

The PSI MI standard open analysis of protein interaction data



Bioinformatics Open Source Conference, Glasgow, July 2004.
Samuel Kerrien, European Bioinformatics Institute



Engineering 1850

- Nuts and bolts fit perfectly together, but only if they originate from the same factory
- Standardisation proposal in 1864 by William Sellers
- It took until after WWII until it was generally accepted, though ...



Engineering 1850

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Proteomics 2004

- Proteomics results are perfectly compatible, but only if they are from the same lab, from the same software
- Fragmentation of proteomics data
- “Publish and vanish”
- Urgent need for standardisation

HUPO Proteomics Standards Initiative

- Develop data *format* standards
- Data *representation* and *annotation* standards
- Involve data producers, database providers, software producers, publishers

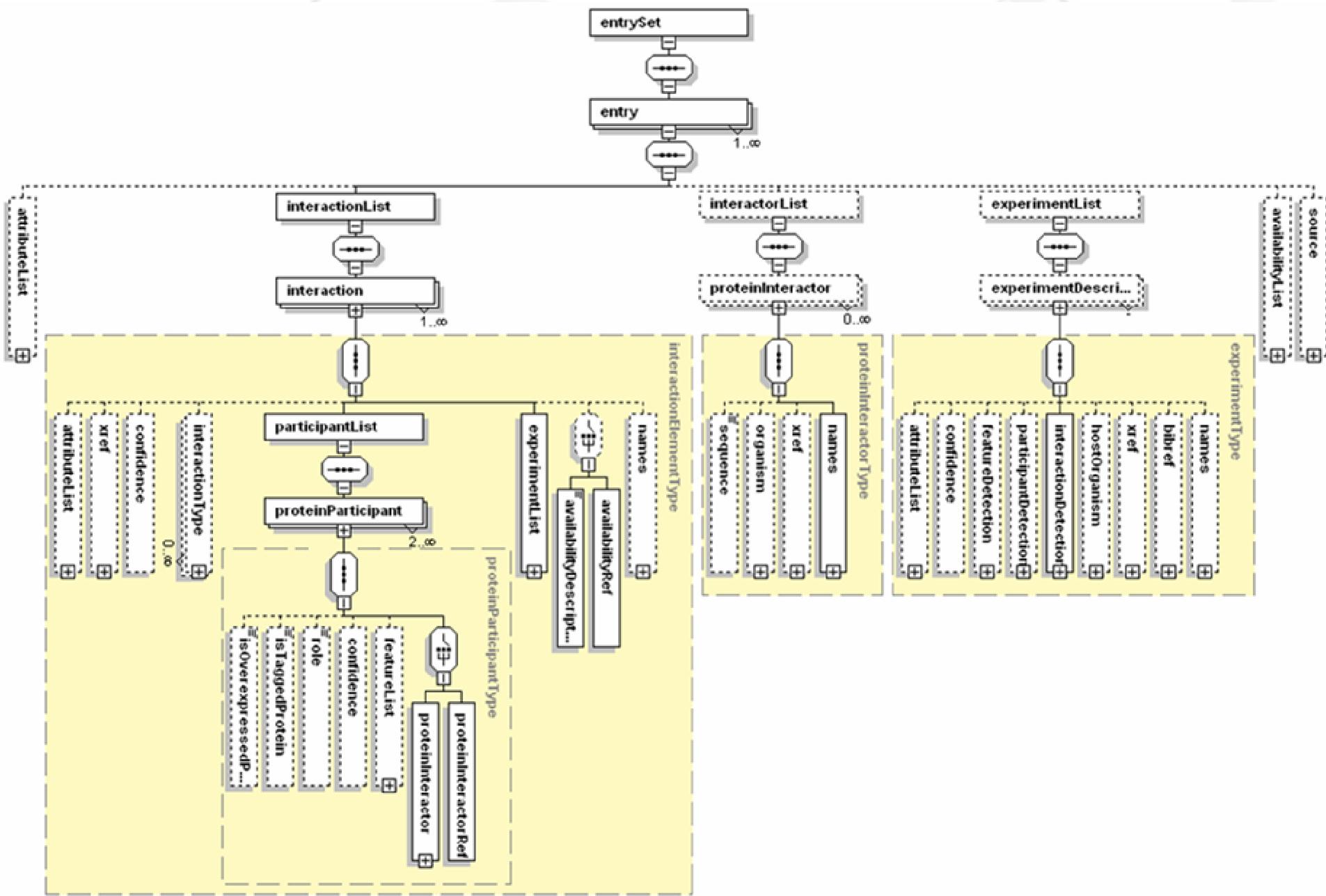


PSI-MI XML format

- **Community standard for Molecular Interactions**
- **XML schema and detailed controlled vocabularies**
- **Jointly developed by major data providers:**
BIND, CellZome, DIP, GSK, HPRD, Hybrigenics, IntAct, MINT, MIPS, Serono, U. Bielefeld, U. Bordeaux, U. Cambridge, and others
- **Version 1.0 published in February 2004**

The HUPO PSI Molecular Interaction Format - A community standard for the representation of protein interaction data.
Henning Hermjakob et al, Nature Biotechnology 2004, 22, 176-183.





PSI-MI XML evolution

- Well-defined schema evolution, yearly releases
- Next release September 2004, version 2.0
 - Better identifier handling
 - New interactor types: DNA, RNA, small molecules
- Well-defined evolution of controlled vocabularies
 - Modeled on GO procedures
 - Requests mailing list
 - Editorial board



PSI-MI XML format support

- **Data**

- DIP, MINT, IntAct, Hybrigenics, HPRD, ...

- **Tools:**

- **Viewer:**

- Cytoscape (MSKCC, ISB, Whitehead)
 - PIMWalker (Hybrigenics)
 - ProViz (U. Bordeaux)

- **Converter:**

- Tabular ↔ PSI MI (MINT)
 - PSI MI ↔ HTML (PSI)



PSI-MI XML benefits

- Collecting and combining data from different sources has become easier,
- standardized annotation through PSI-MI ontologies,
- tools from different organizations can be chained, e.g. analysis of IntAct data in Cytoscape.

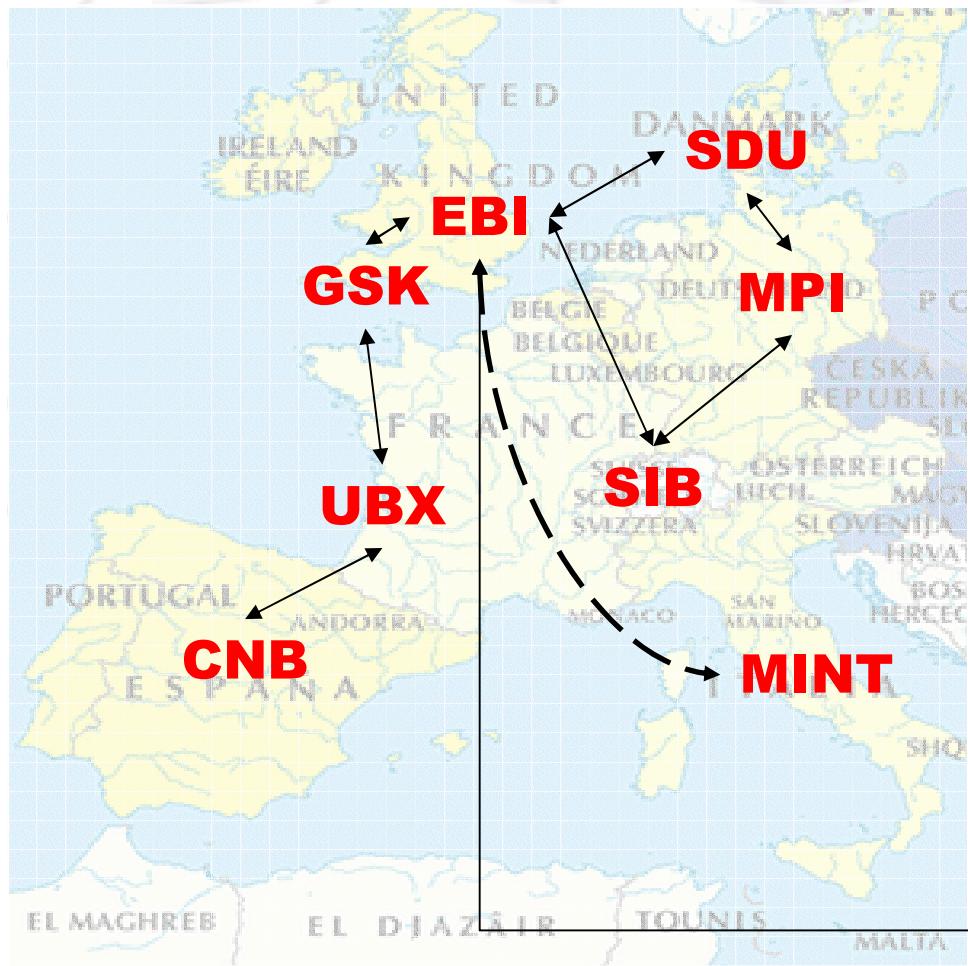




An open source molecular interaction database



IntAct project



- Start January 2002
- Part of EU framework 5, Temblor grant
- Coordinated by EBI
- 8 partners across Europe
- Collaboration with major interaction databases (Mint, Bind ...)

