORS	EXPERIMENTS	PROVENANCE	More Info
SERA_YEAST	APT_X_YEAST	1	IntAct MINT DIP BIND +info_inter
YNM4_YEAST	APT_X_YEAST	1	IntAct +info_inter

INTERACTION FILTER AND SELECTION

Select interactions demonstrated for **at least 1** experiments and with **IPfam validation** Select

3DID

PDB ID	chain 1	residues	chain 2	residues	score	Z-score	more information	RasMol
1ibr	D	318-359	C	12-170	7.85	3.38228	1ibr	
1ibr	B	318-359	A	12-170	6.32	3.01999	1ibr	
1ibr	D	214-248	C	12-170	3.35	2.82048	1ibr	

IntAct

Description	-																		
Annotation	author-confidence LacZ4																		
Interacting molecules	<table border="1"> <thead> <tr> <th>Name</th> <th>Ac</th> <th>Interactor type</th> <th>Stoichiometry</th> <th>Interactor description</th> <th>Expression</th> <th>Identifier</th> <th>Gene</th> <th>Role</th> </tr> </thead> <tbody> <tr> <td>confidence-mapping</td> <td></td> <td></td> <td></td> <td>The authors have assigned confidence based on reporter gene activation. The Y2H interactions that can be identified by activation of three reporter genes HIS3, URA3 and lacZ were regarded as of higher confidence and classified as LacZ4 set. The Y2H interactions identified only with HIS3 and URA3 reporter genes were classified as lower confidence data set SD4.</td> <td></td> <td></td> <td></td> <td></td> </tr> </tbody> </table>	Name	Ac	Interactor type	Stoichiometry	Interactor description	Expression	Identifier	Gene	Role	confidence-mapping				The authors have assigned confidence based on reporter gene activation. The Y2H interactions that can be identified by activation of three reporter genes HIS3, URA3 and lacZ were regarded as of higher confidence and classified as LacZ4 set. The Y2H interactions identified only with HIS3 and URA3 reporter genes were classified as lower confidence data set SD4.				
Name	Ac	Interactor type	Stoichiometry	Interactor description	Expression	Identifier	Gene	Role											
confidence-mapping				The authors have assigned confidence based on reporter gene activation. The Y2H interactions that can be identified by activation of three reporter genes HIS3, URA3 and lacZ were regarded as of higher confidence and classified as LacZ4 set. The Y2H interactions identified only with HIS3 and URA3 reporter genes were classified as lower confidence data set SD4.															



Solution: Distributed System

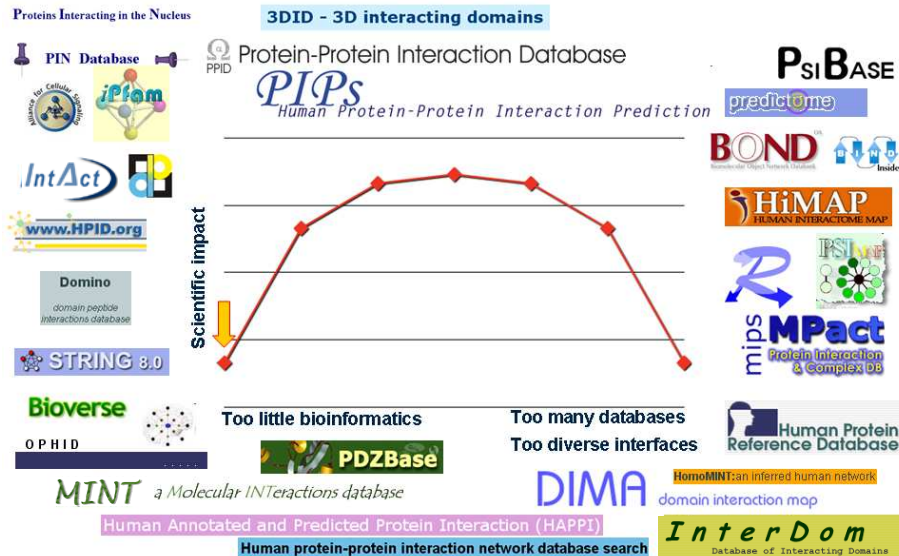
Interaction data servers



Interaction confidence scoring servers



Problem I: Data abundance and distribution



Problem II: Data quality

Your Input:

ATXN1 Ataxin-1 (Spinocerebellar ataxia type 1 protein) (815 aa)
(Homo sapiens)

Predicted Functional Partners:

Protein 1	Protein 2	Name of Protein 2	Expression	Ontology	Combined Transitive	Module Scores	Scores	Evidence	Database
RFC4	RFC3	RFC3: Replication factor C subunit 3				2.41E6	Evidence	72	o
RFC4	RFC5	RFC5: Replication factor C subunit 5				1.58E5	Evidence	72	o
RFC4	RFC2	RFC2: Replication factor C subunit 2				1.43E4	Evidence		
RFC4	PCNA	PCNA: Proliferating cell nuclear antigen				1.25E4	Evidence		

APID

PROTEIN INTERACTORS	EXPERIMENTS	PROVENANCE	More Info
SERA_YEAST	APTIX_YEAST	1	IntAct MINT DIP BIND
YNM4_YEAST	APTIX_YEAST	1	IntAct

3DID

Protein ID	chain	1 residues	chain 2 residues	score	Z-score	more information	ResMap
libr	D	318-359	C	12-170	7.85	3.38228	libr
libr	B	318-359	A	12-170	6.32	3.01999	libr
libr	D	214-248	C	12-170	3.35	2.82048	libr

