

**The PSI MI standard
open analysis of protein interaction data**

IntAct

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.

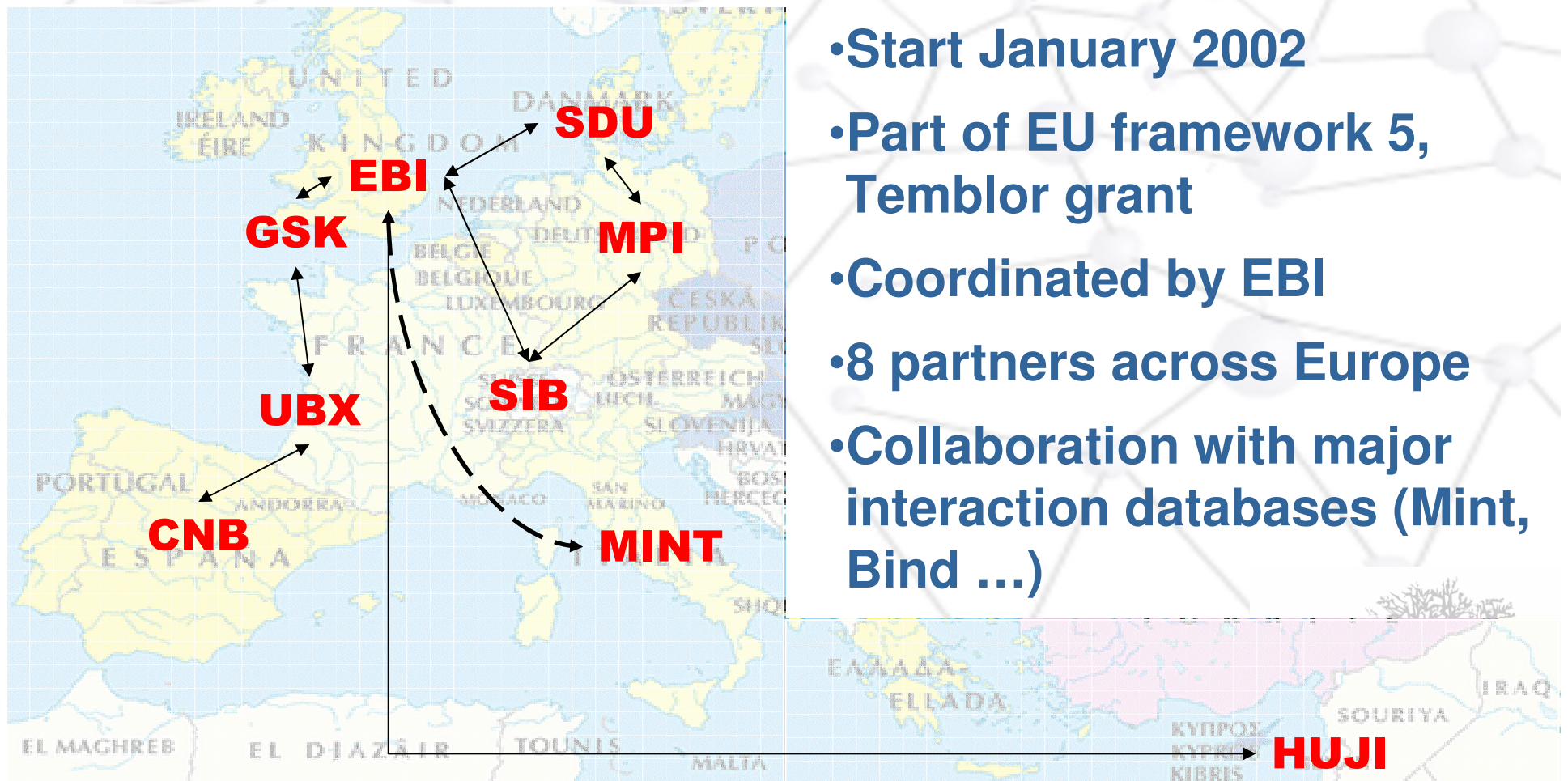


IntAct

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 ...)