HUJI

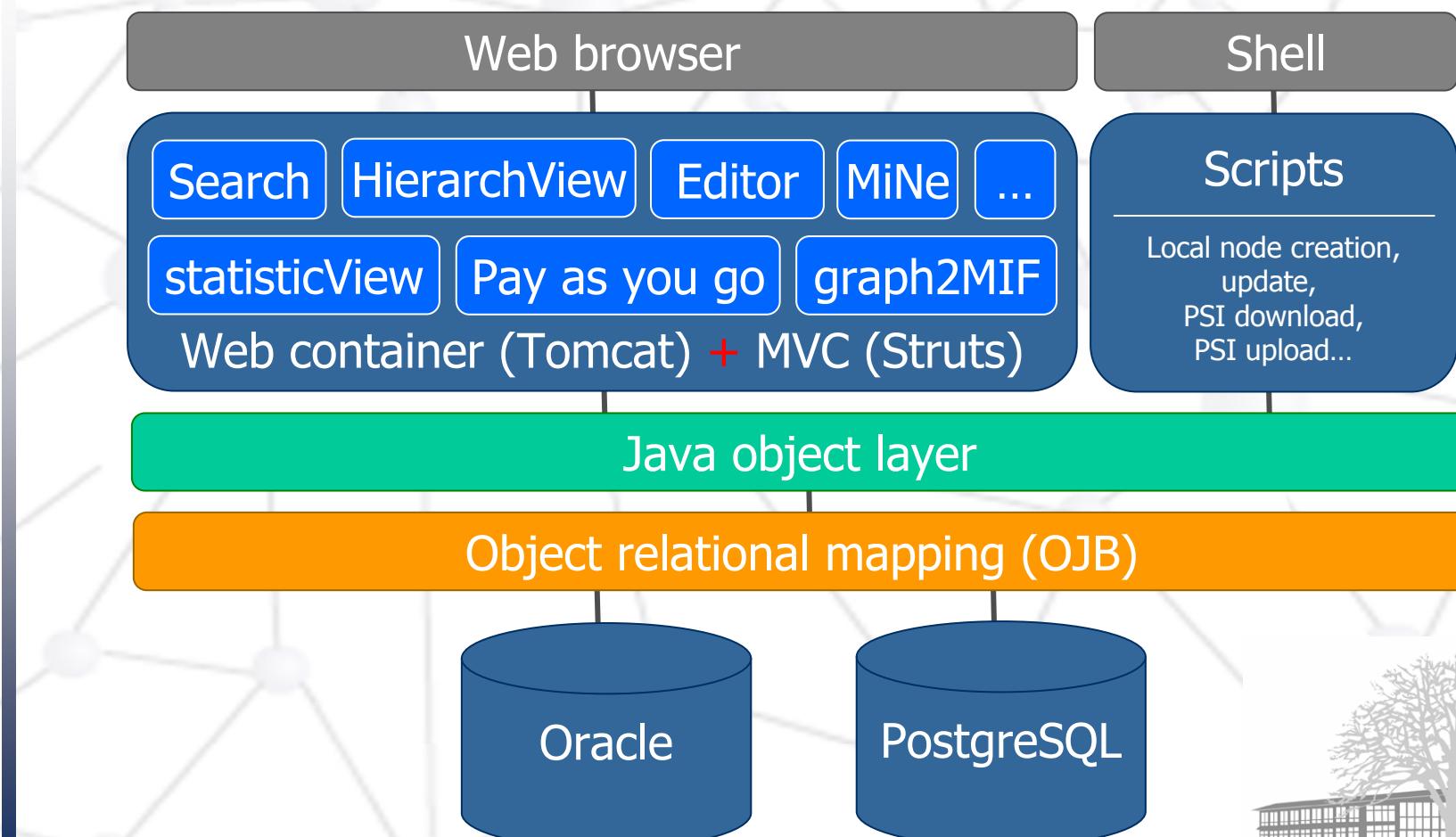
Software architecture

- Open Source Project (hosted at sourceforge)
- No restrictions on source code
- Only “free” software used



- Explicitly written to support local installation

Software architecture



Quick overview of applications

- **Search** (interaction browser)
- **HierarchView** (graphical view)
- **{Proviz and Cytoscape}** (stand-alone network analysis)
- **MiNe** (Minimal connecting Network)
- **Editor** (curation tool)
- **PSI Loader** (integration of PSI-MI data)





Database Search

Search Results for shortLabel=q08491

(short labels of search criteria matches highlighted in *bold italic*)

q08491

[Search](#)

Links

[Home](#)

[Check All](#) [Clear All](#) [Help](#)

<input type="checkbox"/>	q08491	Chromosome XV reading frame ORF YOR076C		Query with q08491
interacts with				
<input type="checkbox"/>	yho1_yeast	Hypothetical 21.0 kDa protein in IRE1-KSP1 intergenic region	View 1 Interaction	Query with yho1_yeast
<input type="checkbox"/>	yba4_yeast	Hypothetical 287.5 kDa protein in PDR3-HTA2 intergenic region	View 1 Interaction	Query with yba4_yeast
<input type="checkbox"/>	rr43_yeast	Exosome complex exonuclease RRP43	View 4 Interactions	Query with rr43_yeast
<input type="checkbox"/>	rr41_yeast	Exosome complex exonuclease RRP41	View 4 Interactions	Query with rr41_yeast
<input type="checkbox"/>	rr46_yeast	Exosome complex exonuclease RRP46	View 3 Interactions	Query with rr46_yeast
<input type="checkbox"/>	rrp6_yeast	Exosome complex exonuclease RRP6	View 4 Interactions	Query with rrp6_yeast
<input type="checkbox"/>	mtr3_yeast	Exosome complex exonuclease MTR3	View 4 Interactions	Query with mtr3_yeast
<input type="checkbox"/>	dhr1_yeast	Probable ATP-dependent RNA helicase DHR1	View 2 Interactions	Query with dhr1_yeast
<input type="checkbox"/>	yiv5_yeast	Hypothetical oxidoreductase in LYS1-HYR1 intergenic region	View 1 Interaction	Query with yiv5_yeast
<input type="checkbox"/>	rr42_yeast	Exosome complex exonuclease RRP42	View 4 Interactions	Query with rr42_yeast
<input type="checkbox"/>	csl4_yeast	3'-5' exoribonuclease CSL4	View 4 Interactions	Query with csl4_yeast
<input type="checkbox"/>	rrp4_yeast	Exosome complex exonuclease RRP4	View 4 Interactions	Query with rrp4_yeast
<input type="checkbox"/>	yg2l_yeast	Hypothetical 140.5 kDa protein in CTT1-PRP31 intergenic region	View 2 Interactions	Query with yg2l_yeast
<input type="checkbox"/>	ima1_yeast	Importin alpha subunit	View 4 Interactions	Query with ima1_yeast
<input type="checkbox"/>	ski3_yeast	Superkiller 3 protein	View 1 Interaction	Query with ski3_yeast
<input type="checkbox"/>	yjk9_yeast	Hypothetical 200.0 kDa protein in GZF3-IME2 intergenic region	View 2 Interactions	Query with yjk9_yeast
<input type="checkbox"/>	ski2_yeast	Antiviral protein SKI2	View 1 Interaction	Query with ski2_yeast
<input type="checkbox"/>	yha2_yeast	Hypothetical 51.2 kDa protein in LAG1-RPL14B intergenic region	View 1 Interaction	Query with yha2_yeast
<input type="checkbox"/>	rr44_yeast	Exosome complex exonuclease RRP44	View 4 Interactions	Query with rr44_yeast
<input type="checkbox"/>	rr45_yeast	Exosome complex exonuclease RRP45	View 3 Interactions	Query with rr45_yeast
<input type="checkbox"/>	rr40_yeast	Exosome complex exonuclease RRP40	View 3 Interactions	Query with rr40_yeast