MINT

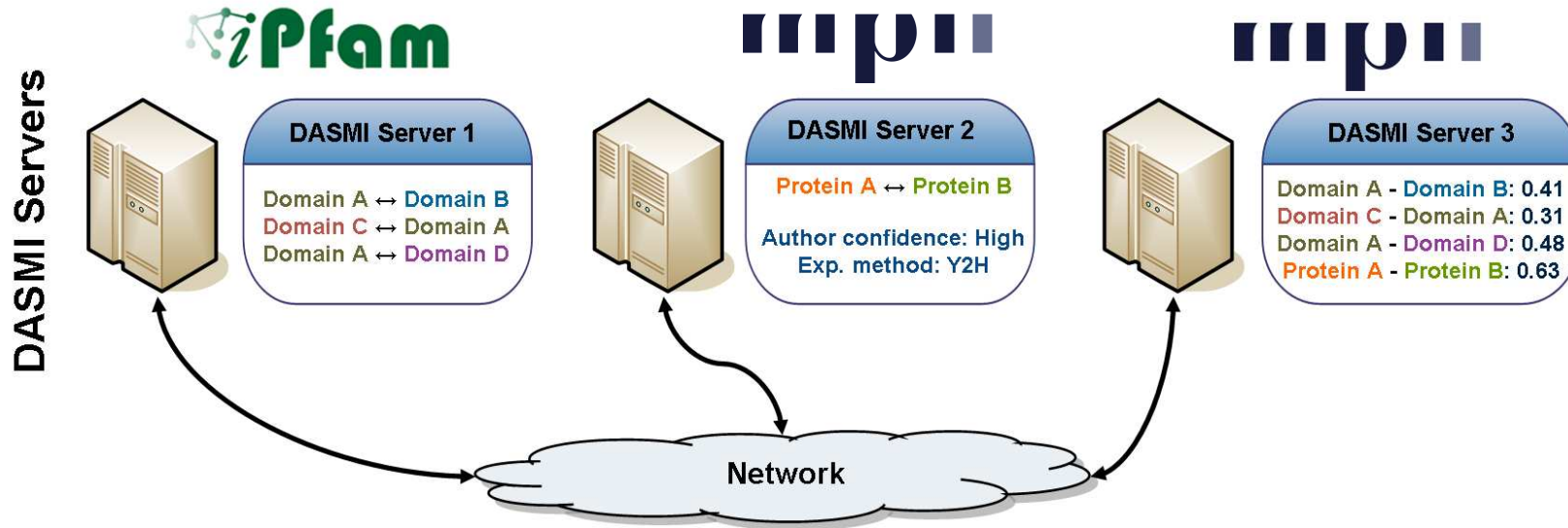
Protein	Interactions	Score
XRCC4 Homo sapiens (P18927)	10	0.95
PARP1 Homo sapiens (P08274)	2	0.52
XRCC4 Homo sapiens (Q13426)	2	0.43
CEP350 Homo sapiens (Q5Y708)	1	0.24
CNTROB Homo sapiens (Q8N137)	1	0.24
HIVEP1 Homo sapiens (P15822)	2	0.24
HRHFB2216 Homo sapiens (Q94799)	2	0.24
KUAA0506 Homo sapiens (Q60336)	1	0.24
P02686 Homo sapiens (P02686)	1	0.24
PICK1 Homo sapiens (Q9NF02)	1	0.24
ASPM4 Human Homo sapiens (Q53H04)	1	0.24
SYT17 Homo sapiens (Q98597)	1	0.24
TRIM37 Homo sapiens (Q94972)	2	0.24
ZNF639 Homo sapiens (Q9UID6)	2	0.24

IntAct

Interacting molecules	Name	Ac	Interactor type	Stoichiometry	Interactor description	Expression	Identifier	Gene	Role
	confidence-mapping				The authors have assigned confidence based on reporter gene activation. The Y2H interactions that can be identified by activation of these reporter genes HIS3, URA3 and LacZ are divided based on their confidence and classified as LacZ set 1. The Y2H interactions identified only with HIS3 and URA3 reporter genes were classified as lower confidence data set SD4.				domain-containing protein 1



DAS for Molecular Interactions (DASMI) - Servers

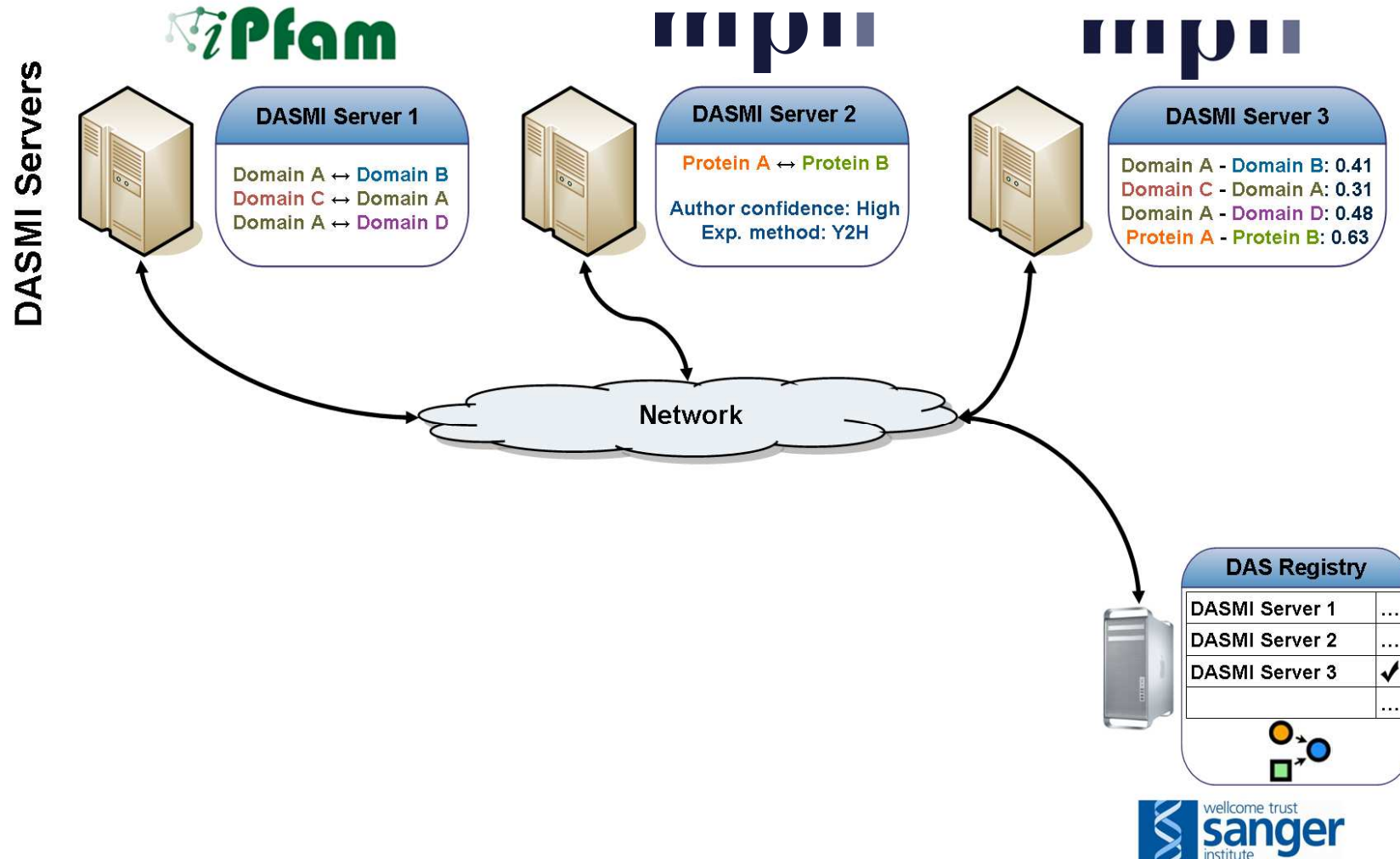


- Servers have coordinate / identifier systems

UniProtKB:	P51587, BRCA2_HUMAN
Entrez Gene:	675
GenInfo:	119395734, 28400649, 1177438, 14424438, 2315186, 27065822, 37675289, 1161384, 16116616,
RefSeq:	NP_000050.2, NM_000059
IPI:	IPI00412408
Ensembl:	ENSG00000139618