Software architecture

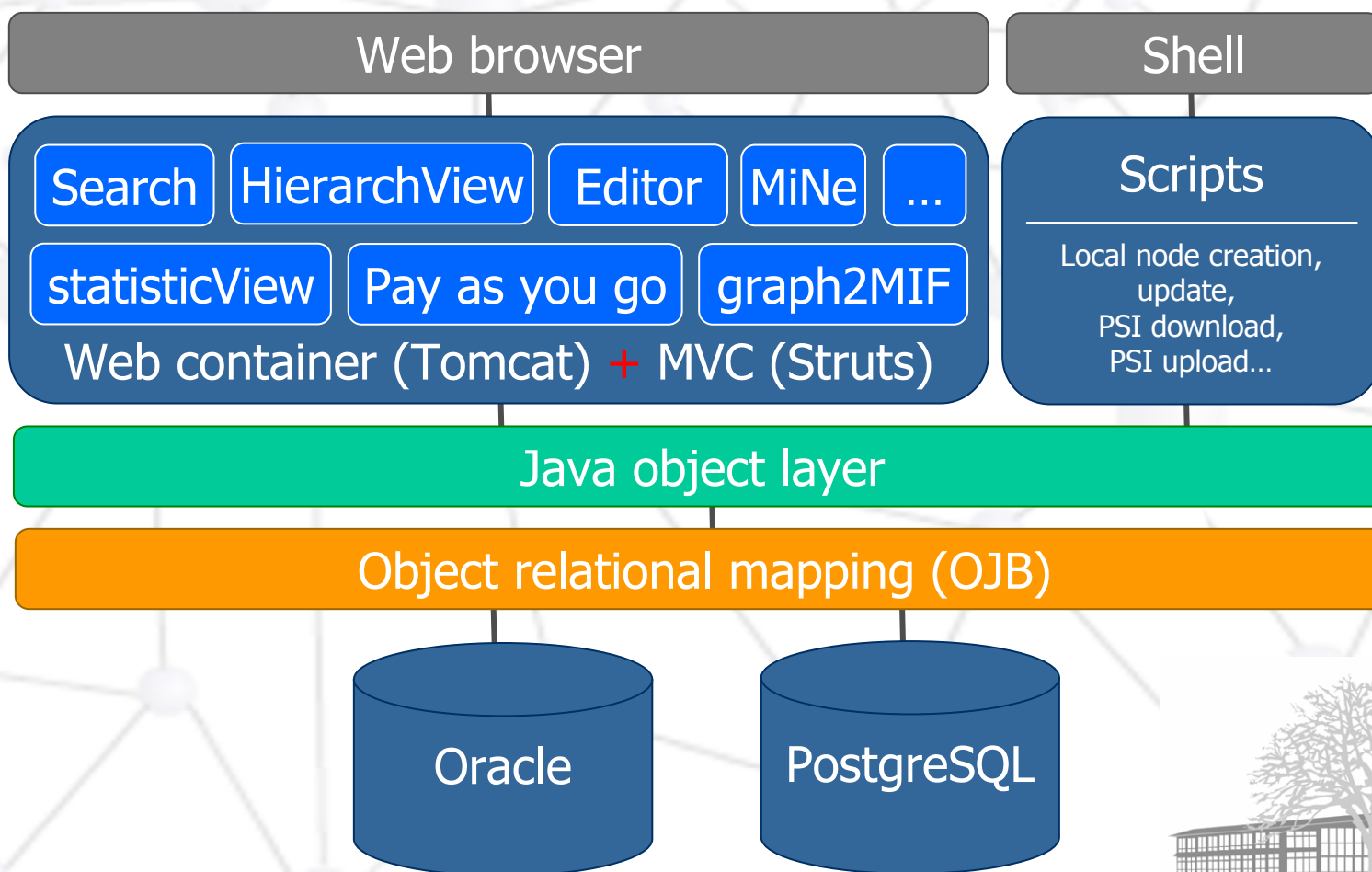
- Open Source Project (hosted at sourceforge)
- No restrictions on source code
- Only “free” software used



- 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

q08491

Search

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

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

Links

[Home](#)

<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"/>	csi4_yeast	3'-5' exoribonuclease CSL4	View 4 Interactions	Query with csi4_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

Search Results for ac=EBI-196429

EBI-196429

Search

Links

[New Search](#)

[Intact Home](#)