Database Search

EBI-196429

[Search](#)**Links**[New Search](#)[Intact Home](#)

Search Results for ac=EBI-196429

(short labels of search criteria matches highlighted in *bold italic*)[Check All](#) [Clear All](#) [Help](#)Results 381 to 401 of 20672 interactions [?](#)[Previous](#) [10](#) [11](#) [12](#) [13](#) [14](#) [15](#) [16](#) [17](#) [18](#) [19](#) **20** [21](#) [22](#) [23](#) [24](#) [25](#) [26](#) [27](#) [28](#) [29](#) [30](#) [Next](#)

Experiment [?]	Ac: EBI-196429	Name: <i>giot-2003-ext</i>	
Interaction identification: classical two hybrid	Participant identification: nucleotide sequence	Host: <i>s cerevisiae</i>	A protein interaction map of <i>Drosophila melanogaster</i> .
comment	Preys used for Y2H screens: 1)cDNA libraries made from embryo and adult fly (Clontech) and 2)using predicted ORF from BDGP (Berkeley Drosophila Genome Project) release 1 and 2 and a mixture of cDNA libraries from embryo, larvae 1,2 and 3, and adult fly to obtain 10306 validated preys.		
comment	11159 validated baits were obtained using predicted ORF from BDGP release 1 and 2 and a mixture of cDNA libraries from embryo, larvae 1,2 and 3, and adult fly.		
pubmed	14605208	-	Type: primary-reference
<input checked="" type="checkbox"/> Interaction [?]	Ac: EBI-198629	Name: <i>cg10139-cg8415-1</i>	Interaction detected by Y2H.
kD: 0.0	Type: aggregation		
comment	Author confidence score for the interaction was: 0.207546778		
<input checked="" type="checkbox"/> q9v740^b , <input checked="" type="checkbox"/> q8t3u^b			
<input checked="" type="checkbox"/> Interaction [?]	Ac: EBI-198634	Name: <i>cg10139-beta_tub56-1</i>	Interaction detected by Y2H.
kD: 0.0	Type: aggregation		
comment	Author confidence score for the interaction was: 0.329140733		
<input checked="" type="checkbox"/> q9v740^b , <input checked="" type="checkbox"/> tbb1_drome^b			
<input checked="" type="checkbox"/> Interaction [?]	Ac: EBI-198638	Name: <i>robl62a-cg10834-1</i>	Interaction detected by Y2H.
kD: 0.0	Type: aggregation		
comment	Author confidence score for the interaction was: 0.659751185		
<input checked="" type="checkbox"/> q9w0f0^b , <input checked="" type="checkbox"/> q9v9p1^b			
<input checked="" type="checkbox"/> Interaction [?]	Ac: EBI-198642	Name: <i>robl62a-cg10927-1</i>	Interaction detected by Y2H.
kD: 0.0	Type: aggregation		
comment	Author confidence score for the interaction was: 0.910044319		
<input checked="" type="checkbox"/> q9w0f0^b , <input checked="" type="checkbox"/> q9v8j4^b			



Database Search

GO:0000176

[Search](#)**Links**[Home](#)

Search Results for ac=GO:0000176

(short labels of search criteria matches highlighted in *bold italic*)

Nuclear exosome

[Check All](#) [Clear All](#) [Help](#)

Experiment²	EBI-13	ho-2002	Systematic identification of protein complexes in <i>Saccharomyces cerevisiae</i> by mass spectrometry.
-	peptide massfingerpr	yeast	
comment	493 bait proteins Flag-tagged		
pubmed	11805837	-	primary-reference
Interaction²	EBI-47793	ho-487	
-	-	-	
	<input type="checkbox"/> yjz2 yeast^b , <input type="checkbox"/> ucr2 yeast^E , <input checked="" type="checkbox"/> rr42 yeast^E , <input type="checkbox"/> lsm2 yeast^E , <input type="checkbox"/> q08723E , <input type="checkbox"/> rsmb yeast^E , <input type="checkbox"/> apal yeast^E , <input type="checkbox"/> gar1 yeast^E , <input type="checkbox"/> if6 yeast^E , <input type="checkbox"/> ygl7 yeast^E , <input type="checkbox"/> rpnc yeast^E ,		
Interaction²	EBI-47399	ho-436	
-	-	-	
	<input type="checkbox"/> imal yeast^b , <input checked="" type="checkbox"/> rr44 yeast^E , <input type="checkbox"/> q05543E , <input type="checkbox"/> sif2 yeast^E , <input type="checkbox"/> gcr3 yeast^E , <input type="checkbox"/> q03782E , <input type="checkbox"/> yah2 yeast^E , <input type="checkbox"/> pap yeast^E , <input type="checkbox"/> imbl yeast^E , <input type="checkbox"/> nup2 yeast^E , <input type="checkbox"/> q07623E , <input type="checkbox"/> q06825E , <input type="checkbox"/> nup1 yeast^E , <input type="checkbox"/> mft1 yeast^E , <input type="checkbox"/> sin3 yeast^E , <input checked="" type="checkbox"/> rrp6 yeast^E , <input type="checkbox"/> fipl yeast^E , <input checked="" type="checkbox"/> rr43 yeast^E , <input type="checkbox"/> nam8 yeast^E , <input type="checkbox"/> rnt1 yeast^E , <input type="checkbox"/> hpr1 yeast^E , <input type="checkbox"/> reb1 yeast^E , <input checked="" type="checkbox"/> rrp4 yeast^E , <input type="checkbox"/> eaf3 yeast^E , <input type="checkbox"/> hasl yeast^E , <input type="checkbox"/> ctpt yeast^E , <input type="checkbox"/> sync yeast^E , <input type="checkbox"/> rlrl yeast^E , <input type="checkbox"/> yhp9 yeast^E , <input type="checkbox"/> umel yeast^E ,		
Experiment²	EBI-12	gavin-2002	Functional organization of the yeast proteome by systematic analysis of protein complexes.
-	peptide massfingerpr	yeast	
comment	589 bait proteins TAP-tagged.		
pubmed	11805826	-	primary-reference
Interaction²	EBI-1730	ga-89	
-	-	-	
	<input type="checkbox"/> csl4 yeast^E , <input type="checkbox"/> csl4 yeast^b , <input type="checkbox"/> rr44 yeast^E , <input type="checkbox"/> mtr3 yeast^E , <input type="checkbox"/> rrp4 yeast^E , <input type="checkbox"/> rr42 yeast^E , <input type="checkbox"/> rr43 yeast^E , <input checked="" type="checkbox"/> rrp6 yeast^E , <input type="checkbox"/> rr41 yeast^E , <input type="checkbox"/> q08491E , <input type="checkbox"/> imal yeast^E , <input type="checkbox"/> yiv5 yeast^E ,		
Interaction²	EBI-1809	ga-367	
-	-	-	



rr42_yeast

Search

Links

[New Search](#)
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Database Search

Search Results for shortLabel=rr42_yeast

(short labels of search criteria matches highlighted in *bold italic*)[Check All](#) [Clear All](#) [Help](#)

<input checked="" type="checkbox"/> Protein	Ac: EBI-1765	Name: <i>rr42_yeast</i>	Exosome complex exonuclease RRP42
Source: <i>s cerevisiae</i>	Crc64: 806C60979642C67E		
sgd	S0002269	RRP42	-
go	GO:0000177	C:cytoplasmic exosome (RNase c)	-
go	GO:0000176	C:nuclear exosome (RNase compl)	-
go	GO:0006402	P:mRNA catabolism	-
uniprot	Q12277	rr42_yeast	Type: identity
interpro	IPR001247	3_ExoRNase	-
MSLSVAEKSY LYDSLASTPS IRPDGRLPHQ FRPIEIFTDF LPSSNGSSRI IASDGSECIV SIKSKVVDHH VENELLQVDV DIAGQRDDAL VVETITSLLN KVLKSGSGVD SSKLQLTKKY SFKIFVDVILV ISSHSHPVSL ISFAIYSALN STYLPKLISA FDDLEVEELP TFHDYDMVKL DINPPLVFL AVVGNNMLD PAANESEEVAN NGLIISWSNG KITSPIRSV A LNDNSNVKSFK PHLLKQGLAM VEKYAPDVVR SLENL			

[Graph](#)[Path](#)[Reset](#)User: INTACTWEB
Database: iwebPlease send any questions or suggestions to intact-help@ebi.ac.uk

Last modified: 19-July-2004 11:34 AM by Samuel

Powered by
Struts



HierarchView?