DAS for Molecular Interactions (DASMI) - Registry



DAS registry – <http://www.dasregistry.org>

- Maintained at Sanger Institute

All DAS servers with interaction capability

[home | list | validate | register new | statistics | docu | DAS 1.53E] [login]

[home | list | validate | register new | statistics | docu | DAS 1.53E] search

AVAILABLE DAS SOURCES

available DAS services

organism: any authority: any type: any

capability: interaction label: any display

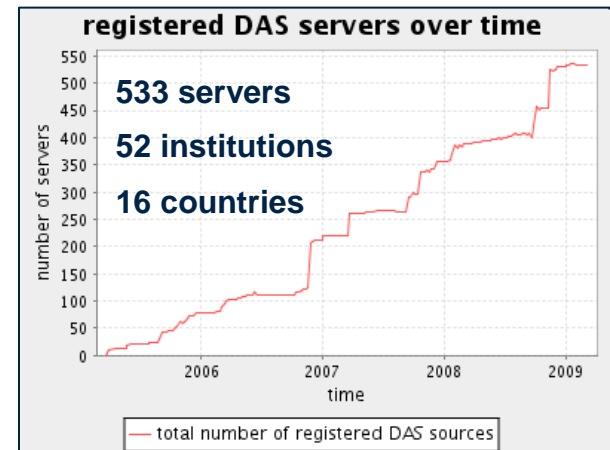
[1 - 10 | 28] next > last >> | show all

pos id	clients	nickname	status	capabilities	coordinateSystem	description	project
1	DS_529	ldsc-core	interaction	Pfam,Protein Sequence		show > go to site	
2	DS_527	interdom	interaction	Pfam,Protein Sequence		show > go to site	
3	DS_526	3did	interaction	Pfam,Protein Sequence		show > go to site	
4	DS_531	apmm2	interaction	Pfam,Protein Sequence		show > go to site	
5	DS_530	apmm1	interaction	Pfam,Protein Sequence		show > go to site	
6	DS_528	ldsc	interaction	Pfam,Protein Sequence		show > go to site	
7	DS_498	homomint	interaction	Entrez, Gene_ID		show > go to site	
8	DS_499	ccsb-hi1	interaction	Entrez, Gene_ID		show > go to site	
9	DS_500	sanger	interaction	Entrez, Gene_ID		show > go to site	
10	DS_501	sanger-core	interaction	Entrez, Gene_ID		show > go to site	

[1 - 10 | 28] next > last >> | show all

DAS - client legend:
 ... SPICE
 ... Ensembl
 ... Dasty

[home | list sources | validate | register new | statistics | history | docu] © 2008

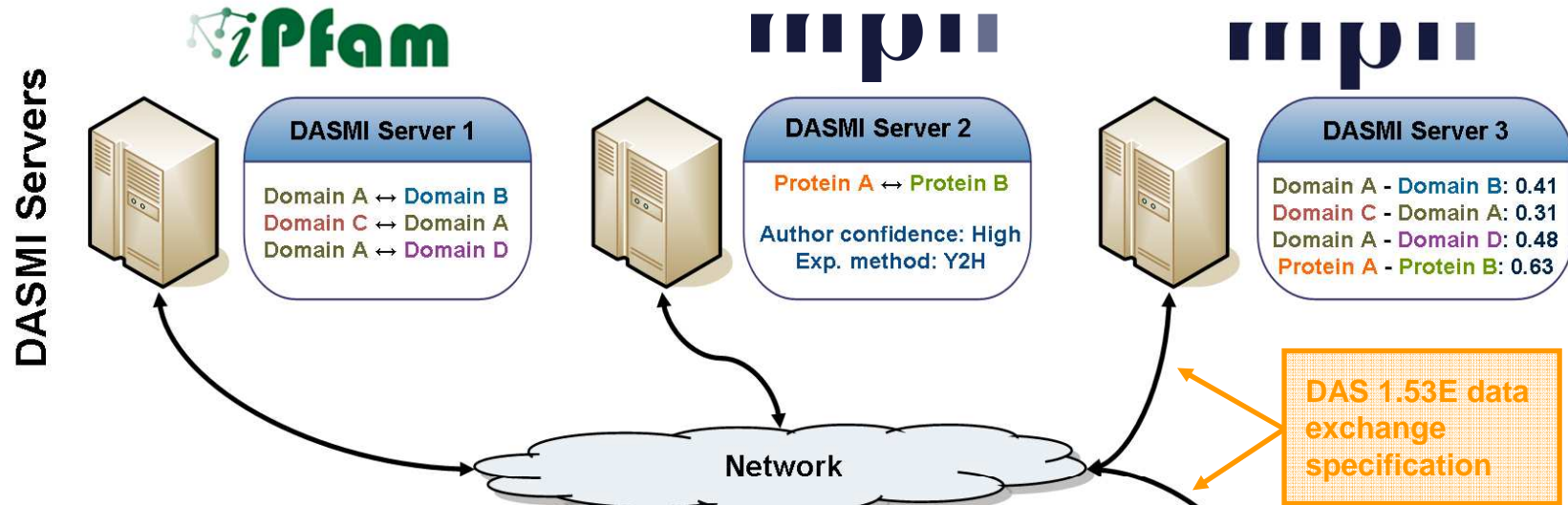


Domain interactions

Protein interactions



DAS for Molecular Interactions (DASMI) - Data exchange



DAS Request

<http://www.dasmi.de/das/funsimmat/interaction?interactor=P09497&interactor=O60828&detail=property:bpscore>