(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-ext1</i>	A protein interaction map of Drosophila melanogaster.
Interaction identification: classical two hybrid	Participant identification: nucleotide sequence	Host: <i>s. cerevisiae</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: cg10139-cg8415-1	Interaction detected by Y2H.
kD: 0.0	Type: aggregation		
comment	Author confidence score for the interaction was: 0.207546778		
<input type="checkbox"/> g9v740^b , <input type="checkbox"/> g8t3u2^b			
<input checked="" type="checkbox"/> Interaction[?]	Ac: EBI-198634	Name: cg10139-beta tub56-1	Interaction detected by Y2H.
kD: 0.0	Type: aggregation		
comment	Author confidence score for the interaction was: 0.329140733		
<input type="checkbox"/> g9v740^b , <input type="checkbox"/> tbb1 drome^b			
<input checked="" type="checkbox"/> Interaction[?]	Ac: EBI-198638	Name: robl62a-cg10834-1	Interaction detected by Y2H.
kD: 0.0	Type: aggregation		
comment	Author confidence score for the interaction was: 0.859751185		
<input type="checkbox"/> g9w0m^b , <input type="checkbox"/> g9v9p1^b			
<input checked="" type="checkbox"/> Interaction[?]	Ac: EBI-198642	Name: robl62a-cg10927-1	Interaction detected by Y2H.
kD: 0.0	Type: aggregation		
comment	Author confidence score for the interaction was: 0.910044319		
<input type="checkbox"/> g9w0m^b , <input type="checkbox"/> g9v8j4^b			



Database Search

Search Results for ac=GO:0000176

Nuclear exosome

GO:0000176

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

Search

Links

[Home](#)

[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"/> yjl2 yeast^b , <input type="checkbox"/> ucr2 yeast^R , <input type="checkbox"/> rr42 yeast^R , <input type="checkbox"/> lsm2 yeast^R , <input type="checkbox"/> q08723^R , <input type="checkbox"/> rsmb yeast^R , <input type="checkbox"/> apal yeast^R , <input type="checkbox"/> garl yeast^R , <input type="checkbox"/> if6 yeast^R , <input type="checkbox"/> ygl7 yeast^R , <input type="checkbox"/> rpnc yeast^R ,			
Interaction²	EBI-47399	ho-436	-
-	-	-	-
<input type="checkbox"/> imal yeast^b , <input type="checkbox"/> rr44 yeast^R , <input type="checkbox"/> q05543^R , <input type="checkbox"/> sif2 yeast^R , <input type="checkbox"/> gcr3 yeast^R , <input type="checkbox"/> q03782^R , <input type="checkbox"/> yah2 yeast^R , <input type="checkbox"/> pap yeast^R , <input type="checkbox"/> iml1 yeast^R , <input type="checkbox"/> nup2 yeast^R , <input type="checkbox"/> q07623^R , <input type="checkbox"/> q06825^R , <input type="checkbox"/> nup1 yeast^R , <input type="checkbox"/> mft1 yeast^R , <input type="checkbox"/> sin3 yeast^R , <input type="checkbox"/> rrp6 yeast^R , <input type="checkbox"/> fip1 yeast^R , <input type="checkbox"/> rr43 yeast^R , <input type="checkbox"/> nam8 yeast^R , <input type="checkbox"/> rnt1 yeast^R , <input type="checkbox"/> hpr1 yeast^R , <input type="checkbox"/> reh1 yeast^R , <input type="checkbox"/> rrp4 yeast^R , <input type="checkbox"/> eaf3 yeast^R , <input type="checkbox"/> has1 yeast^R , <input type="checkbox"/> ctpt yeast^R , <input type="checkbox"/> sync yeast^R , <input type="checkbox"/> rlr1 yeast^R , <input type="checkbox"/> yhp9 yeast^R , <input type="checkbox"/> umel yeast^R ,			
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^R , <input type="checkbox"/> csl4 yeast^b , <input type="checkbox"/> rr44 yeast^R , <input type="checkbox"/> mtr3 yeast^R , <input type="checkbox"/> rrp4 yeast^R , <input type="checkbox"/> rr42 yeast^R , <input type="checkbox"/> rr43 yeast^R , <input type="checkbox"/> rrp6 yeast^R , <input type="checkbox"/> rr41 yeast^R , <input type="checkbox"/> q08491^R , <input type="checkbox"/> imal yeast^R , <input type="checkbox"/> yiv5 yeast^R ,			
Interaction²	EBI-1809	ga-367	-
-	-	-	-



rr42_yeast

Search

Links

[New Search](#)

[Intact Home](#)

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 SSKLQLIKKY SFKIFVDVLV ISSHSHPVSL ISFAIYSALN STYLPKLISA FDDLEVEELP TFHDYDMVKL DINPPLVFIL AVVGNMMLLD PAANESEVAN NGLIISWSNG KITSPIRSVA LNDSNVKSKF PHLKQGLAM VEKYAPDVVR SLENL			

[Graph](#)

[Path](#)

[Reset](#)

User: INTACTWEB
Database: iweb

Please send any questions or suggestions to intact-help@ebi.ac.uk
Last modified: 19-July-2004 11:34 AM by Samuel

Powered by
Struts

Interactor?