Interactor ?

EBI-1765

[Search](#) [Add](#)

Graph ?

[Expand](#)

Clicking on a node of the graph will :

- center the view ?
- add a network ?

PSI-XML ?

[Download](#)

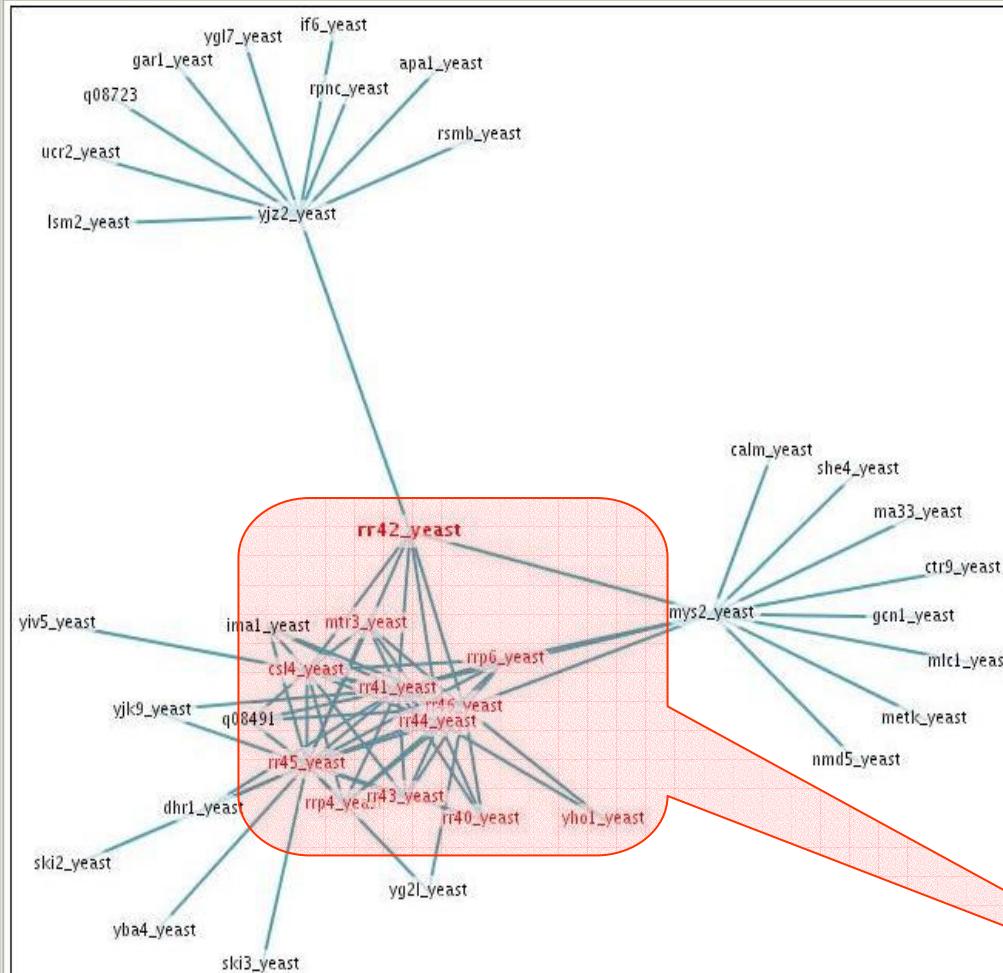
Links

[IntAct home](#)
[Back to search](#)

Interaction network for ac: [EBI-1765](#)

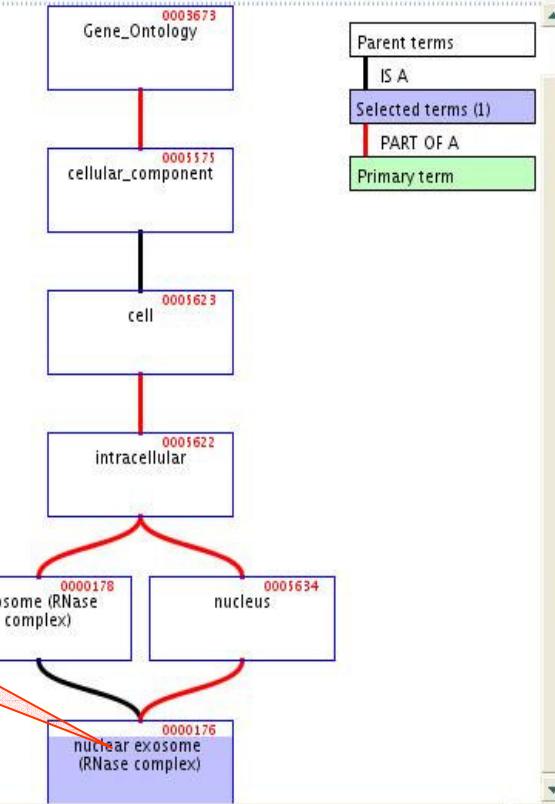
Highlight by GO:0000176

#nodes:40 #edges:81



Existing highlight source for the central protein(s). ?

ID	Description	Use
GO:0000177	C:cytoplasmic exosome (RNase c)	
GO:0000176	C:nuclear exosome (RNase compl)	
GO:0006402	P:mRNA catabolism	





HierarchView?

Interactor ?

EBI-1765

Graph ?

Clicking on a node of the graph will :

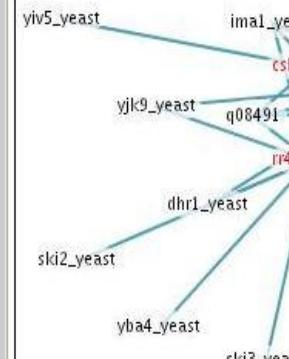
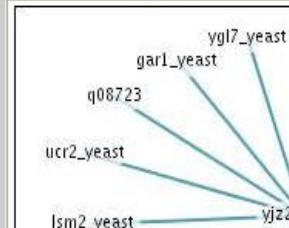
- center the view ?
- add a network ?

PSI-XML ?

Links

[IntAct home](#)
[Back to search](#)

Interaction network for ac: EBI-1765
Highlight by GO:0000176
#nodes:40 #edges:81



```
<?xml version="1.0" encoding="UTF-8" ?>
- <entrySet level="1" version="1" xmlns="net:sf:psidev:mi"
  xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xsi:schemaLocation="net:sf:psidev:mi
  http://psidev.sourceforge.net/mi/xml/src/MIF.xsd">
- <entry>
  <source releaseDate="2004-05-05" />
- <experimentList>
  - <experimentDescription id="EBI-12">
    - <names>
      <shortLabel>gavin-2002</shortLabel>
      <fullName>Functional organization of the yeast proteome by systematic analysis
      of protein complexes.</fullName>
    </names>
- <hostOrganism ncbiTaxId="4932">
  - <names>
    <shortLabel>s cerevisiae</shortLabel>
    <fullName>Saccharomyces cerevisiae</fullName>
  </names>
</hostOrganism>
- <interactionDetection>
  - <names>
    <shortLabel>tandem affinity puri</shortLabel>
    <fullName>tandem affinity purification</fullName>
  </names>
- <xref>
  <primaryRef db="psi-mi" id="MI:0109" secondary="" version="" />
  <secondaryRef db="pubmed" id="10504710" secondary="" version="" />
</xref>
</interactionDetection>
- <participantDetection>
  - <names>
    <shortLabel>peptide massfingerpr</shortLabel>
    <fullName>peptide massfingerprinting</fullName>
  </names>
- <xref>
  <primaryRef db="psi-mi" id="MI:0082" secondary="" version="" />
  <secondaryRef db="pubmed" id="10967324" secondary="" version="" />
  <secondaryRef db="pubmed" id="111752500" secondary="" version="" />
</xref>
</participantDetection>
```

The screenshot shows the Cytoscape website at <http://www.cytoscape.org/>. The page features a large molecular interaction network graph in the background. On the left, the word "Cytoscape" is written in large white letters. Below it is a description: "A bioinformatics software platform for **visualizing** molecular interaction networks and **integrating** these interactions with gene expression profiles and other state data." A "Read more »" link is present. On the right, there is a "Download Cytoscape!" section with a "Read more »" link for version 1.1.1. Another "Read more »" link points to the latest Cytoscape Plugins. A navigation bar at the bottom includes links for "Cytoscape: Features | Screenshots | Dev team | PlugIns | Download | Report a Bug". Below the navigation bar are five boxes with links: "Download Cytoscape Version 1.1.1", "Download Source Version 1.1.1", "Click here to run Cytoscape from the web!", "Online Tutorial", and "Manual".