DASINT XML Response

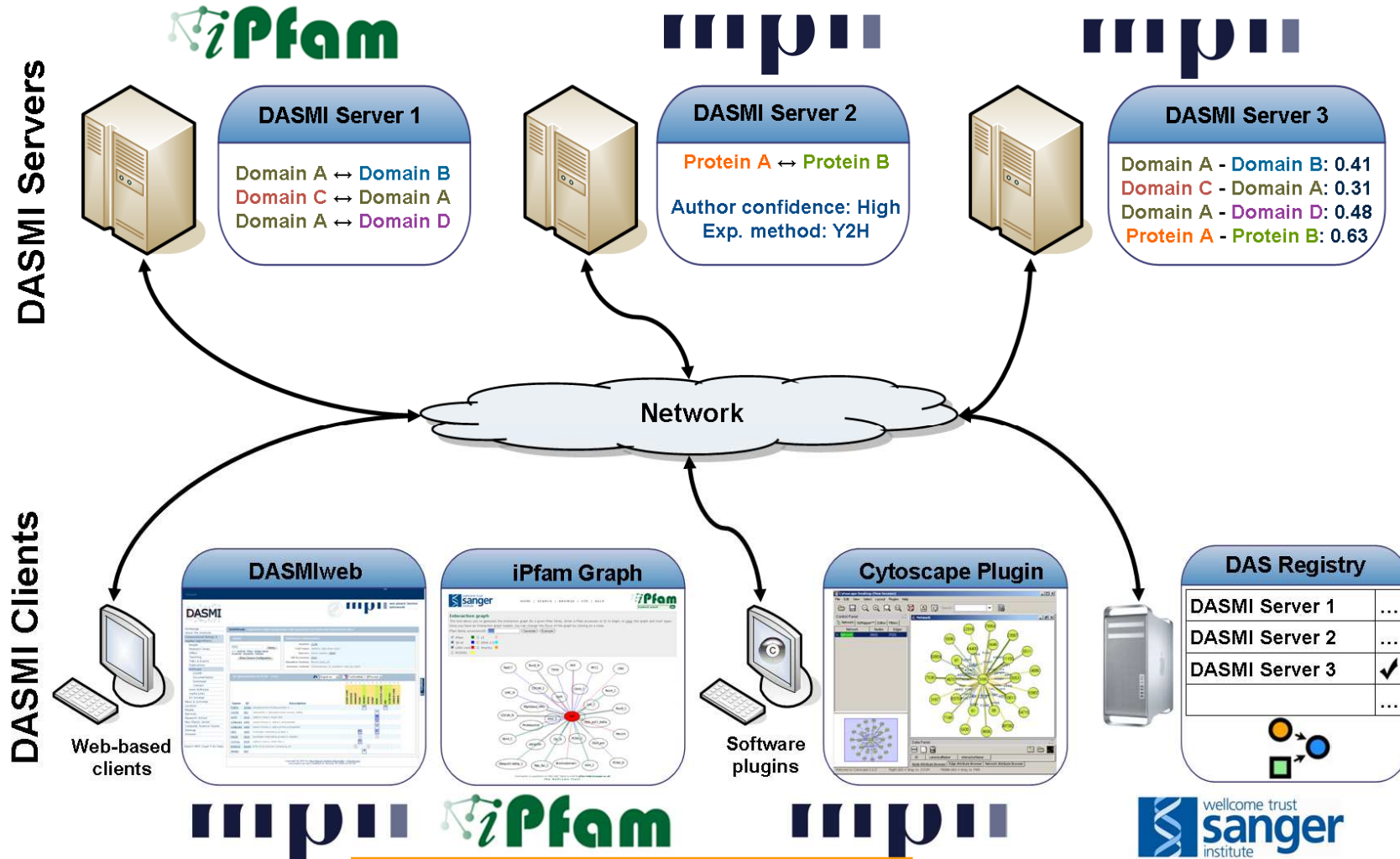
```

<?xml version="1.0" encoding="UTF-8"?>
<DASINT xmlns="http://www.dasmi.de/" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance"
  xsi:schemaLocation="http://www.dasmi.de/ http://www.dasmi.de/dasint.xsd">
  <INTERACTOR intId="1" shortLabel="CLCB_HUMAN" dbSource="uniprotkb" dbSourceCvId="MI:0486"
    dbVersion="12.1" dbAccessionId="P09497" dbCoordSys="UniProt,Protein Sequence"/>
  <INTERACTOR intId="2" shortLabel="PQBP1_HUMAN" dbSource="uniprotkb" dbSourceCvId="MI:0486"
    dbVersion="12.1" dbAccessionId="O60828" dbCoordSys="UniProt,Protein Sequence"/>
  <INTERACTION name="P09497-O60828" dbSource="" dbAccessionId="">
    <DETAIL property="bpscore" value="0.154429056459711"/>
    <PARTICIPANT intId="1"/>
    <PARTICIPANT intId="2"/>
  </INTERACTION>
</DASINT>
  
```

DAS Registry

DASMI Server 1	...
DASMI Server 2	...
DASMI Server 3	✓
	...

DAS for Molecular Interactions (DASMI) - Clients



Clients merge interactors / interactions



iPfam graphical domain interaction browser

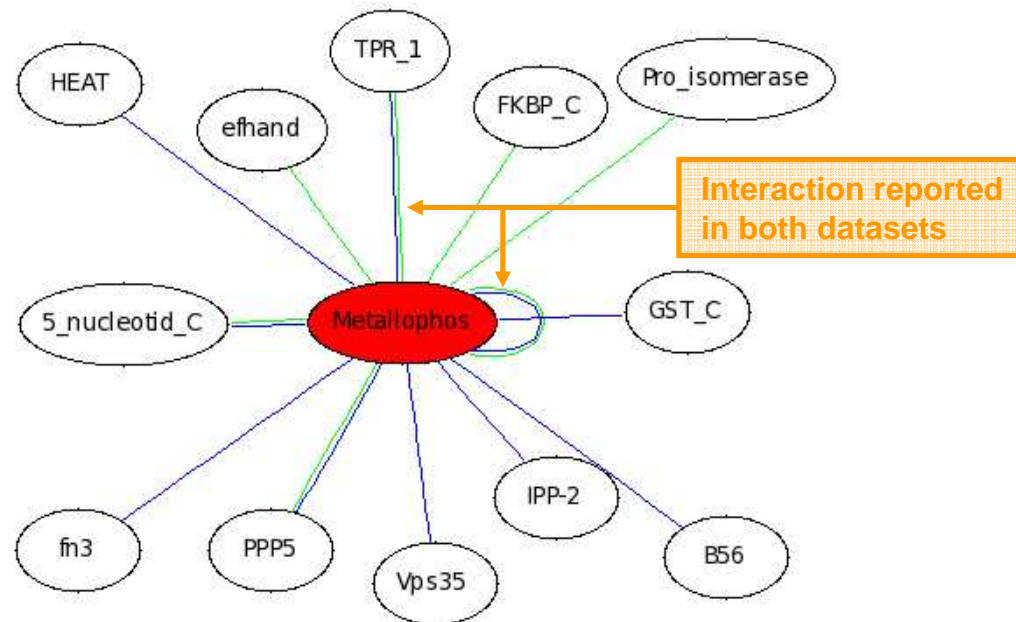
Interaction graph

This tool allows you to generate the interaction graph for a given Pfam family. Enter a Pfam accession or ID to begin, or [clear](#) this graph and start again. Once you have an interaction graph loaded, you can change the focus of the graph by clicking on a node.