EBI-1765

Graph?

Clicking on a node of the graph will:

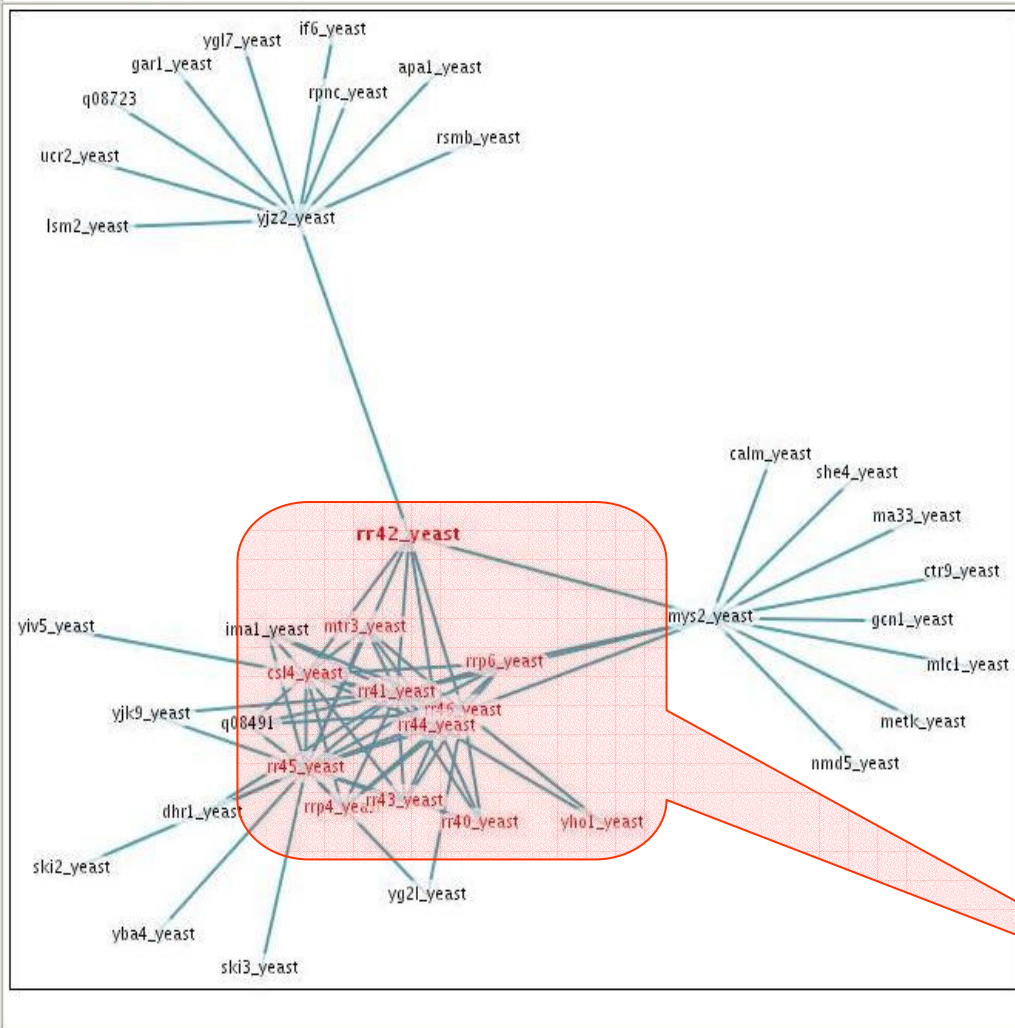
- center the view?
- add a network?

PSI-XML?