Cytoscape

A bioinformatics software platform for **visualizing** molecular interaction networks and **integrating** these interactions with gene expression profiles and other state data.

[Read more »](#)

Download Cytoscape!

New! Version 1.1.1 is now available.
[Read more »](#)

New! Check out the latest Cytoscape Plugins:
jActiveModules, SBML Reader, PSI-MI Reader,
and Expression Data Viewers.
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[Cytoscape: Features](#) | [Screenshots](#) | [Dev team](#) | [PlugIns](#) | [Download](#) | [Report a Bug](#)

Download Cytoscape <u>Version 1.1.1</u> Requires Java 1.4.1	Download Source <u>Version 1.1.1</u> Source code is written for Java 1.4.1	Click here to run Cytoscape from the web! (if you already have Java Web Start .)	Online Tutorial The tutorial uses Java Web Start .	Manual PDF format, explains all basic features of Cytoscape. Get Acrobat reader
---	---	---	---	--

The page features logos of four partner institutions: Institute for Systems Biology (blue stylized logo), Memorial Sloan-Kettering Cancer Center (circle with vertical bars logo), University of California at San Diego (orange circle logo), and Institut Pasteur (purple stylized logo). To the right is a drawing of a building with a tree in front of it.

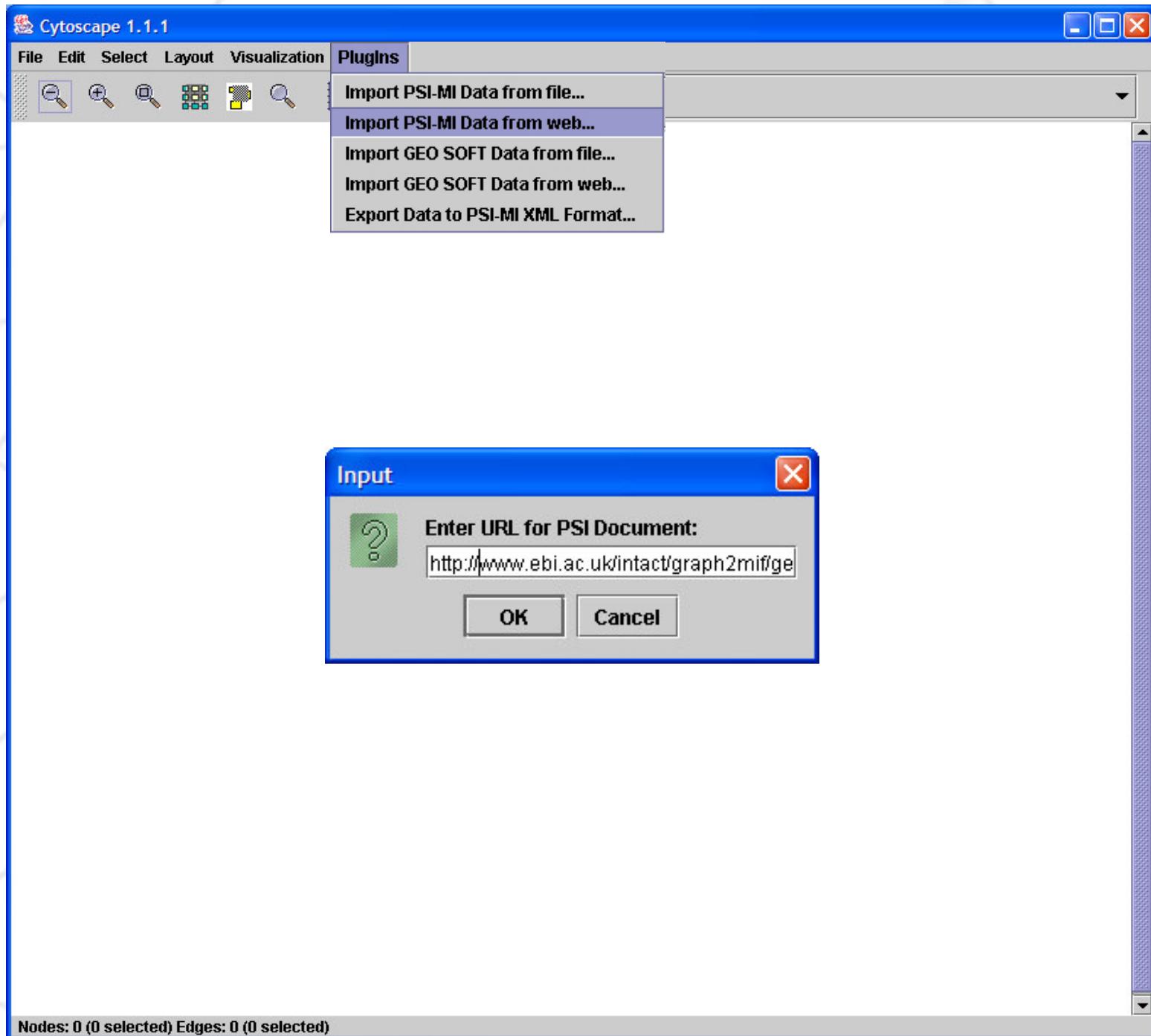
Institute for Systems Biology

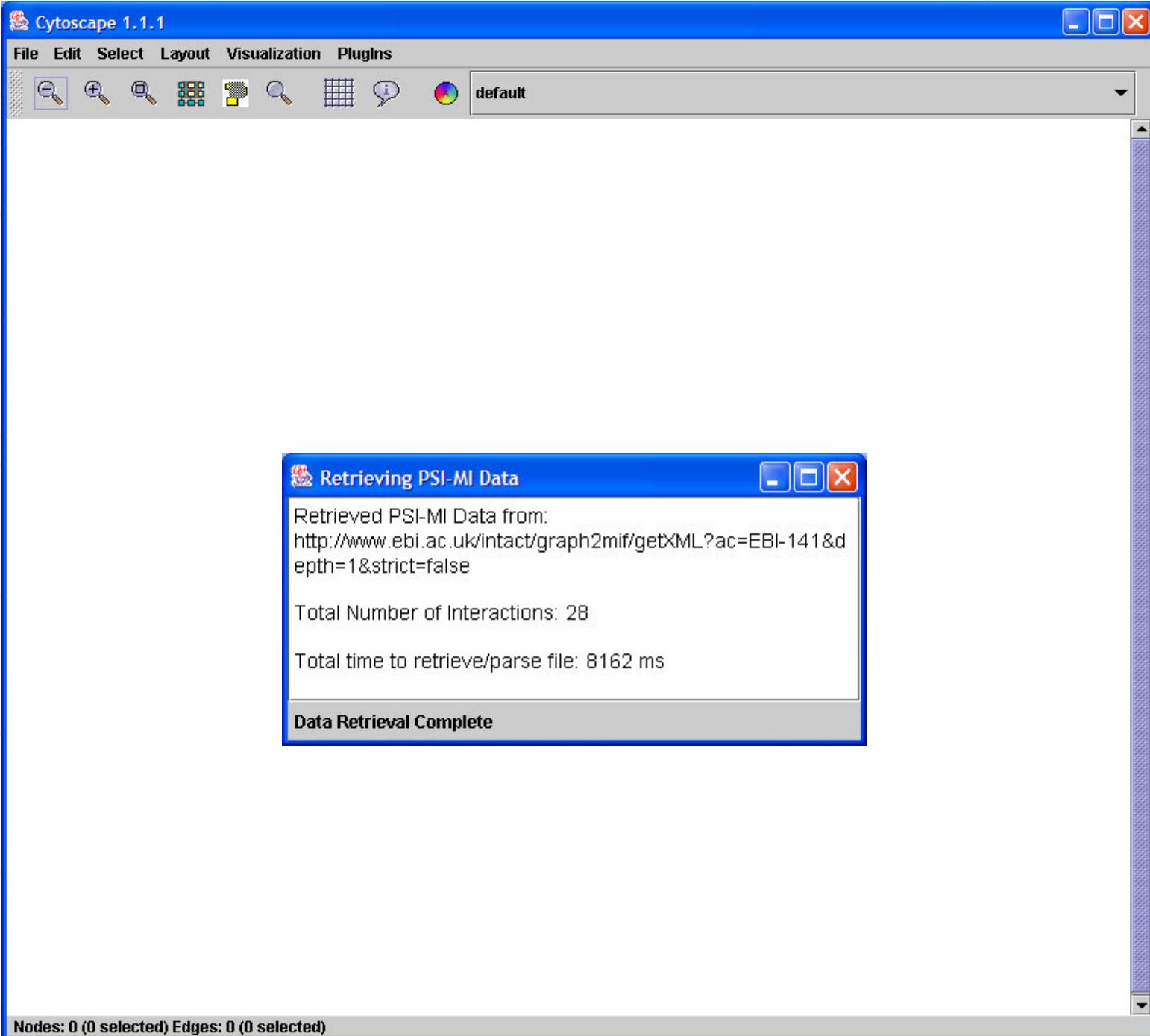
Memorial Sloan-Kettering Cancer Center

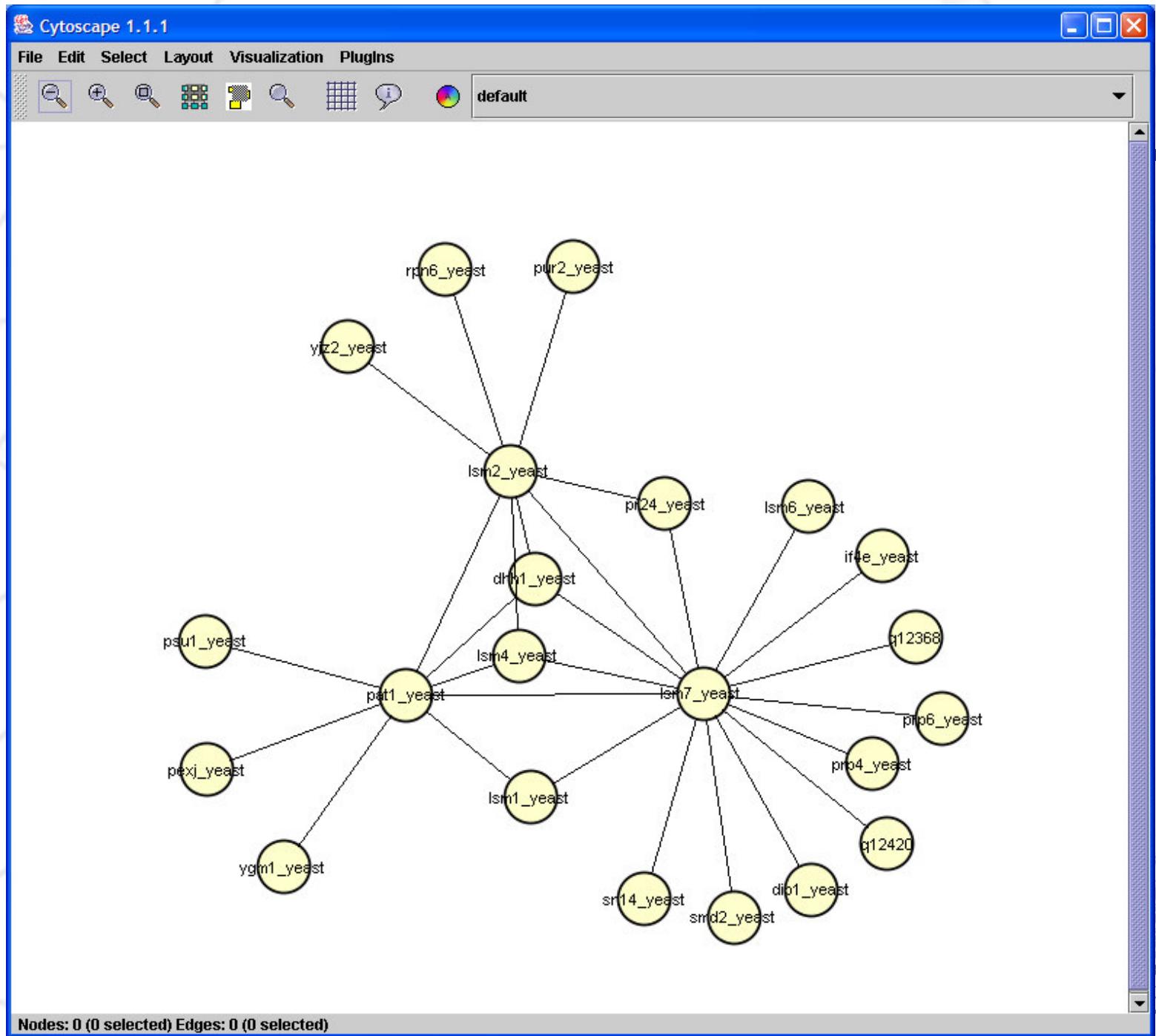
University of California at San Diego

Institut Pasteur

21/25









Database Search

Search Results for ac=EBI-39933, ac=EBI-1893

(short labels of search criteria matches highlighted in *bold italic*)

[Search](#)

[Check All](#) [Clear All](#) [Help](#)

Links

[New Search](#)

[Intact Home](#)