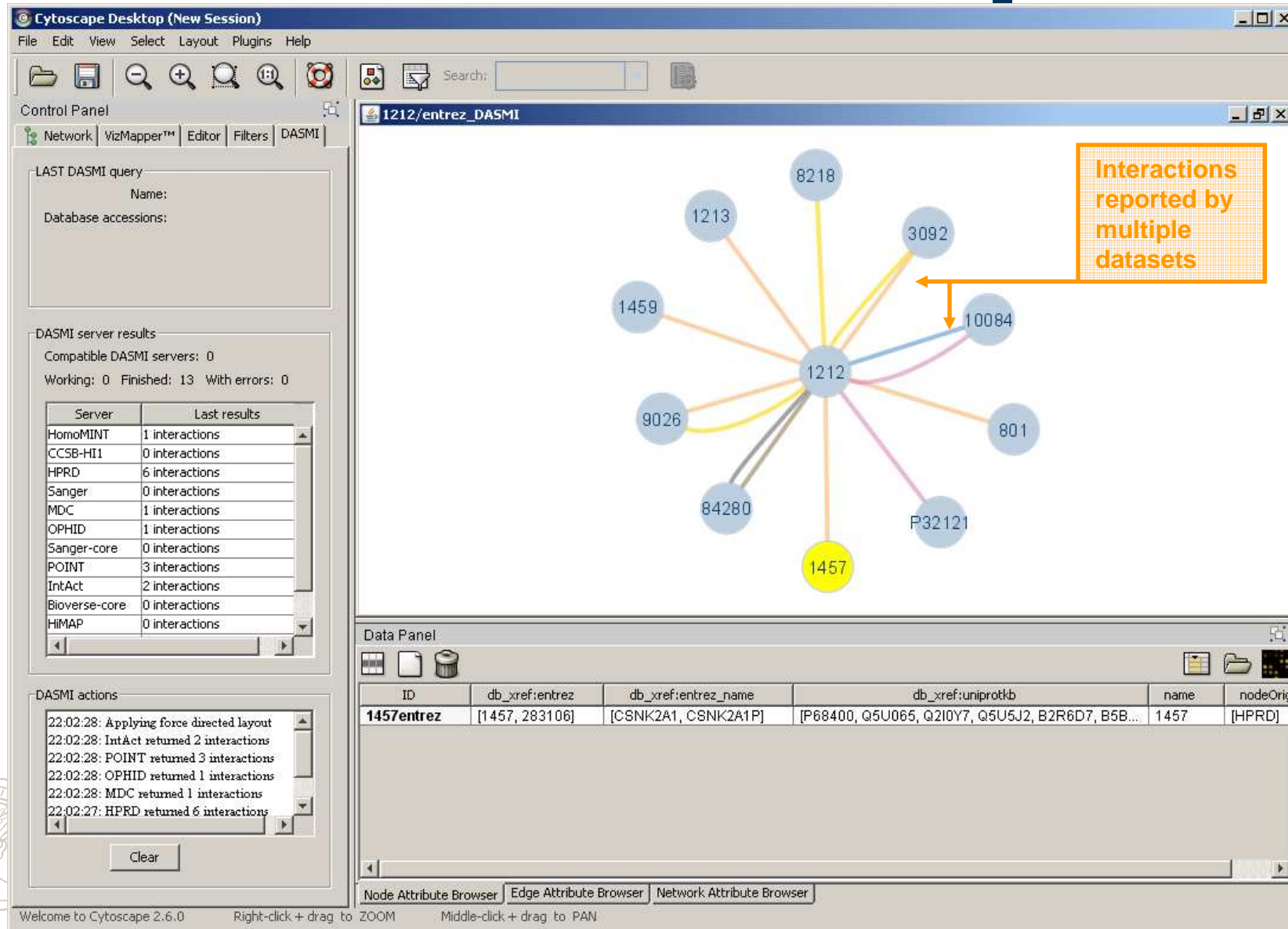
Pfam family accession/ID:

- | | | | | | | |
|---|---|------------------------------------|---------------------------------|-----------------------------|-----------------------------------|---------------------------------|
| <input checked="" type="checkbox"/> iPfam | <input checked="" type="checkbox"/> 3D-id | <input type="checkbox"/> LDSC core | <input type="checkbox"/> RCDP50 | <input type="checkbox"/> LP | <input type="checkbox"/> DIMA 2.0 | <input type="checkbox"/> Wuchty |
|---|---|------------------------------------|---------------------------------|-----------------------------|-----------------------------------|---------------------------------|

Selected domain
interaction servers



DASMI Cytoscape Client



The screenshot shows the Cytoscape Desktop interface with a network graph and several control panels.

Control Panel (DASMI):

- LAST DASMI query:
 - Name:
 - Database accessions:
- DASMI server results:
 - Compatible DASMI servers: 0
 - Working: 0 Finished: 13 With errors: 0

Server	Last results
HomoMINT	1 interactions
CCSB-HI1	0 interactions
HPRD	6 interactions
Sanger	0 interactions
MDC	1 interactions
OPHID	1 interactions
Sanger-core	0 interactions
POINT	3 interactions
IntAct	2 interactions
Bioverse-core	0 interactions
HIMAP	0 interactions
- DASMI actions:
 - 22:02:28: Applying force directed layout
 - 22:02:28: IntAct returned 2 interactions
 - 22:02:28: POINT returned 3 interactions
 - 22:02:28: OPHID returned 1 interactions
 - 22:02:28: MDC returned 1 interactions
 - 22:02:27: HPRD returned 6 interactions

Network Graph: A central node (1212) is connected to several other nodes (1213, 8218, 3092, 10084, 801, P32121, 1457, 84280, 9026, 1459). An orange box highlights the interactions between nodes 1212 and 10084, with the text "Interactions reported by multiple datasets".