Links

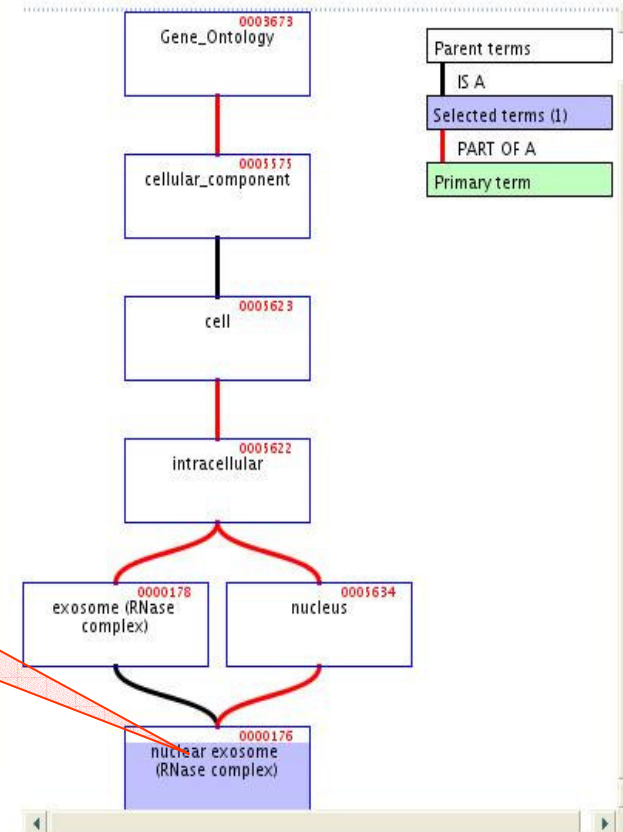
[IntAct home](#)
[Back to search](#)

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



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

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





HierarchView?

Interactor?

EBI-1765

Search Add

Graph?

Expand

Clicking on a node of the graph will:

- center the view?
- add a network?

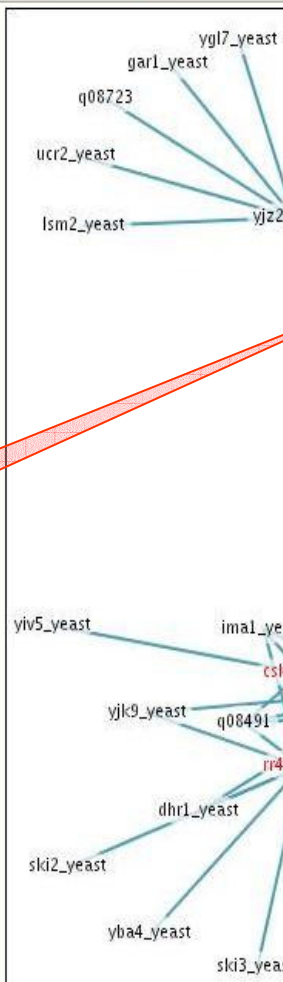
PSI-XML?

Download

Links

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



http://www.ebi.ac.uk/intact/graph2mif/getXML?ac=EBI-1765&depth=1&strict=false - Microsoft Internet Explorer

```

File Edit View Favorites Tools Help

<?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="11752500" secondary="" version="" />
  </xref>
  </participantDetection>
  </entry>
  </entrySet>
  
```

Done Internet

Back Forward Reload Stop <http://www.cytoscape.org/>

Mail AIM Home Radio Netscape Search Shop IntAct Project IntAct local technical i... SeqDB swissWatch GMX

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. [Read more »](#)

[Cytoscape: Features](#) | [Screenshots](#) | [Dev team](#) | [PlugIns](#) | [Download](#) | [Report a Bug](#)

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



Memorial Sloan-Kettering Cancer Center



University of California at San Diego



Institut Pasteur



Cytoscape 1.1.1

File Edit Select Layout Visualization **Plugins**

- Import PSI-MI Data from file...
- Import PSI-MI Data from web...**
- Import GEO SOFT Data from file...
- Import GEO SOFT Data from web...
- Export Data to PSI-MI XML Format...