Experiment?	Ac: EBI-12	Name: gavin-2002	Functional organization of the yeast proteome by systematic analysis of protein complexes.
Interaction identification: tandem affinity puri	Participant identification: peptide massfingerpr	Host: s cerevisiae	
comment	589 bait proteins TAP-tagged.		
pubmed	11805826	-	Type: primary-reference
pubmed	15044803	-	Type: see-also
■ Interaction?	Ac: EBI-39933	Name: ga-99	
	Type: aggregation		
<input type="checkbox"/> rr44 yeast^b , <input type="checkbox"/> csl4 yeast^P , <input type="checkbox"/> rr44 yeast^P , <input type="checkbox"/> mtr3 yeast^P , <input type="checkbox"/> rrp4 yeast^P , <input type="checkbox"/> rr40 yeast^P , <input checked="" type="checkbox"/> rr42 yeast^P ,			
<input type="checkbox"/> rr43 yeast^P , <input type="checkbox"/> rr46 yeast^P , <input type="checkbox"/> rrp6 yeast^P , <input type="checkbox"/> rr41 yeast^P , <input type="checkbox"/> yhol yeast^P			
■ Interaction?	Ac: EBI-1893	Name: ga-368	
	Type: aggregation		
<input type="checkbox"/> rr46 yeast^b , <input type="checkbox"/> csl4 yeast^P , <input type="checkbox"/> rr44 yeast^P , <input type="checkbox"/> mtr3 yeast^P , <input type="checkbox"/> rrp4 yeast^P , <input type="checkbox"/> rr40 yeast^P , <input type="checkbox"/> rr42 yeast^P ,			
<input type="checkbox"/> rr43 yeast^P , <input type="checkbox"/> rr45 yeast^P , <input type="checkbox"/> rr46 yeast^P , <input type="checkbox"/> rrp6 yeast^P , <input type="checkbox"/> rr41 yeast^P , <input checked="" type="checkbox"/> q08491 , <input type="checkbox"/> imal yeast^P ,			
<input type="checkbox"/> yg21 yeast^P , <input type="checkbox"/> yhol yeast^P			

[Graph](#) [Path](#) [Reset](#)



HierarchView?

Interactor ?

rr41_yeast,q084

[Search](#) [Add](#)

Graph ?

[Expand](#)

Clicking on a node of the graph will :

- center the view ?
- add a network ?