Data Panel:

ID	db_xref:entrez	db_xref:entrez_name	db_xref:uniprotkb	name	nodeOrig
1457entrez	[1457, 283106]	[CSNK2A1, CSNK2A1P]	[P68400, Q5U065, Q210Y7, Q5U5J2, B2R6D7, B5B...	1457	[HPRD]

Node Attribute Browser | Edge Attribute Browser | Network Attribute Browser

Welcome to Cytoscape 2.6.0 Right-click + drag to ZOOM Middle-click + drag to PAN

DASMI Cytoscape Client

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Control Panel

Network VizMapper™ Editor Filters DASMI

LAST DASMI query

Name:

Database accessions:

DASMI server results

Compatible DASMI servers: 0

Working: 0 Finished: 26 With errors: 0

Server	Last results
CCSB-HI1	0 interactions
MDC	2 interactions
OPHID	4 interactions
HomoMINT	39 interactions
HIMAP	5 interactions
HPRD	186 interactions
POINT	112 interactions
HIMAP-core	3 interactions
Bioverse-core	1 interactions
Bioverse	665 interactions
Sanger	220 interactions
Sanger-core	11 interactions

DASMI actions

22:09:26: Applying force directed layout

22:09:25: Sanger-core returned 11 interactions

22:09:09: IntAct returned 307 interactions

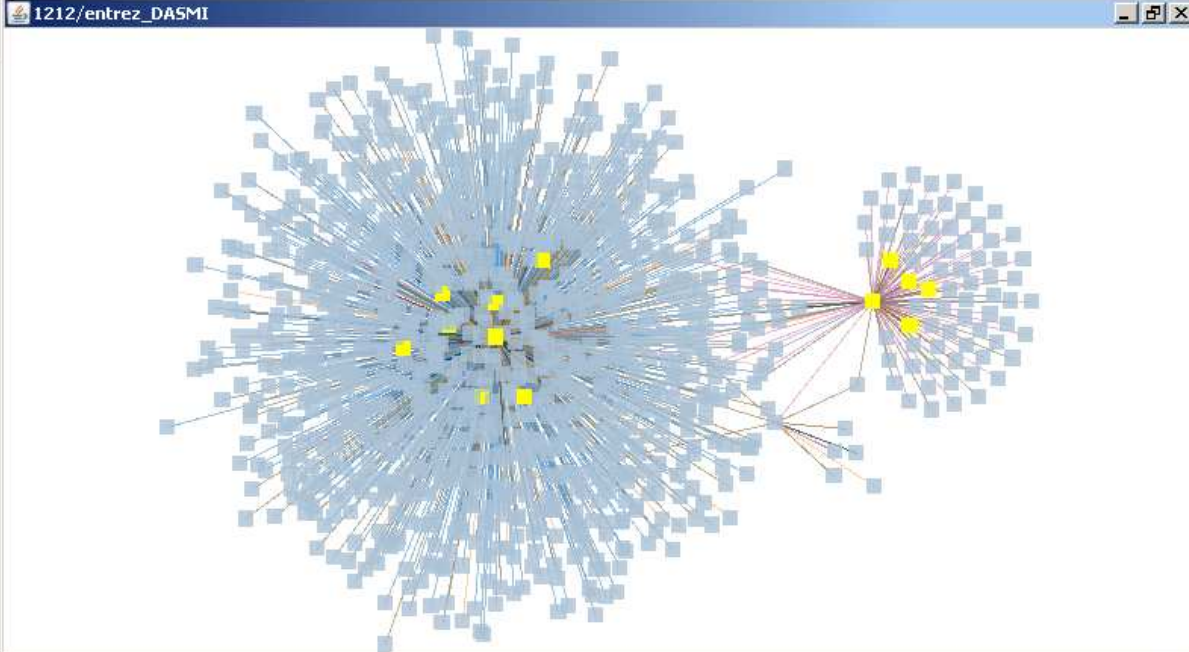
22:08:31: Sanger returned 220 interactions

22:06:31: Bioverse returned 666 interactions

22:06:31: Bioverse-core returned 1 interaction

Clear

1212/entrez_DASMI



Data Panel

ID	db_xref:entrez	db_xref:entrez_name	db_xref:uniprotkb	name
11198entrez	[11198]	[SUPT16H]	[Q9Y5B9, Q0VGA3]	11198
79577entrez	[79577]	[CDC73]	[Q6P1J9, B2RBR2, A8MPR2, Q6PHR8]	79577
25790entrez	[25790]	[CCDC19]	[Q9UL16, A8K884, Q05BA3, Q5VU18]	25790
1460entrez	[1460, 58496]	[CSNK2B, LY6G5B]	[P67870, B0UXA9, Q8NDX9-1, Q8NDX9, B0UXB2, ...]	1460
P32121uniprotkb	[409]	[ARRB2]	[P32121, P32121-1, A8K4I6, B5B0C0, Q59EM5, P3...]	P32121
271entrez	[271]	[AMPD2]	[Q01433-2, Q01433, B4DK50, Q5T695, Q01433-3, ...]	271
54558entrez	[54558]	[SPATA6]	[Q9NWH7-1, Q9NWH7, B4DX17, Q9NWH7-2, A8M...]	54558
65083entrez	[65083]	[NOL6]	[Q9H6R4-1, Q9H6R4, Q9H6R4-3, Q9H6R4-4, B3K...]	65083

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

Welcome to Cytoscape 2.6.0 Right-click + drag to ZOOM Middle-click + drag to PAN



- Homepage
- About the Institute
- Computational Biology & Applied Algorithmics
- People
- Research Areas
- Offers
- Teaching
- Talks & Events
- Publications
- Software
 - DASMI
 - DASMIweb
 - Documentation
 - Download
 - Contact
 - more Software
 - Useful Links
- News & Activities
- Location
- People
- Services
- Research School
- Max Planck Center
- Computer Science Cluster
- Sitemap

Search MPII (type ? for help)

DASMIweb - dynamic online integration and annotation of molecular interaction data

Query

961

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

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](#),

UniParc [UPI0000049C6C](#), [UPI00001BDF27](#),

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

Name	ID	Description	Confidence Sources															
			SANGER-CORE	INTACT	CCSB-HI1	HPRD	BIOVERSE	SANGER	MINT	HOMOMINT	HIMAP	HIMAP-CORE	POINT	OPHID	HPIDB	MDC	DIP	BIOVERSE-CORE
P2RY2	5029	P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)(Purinergic receptor).																
EPB42	2038	Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)(P4.2).																
THBS1	7057	Hypothetical protein (Fragment).																
UBQLN1	29979	Ubiquilin-1 (Protein linking IAP with cytoskeleton 1) (PLIC-1) (hPLIC-1).																
RHAG	6005	Rhesus blood group-associated glycoprotein (Rhesus blood group-associated ammonia channel) (Erythrocyte plasma membrane 50 kDaglycoprotein) (Rh50A) (CD241 antigen).																
PTK2	5747	Focal adhesion kinase 1 (EC 2.7.10.2) (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2).																
ITGA6	3655	Integrin alpha-6 variant (Fragment).																
COMP	1311	Cartilage oligomeric matrix protein variant (Fragment).																
THBS2	7058	Hypothetical protein DKFZp686G02190 (Fragment).																
THBS3	7059	Thrombospondin 3 variant (Fragment).																
THBS4	7060	Thrombospondin-4 precursor.																