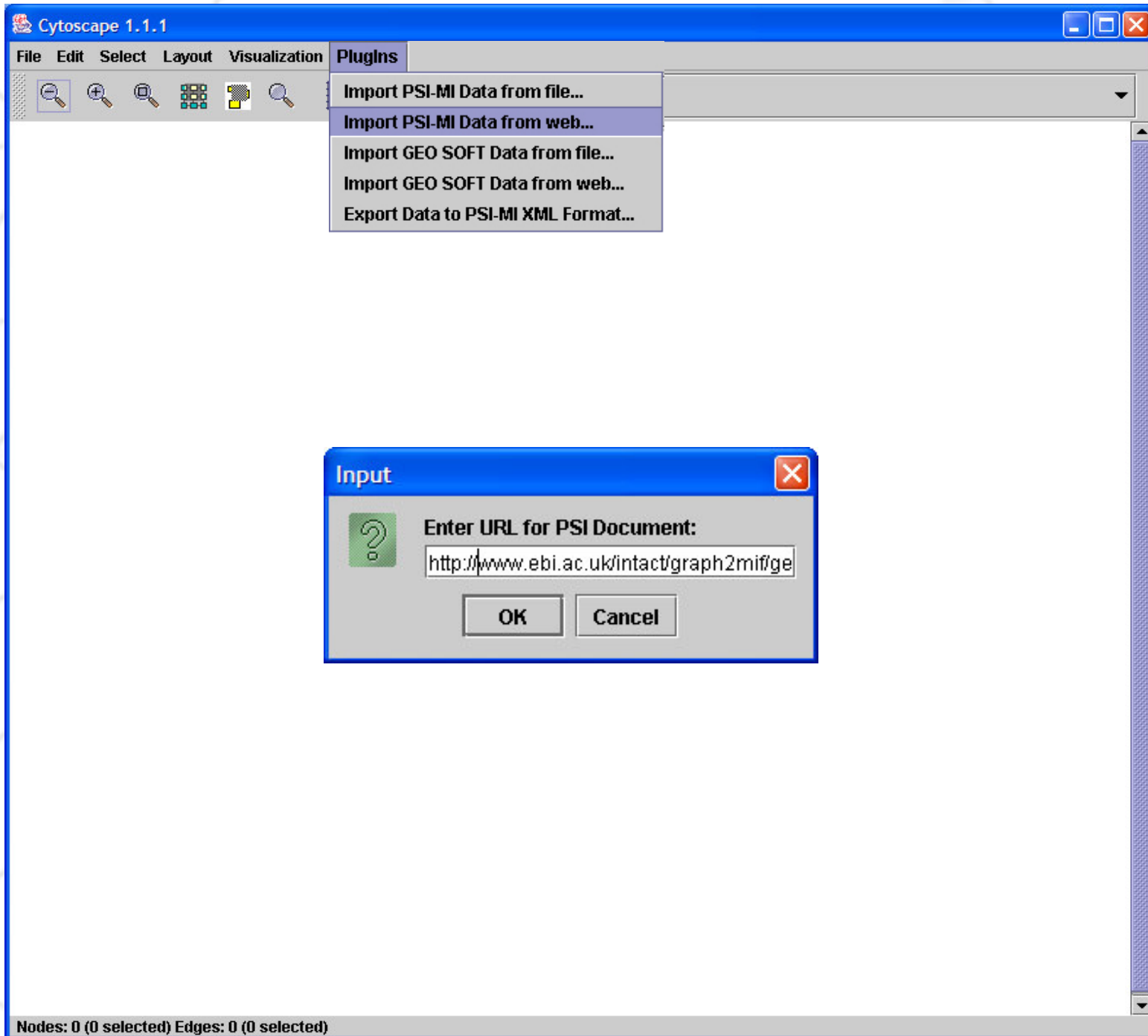
Input

Enter URL for PSI Document:

<http://www.ebi.ac.uk/intact/graph2mif/ge>

OK Cancel

Nodes: 0 (0 selected) Edges: 0 (0 selected)

The image shows the Cytoscape 1.1.1 software interface. The main window has a menu bar with 'File', 'Edit', 'Select', 'Layout', 'Visualization', and 'Plugins'. The 'Plugins' menu is open, showing options for importing and exporting PSI-MI and GEO SOFT data. An 'Input' dialog box is centered on the screen, prompting the user to enter a URL for a PSI document. The URL 'http://www.ebi.ac.uk/intact/graph2mif/ge' is entered in the text field. The dialog box has 'OK' and 'Cancel' buttons. At the bottom of the Cytoscape window, the status bar displays 'Nodes: 0 (0 selected) Edges: 0 (0 selected)'. The background of the slide features a faint network diagram and a tree icon in the bottom right corner.