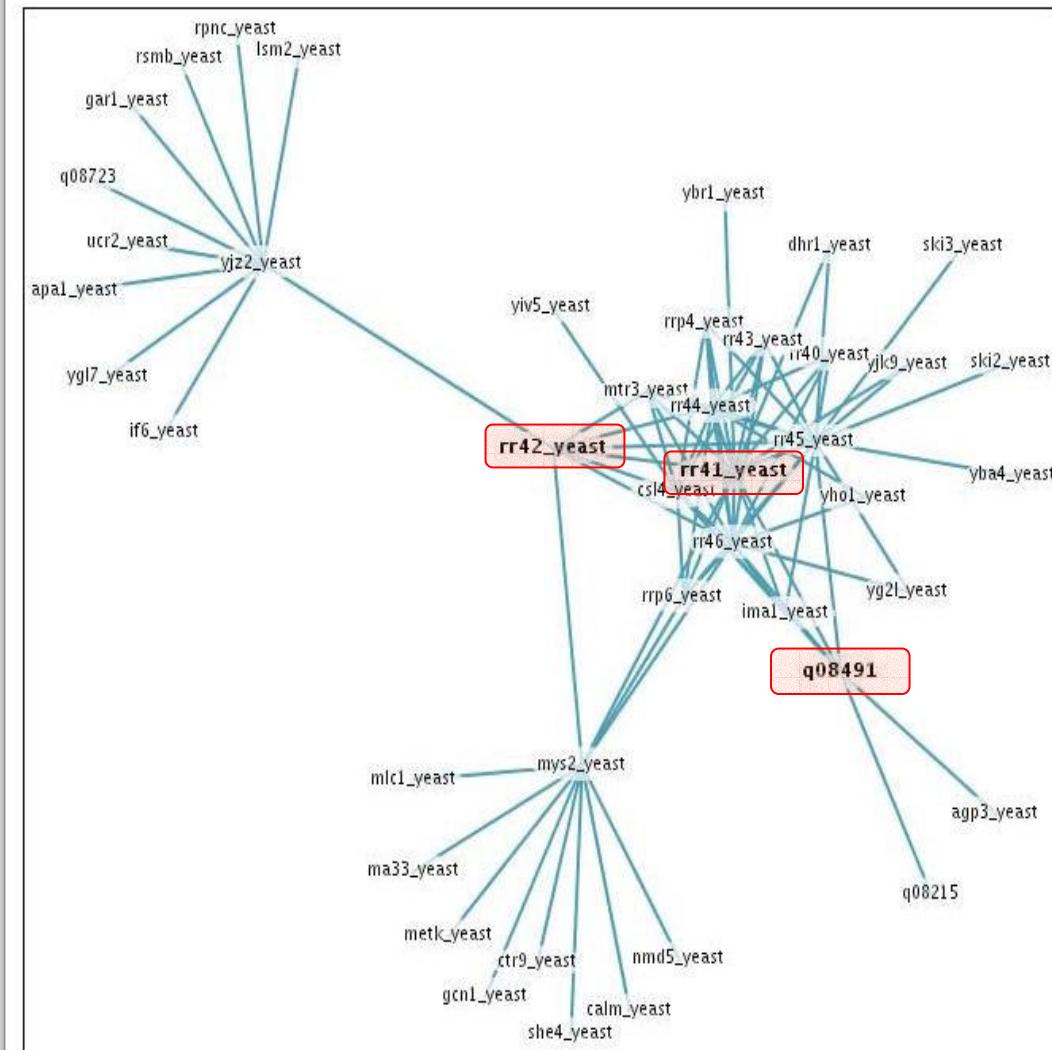
PSI-XML ?

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Interaction network for shortLabel: [rr41_yeast](#), shortLabel: [q08491](#), shortLabel: [rr42_yeast](#)
#nodes:43 #edges:85



Existing highlight source for the central protein(s). ?

ID	Description	Use
GO:0000177	C:cytoplasmic exosome (RNase c)	<input checked="" type="checkbox"/>
GO:0000176	C:nuclear exosome (RNase compl)	<input checked="" type="checkbox"/>
GO:0006402	P:mRNA catabolism	<input checked="" type="checkbox"/>
GO:0000178	C:exosome (RNase complex)	<input checked="" type="checkbox"/>
GO:0005737	C:cytoplasm	<input checked="" type="checkbox"/>

Editor - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Back Favorites Media

IntAct

Experiment

Editor - Experiment

Help Topics FAQ

Intact AC	Short Label	Full Name
EBI-74703	altmann-1997-ex1	A novel inhibitor of cap-dependent translation initiation in yeast: p20 competes with eIF4G for binding to eIF4E

Host Organism	Interaction Detection	Participant Detection
s cerevisiae	gst pull down	polyclonal antibody

[Logout](#)

Interactions

2 items found, displaying 1 to 2 1

Action	Short Label	Ac	Full Name
Edit Interaction	if43yeast-if4eveast	EBI-74705	A novel inhibitor of cap-dependent translation initiation in yeast: p20 competes with eIF4G for binding to eIF4E
Edit Interaction	if4yeast-if43yeast	EBI-74709	A novel inhibitor of cap-dependent translation initiation in yeast: p20 competes with eIF4G for binding to eIF4E

Interactions not yet added to the Experiment

Action	Short Label	Intact AC
Recent Interaction		
Search Interaction		

Annotations

Action	Topic	Description
Add Annotation	--- Select ---	

Crossreferences

Action	Database	Primary Id	Secondary Id	Release Number	Reference Qualifier
Edit Crossreference	pubmed	9118949			primary-reference
Action	Database	Primary Id	Secondary Id	Release Number	Reference Qualifier
Add Crossreference	--- Select ---				primary-reference

Buttons

Submit Save & Continue Cancel Delete

Internet

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IntAct

Experiment

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Editor - Experiment+

Intact AC EBI-74703 altmann-1997-ex1 A novel inhibitor of cap-dependent translation initiation in yeast: p20 competes with eIF4G for binc

Host Organism Interaction Detection Participant Detection

s cerevisiae
nicpl
oceih
oncmv
opsanus
oren
pig
piadu
prote
rabbit
rat
rat-pc12
rhyam
rots1
s cerevisiae
sacba
sacdo
sacps
sarbu
schpo
shift
spiso
spofr
spofr-sf_21
spofr-sf_9
tetpy
theth
tigca
ureca
xenbo
xenla

gst pull down
gst pull down
ha tag
his pull down
his tag
in silico
interaction detection
interologs
isothermal titration
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light scattering
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mrna display
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Ac
EBI-74705
EBI-74709

A novel inhibitor of cap-dependent
eIF4E
A novel inhibitor of cap-dependent
eIF4E

Label Intact AC

Intact AC

--- Select ---
cabri
flybase
go
intact
interpro
newt
pdb
psi-mi
pubmed
sgd
uniprot

Database
bmed

Primary Id
9118949

Secondary Id
Release Number
Reference Qualifier

Action Database Primary Id Secondary Id Release Number Reference Qualifier

Edit Crossreference Delete Crossreference

Add Crossreference --- Select ---

Submit Save & Continue Cancel Delete

Internet

Controlled Vocabulary !!!