Predictions (points to SANGER-CORE, INTACT, CCSB-HI1, BIOVERSE, SANGER, MINT, HOMOMINT, HIMAP, HIMAP-CORE, POINT, OPHID, HPIDB, MDC, DIP, BIOVERSE-CORE)

Literature curation / experiments (points to SANGER-CORE, INTACT, CCSB-HI1, BIOVERSE, SANGER, MINT, HOMOMINT, HIMAP, HIMAP-CORE, POINT, OPHID, HPIDB, MDC, DIP, BIOVERSE-CORE)

Interaction reported by multiple datasets (points to THBS1 interaction)

myDASMI



- Homepage
- About the Institute
- Computational Biology & Applied
Algorithmics
- People
- Research Areas
- Offers
- Teaching
- Talks & Events
- Publications
- Software
- DASMI
- DASMIweb
- Documentation
- Download
- Contact
- more Software
- Useful Links
- News & Activities
- Location
- People
- Services
- Research School
- Max Planck Center
- Computer Science Cluster
- Sitemap

Search MPII (type ? for help)

DASMIweb - dynamic online integration and annotation of molecular interaction data

Query

961

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

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](#),

UniParc [UPI0000049C6C](#), [UPI00001BDF27](#),

22 interactions (showing 11 to 20)

All confidence scoring methods that returned results for the current interactions

Select confidence measure ...

- Bioverse (originalConfidenceScore)
- Bioverse-core (originalConfidenceScore)
- Domain support (predicted)
- FunSimMat2.1 (BPscore)
- FunSimMat2.1 (CCscore)
- FunSimMat2.1 (MFscore)
- HiMAP (originalConfidenceScore)

Name	ID	Description	POINT	OPHID	HPIDB	MDC	DIP	BIOVERSE-CORE
P2RY2	5029	P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)(Purinergic receptor).	■					
EPB42	2038	Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)(P4.2).	■					
THBS1	7057	Hypothetical protein (Fragment).	■	■				■
UBQLN1	29979	Ubiquilin-1 (Protein linking IAP with cytoskeleton 1) (PLIC-1) (hPLIC-1).	■					
RHAG	6005	Rhesus blood group-associated glycoprotein (Rhesus blood group-associated ammonia channel) (Erythrocyte plasma membrane 50 kDaglycoprotein) (Rh50A) (CD241 antigen).	■					
PTK2	5747	Focal adhesion kinase 1 (EC 2.7.10.2) (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2).	■					
ITGA6	3655	Integrin alpha-6 variant (Fragment).					■	
COMP	1311	Cartilage oligomeric matrix protein variant (Fragment).						■
THBS2	7058	Hypothetical protein DKFZp686G02190 (Fragment).	■					
THBS3	7059	Thrombospondin 3 variant (Fragment).	■					
THBS4	7060	Thrombospondin-4 precursor.	■					



- Homepage
- About the Institute
- Computational Biology & Applied
Algorithmics
- People
- Research Areas
- Offers
- Teaching
- Talks & Events
- Publications
- Software
- DASMI
- DASMIweb
- Documentation
- Download
- Contact
- more Software
- Useful Links
- News & Activities
- Location
- People
- Services
- Research School
- Max Planck Center
- Computer Science Cluster
- Sitemap

Search MPII (type ? for help)

DASMIweb - dynamic online integration and annotation of molecular interaction data

Query

961

Query

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

Show Source Configuration

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](#),

[UniParc](#) [UPI0000049C6C](#), [UPI00001BDF27](#),

22 interactions (showing 11 to 20) previous next

Export as ...

Bioverse (originalConfidenceScore)

Query Confidence Sources

Original confidence score provided by the authors

Name	ID	Description	SANGER-CORE	INTACT	CCSB-HII	HPRO	BIOVERSE	SANGER	MINT	HOMMINT	HIMAP	HIMAP-CORE	POINT	OPHID	HPIDB	HDC	DIP	BIOVERSE-CORE	
P2RY2	5029	P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)(Purinergic receptor).																	
EPB42	2038	Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)(P4.2).																	
THBS1	7057	Hypothetical protein (Fragment).				0.92	0.92							0.92					0.92
UBQLN1	29979	Ubiquilin-1 (Protein linking IAP with cytoskeleton 1) (PLIC-1) (hPLIC-1).																	
RHAG	6005	Rhesus blood group-associated glycoprotein (Rhesus blood group-associated ammonia channel) (Erythrocyte plasma membrane 50 kDaglycoprotein) (Rh50A) (CD241 antigen).																	
PTK2	5747	Focal adhesion kinase 1 (EC 2.7.10.2) (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2).																	
ITGA6	3655	Integrin alpha-6 variant (Fragment).																	
COMP	1311	Cartilage oligomeric matrix protein variant (Fragment).																	0.28
THBS2	7058	Hypothetical protein DKFZp686G02190 (Fragment).																	0.27
THBS3	7059	Thrombospondin 3 variant (Fragment).																	0.27
THBS4	7060	Thrombospondin-4 precursor.																	0.27

Details for Bioverse (originalConfidenceScore)

The confidence score as reported in the original publication.
Range: 0-1
<http://nar.oxfordjournals.org/cgi/content/abstract/31/13/3736>



- Homepage
- About the Institute
- Computational Biology & Applied Algorithmics
- People
- Research Areas
- Offers
- Teaching
- Talks & Events
- Publications
- Software
 - DASMI
 - DASMIweb
 - Documentation
 - Download
 - Contact
 - more Software
 - Useful Links
- News & Activities
- Location
- People
- Services
- Research School
- Max Planck Center
- Computer Science Cluster
- Sitemap

Search MPII (type ? for help)

DASMIweb - dynamic online integration and annotation of molecular interaction data

Query

961

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

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](#),

UniParc [UPI0000049C6C](#), [UPI00001BDF27](#),

22 interactions (showing 11 to 20) Export as ...

Name	ID	Description	SANGER-CORE	INTACT	CCSB-HII	HPRD	BIOVERSE	SANGER	MINT	HOMMINT	HIMAP	HIMAP-CORE	POINT	OPHID	HPIDB	MDC	DIP	BIOVERSE-CORE	
P2RY2	5029	P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)(Purinergic receptor).																	
EPB42	2038	Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)(P4.2).																	
THBS1	7057	Hypothetical protein (Fragment).																	
UBQLN1	29979	Ubiquilin-1 (Protein linking IAP with cytoskeleton 1) (PLIC-1) (hPLIC-1).																	
RHAG	6005	Rhesus blood group-associated glycoprotein (Rhesus blood group-associated ammonia channel) (Erythrocyte plasma membrane 50 kDaglycoprotein) (Rh50A) (CD241 antigen).																	
PTK2	5747	Focal adhesion kinase 1 (EC 2.7.10.2) (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2).																	
ITGA6	3655	Integrin alpha-6 variant (Fragment).																	
COMP	1311	Cartilage oligomeric matrix protein variant (Fragment).																	
THBS2	7058	Hypothetical protein DKFZp686G02190 (Fragment).																	
THBS3	7059	Thrombospondin 3 variant (Fragment).																	
THBS4	7060	Thrombospondin-4 precursor.																	

Protein interactions supported by underlying domain interactions

Details for Domain support (predicted)

This measure indicates protein-protein interactions that are supported by underlying domain-domain interactions. The domain-domain interaction datasets used in the predicted subset are based on diverse computational prediction algorithms. Please see the respective interaction details for more information on the datasets.

Range: 1
<http://www.dasmi.de>


[Homepage](#)
[About the Institute](#)
[Computational Biology & Applied
Algorithmics](#)
[People](#)
[Research Areas](#)
[Offers](#)
[Teaching](#)
[Talks & Events](#)
[Publications](#)
[Software](#)
[DASMI](#)
[DASMIweb](#)
[Documentation](#)
[Download](#)
[Contact](#)
[more Software](#)
[Useful Links](#)
[News & Activities](#)
[Location](#)
[People](#)
[Services](#)
[Research School](#)
[Max Planck Center](#)
[Computer Science Cluster](#)
[Sitemap](#)

DASMIweb - dynamic online integration and annotation of molecular interaction data

Query

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

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](#),

UniParc [UPI0000049C6C](#), [UPI00001BDF27](#),

22 interactions (showing 11 to 20)



Export as ...



Domain support (predicted)

Name	ID	Description	SANGER-CORE	INTACT	CCSB-HI1	HPRD	BIOVERSE	SANGER	HINT	HOMOMINT	HIMAP	HIMAP-CORE	POINT	OPHID	HPIDB	MDC	DIP	BIOVERSE-CORE
P2RY2	5029	P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)(Purinergic receptor).	0	1	0	11	5	0	0	1	1	0	8	2	0	0	0	1
EPB42	2038	Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)(P4.2).																

Details from source HPRD

 link http://www.hprd.org/interactions?protein=01517&isoform_id=01517_1&isoform_name=

 link http://www.hprd.org/interactions?protein=03017&isoform_id=03017_1&isoform_name=

 DAS query string <http://dasmi.bioinf.mpi-inf.mpg.de/das/hprd/interaction?interactor=Q08722&interactor=A8K198&interactor=Q71A41&operation=union>

Details from source Domain support

predicted PF00927-PF04549: IPPRI core (0.03977)

predicted PF00927-PF08204: IPPRI core (0.03977)

predicted PF00868-PF04549: IPPRI core (0.061411)

predicted PF00868-PF08204: IPPRI core (0.061411)

predicted PF01841-PF04549: IPPRI core (0.061411)

predicted PF01841-PF08204: IPPRI core (0.061411)

Details from source FunSimMat2.1

MFscore 0.976656009021968

CCscore 0.846404924988201

Details on domain interactions

Details for Domain support (predicted)

This measure indicates protein-protein interactions that are supported by underlying domain-domain interactions. The domain-domain interaction datasets used in the predicted subset are based on diverse computational prediction algorithms. Please see the respective interaction details for more information on the datasets.

Range: 1

<http://www.dasmi.de>



- Homepage
- About the Institute
- Computational Biology & Applied Algorithmics
- People
- Research Areas
- Offers
- Teaching
- Talks & Events
- Publications
- Software
 - DASMI
 - DASMIweb
 - Documentation
 - Download
 - Contact
 - more Software
 - Useful Links
- News & Activities
- Location
- People
- Services
- Research School
- Max Planck Center
- Computer Science Cluster
- Sitemap

Search MPII (type ? for help)

DASMIweb - dynamic online integration and annotation of molecular interaction data

Query

961

Query

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

Show Source Configuration

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](#),

[UniParc](#) [UPI0000049C6C](#), [UPI00001BDF27](#),

22 interactions (showing 11 to 20) ← →

Export as ...

FunSimMat2.1 (BPscore)

Query Confidence Sources

Functional similarity based on GO annotation of interactors

Name	ID	Description	SANGER-CORE	INTACT	CCSB-HII	HPRD	BIOVERSE	SANGER	MINT	HOMMINT	HIMAP	HIMAP-CORE	POINT	OPHID	HPIDB	MDC	DIP	BIOVERSE-CORE
P2RY2	5029	P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor)(Purinergic receptor).				0.61												
EPB42	2038	Erythrocyte membrane protein band 4.2 (Erythrocyte protein 4.2)(P4.2).																
THBS1	7057	Hypothetical protein (Fragment).				0.22	0.22							0.22				0.22
UBQLN1	29979	Ubiquilin-1 (Protein linking IAP with cytoskeleton 1) (PLIC-1) (hPLIC-1).																
RHAG	6005	Rhesus blood group-associated glycoprotein (Rhesus blood group-associated ammonia channel) (Erythrocyte plasma membrane 50 kDaglycoprotein) (Rh50A) (CD241 antigen).				0.13												
PTK2	5747	Focal adhesion kinase 1 (EC 2.7.10.2) (FADK 1) (pp125FAK) (Protein-tyrosine kinase 2).				0.59												
ITGA6	3655	Integrin alpha-6 variant (Fragment).									0.71							
COMP	1311	Cartilage oligomeric matrix protein variant (Fragment).						0.20										
THBS2	7058	Hypothetical protein DKFZp686G02190 (Fragment).																
THBS3	7059	Thrombospondin 3 variant (Fragment).																
THBS4	7060	Thrombospondin-4 precursor.																

Details for FunSimMat2.1 (BPscore)

The BPscore is based on biological process annotation of the Gene Ontology.

Range: 0-1

<http://funsimmat.bioinf.mpi-inf.mpg.de/help.php>

- Usage of DASMI servers and clients surprisingly good, but more external DASMI servers are desirable
- DAS client and server libraries (Dazzle, ProServer, (MyDAS), Dasobert, Bio-DAS-lite) support DASMI
- Considerable overlap with HUPO-PSI initiatives for distributed interaction data retrieval (PSICQUIC) and confidence scoring (PSISCORE)
- Develop methods for combining different interaction confidence scoring schemas in DASMI clients

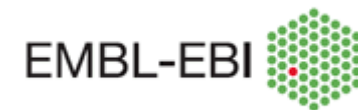


Acknowledgements



- Joachim Büch
- Fidel Ramírez
- Dorothea Emig
- Sven-Eric Schelhorn
- Andreas Schlicker
- Thomas Lengauer
- Mario Albrecht

- Robert Finn
- Andreas Prlić
- Jonathan Warren



- Andrew Jenkinson
- Henning Hermjakob