Controlled Vocabulary

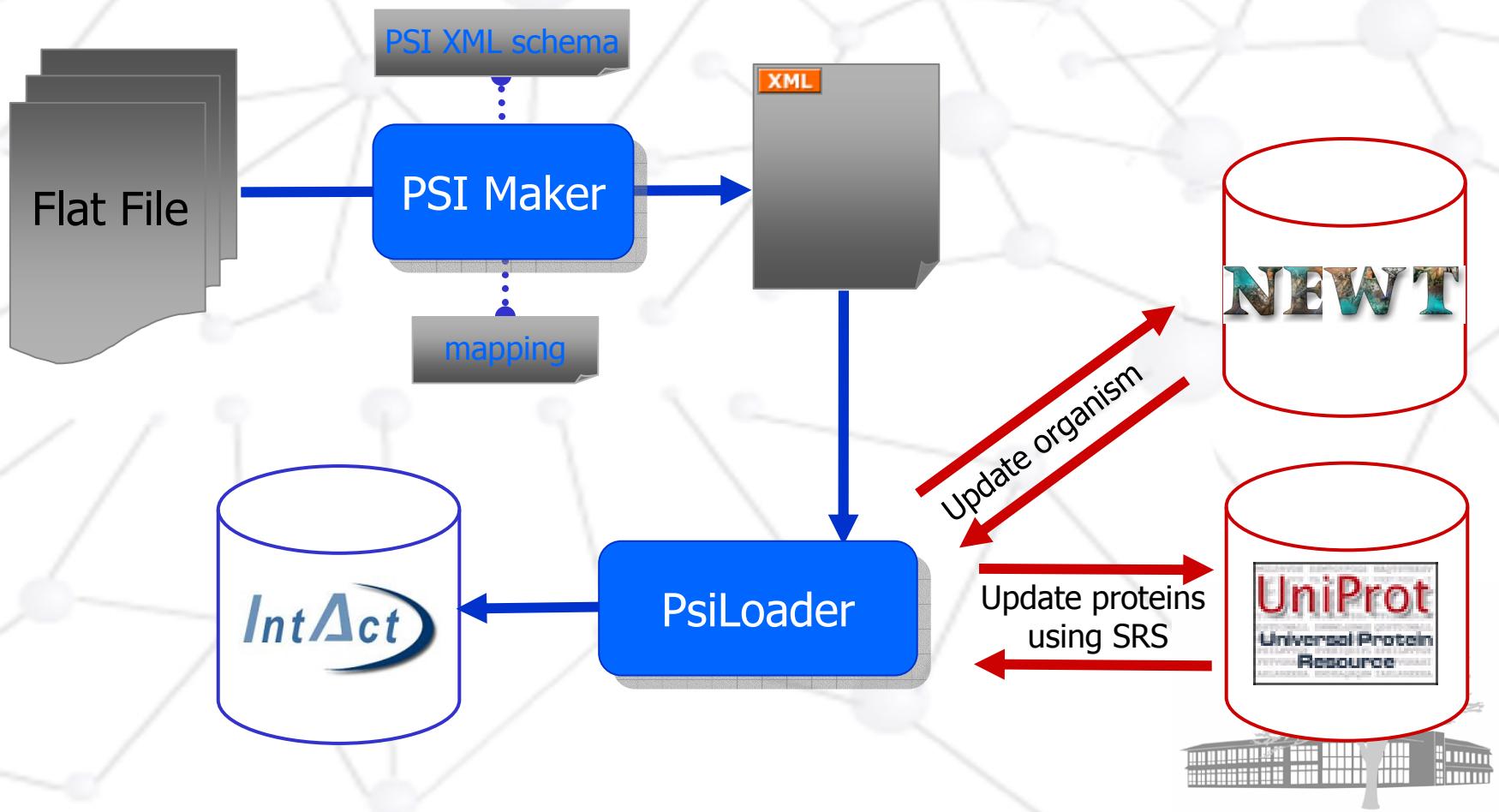
- **IntAct has developed CV specific to Molecular Interactions, this is now maintained and extended by PSI.**

CvInteraction	Ac:	EBI-94	Name:	<i>classical two hybrid</i>	classical two hybrid
definition				The "classical" yeast two-hybrid system is a method that uses transcriptional activity as a measure of protein-protein interaction. It relies on the modular nature of many site-specific transcriptional activators (GAL 4), which consist of a DNA-binding domain and a transcriptional activation domain. The DNA-binding domain serves to target the activator to the specific genes that will be expressed, and the activation domain contacts other proteins of the transcriptional machinery to enable transcription to occur. The two-hybrid system is based on the observation that the two domains of the activator need to be non-covalently brought together by the interaction of any two proteins. The application of this system requires the expression of two hybrid proteins: a DNA-binding domain fused to a protein, X, and a transcription activation domain fused to a second protein, Y. These chimeric proteins are expressed in a cell containing one or more reporter genes under the control of a promoter that is activated by the transcription factor utilized in the assay. If the X and Y proteins do interact, they create a functional activator by bringing the activation domain into close proximity with the DNA-binding domain and as a consequence stimulate the expression reporter gene(s). While the assay has been developed and generally performed in yeast cells, it works similarly in mammalian cells and should be applicable to any other eukaryotic cells. This method has been used with a wide variety of proteins, including some that normally reside in the nucleus, cytoplasm, or mitochondria, or are peripherally associated with membranes. It can be used to detect interactions between candidate proteins, whose genes are available, by constructing the appropriate hybrids and by testing for reporter gene activity. Most significantly, the two-hybrid system can be used to screen libraries in which the activation domain is fused to a collection of cDNA. This allows the identification of proteins, among a large collection, that bind to a protein of interest. This procedure results in the immediate availability of the cloned gene for any newly identified protein. In addition, since multiple clones that encode overlapping regions of protein are often identified, the minimal domain for interaction may be readily apparent from the initial screen.	
psi-mi		MI:0018		-	Type: identity
pubmed		10967325		-	Type: go-definition-ref



PSI Loader

Example of use:
Insertion of large scale experiment



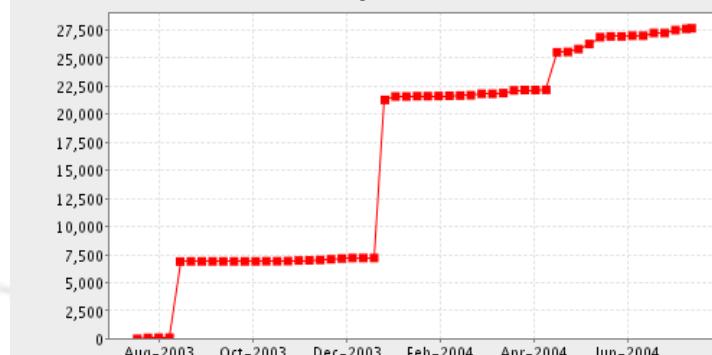
Data

All data publicly available, released monthly

<ftp://ftp.ebi.ac.uk/pub/databases/intact>



Data statistics

IntAct interactions**IntAct binary interactions****IntAct experiments****IntAct proteins**

Summary

- The PSI-MI XML standard has been jointly developed by major interaction database providers to facilitate data exchange and analysis of interaction data

<http://psidev.sf.net>

- IntAct provides a Java-based, freely available, open source database and toolkit for the analysis of interaction data based on the PSI-MI standard

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



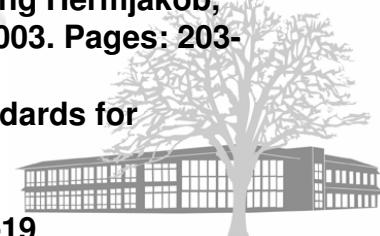
The IMEx consortium

- ***International Molecular-Interaction Exchange*** consortium
- BIND, DIP, IntAct, MINT, MIPS will regularly exchange user-submitted data in PSI-MI format from beginning of 2005 onwards to provide a network of stable, comprehensive resources for molecular interaction data
- Watch out for IMEx announcement during ISMB



Publications

- The HUPO PSI Molecular Interaction Format - A community standard for the representation of protein interaction data.
Henning Hermjakob, Luisa Montecchi-Palazzi, Gary Bader, Jérôme Wojcik, Lukasz Salwinski, Arnaud Ceol, Susan Moore, Sandra Orchard, Ugis Sarkans, Christian von Mering, Bernd Roechert, Sylvain Poux, Eva Jung, Henning Mersch, Paul Kersey, Michael Lappe, Yixue Lix, Rong Zeng, Debashis Rana, Macha Nikolski, Holger Husi, Christine Brun, K. Shanker, Seth G.N. Grant, Chris Sander, Peer Bork, Weimin Zhu, Akhilesh Pandey, Alvis Brazma, Bernard Jacq, Marc Vidal, David Sherman, Pierre Legrain, Gianni Cesareni, Ioannis Xenarios, David Eisenberg, Boris Steipe, Chris Hogue, Rolf Apweiler.
Nature Biotechnology 2004, 22, 176-183.
- Further advances in the development of a data interchange standard for proteomics data.
Sandra Orchard, Weimin Zhu, Randall K. Julian Jnr, Henning Hermjakob and Rolf Apweiler.
Proteomics 2003, 3, 2965-2066.
- The Proteomics Standards Initiative.
Sandra Orchard, Henning Hermjakob, Rolf Apweiler.
Proteomics 2003, 3, 1374-1376.
- Progress in establishing common standards for exchanging proteomics data:
The second meeting of the HUPO Proteomics Standards Initiative.
Sandra Orchard, Paul Kersey, Weimin Zhu, Luisa Montecchi-Palazzi, Henning Hermjakob, Rolf Apweiler. Comparative and Functional Genomics Volume 4, Issue 2, 2003. Pages: 203-206
- The HUPO Proteomics Standards Initiative meeting: towards common standards for exchanging proteomics data
Sandra Orchard, Paul Kersey, Henning Hermjakob, Rolf Apweiler
Comparative and Functional Genomics Volume 4, Issue 1, 2003. Pages: 16-19



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• Misc.

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- GO curators

YOU!

<http://psidev.sf.net>