The image shows a screenshot of the Cytoscape 1.1.1 software interface. The main window has a blue title bar with the text "Cytoscape 1.1.1" and standard window control buttons. Below the title bar is a menu bar with "File", "Edit", "Select", "Layout", "Visualization", and "Plugins". A toolbar with various icons is located below the menu bar. The main workspace is currently empty. A dialog box titled "Retrieving PSI-MI Data" is open in the center of the workspace. The dialog box contains the following text:

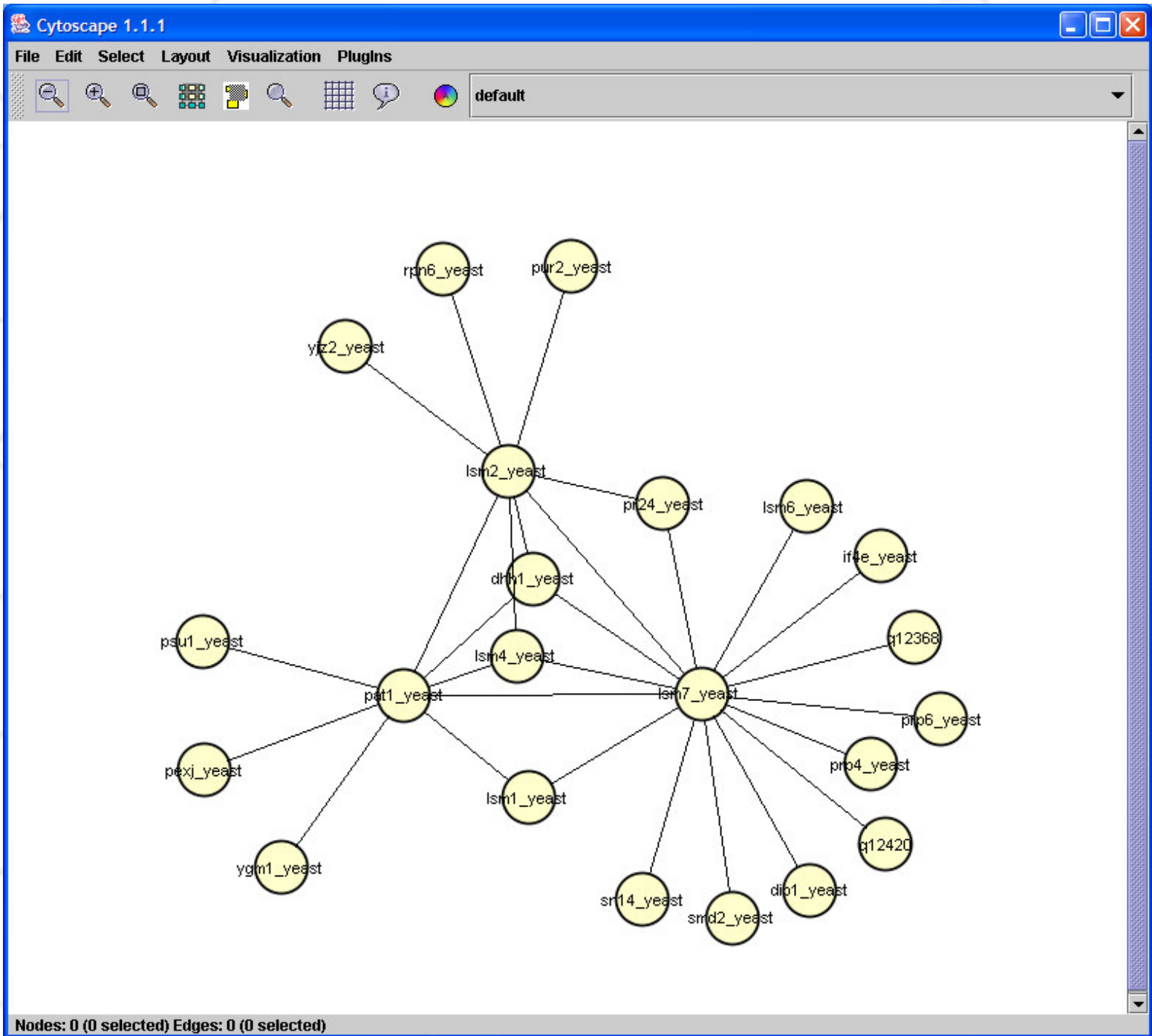
Retrieved PSI-MI Data from:
<http://www.ebi.ac.uk/intact/graph2mif/getXML?ac=EBI-141&depth=1&strict=false>

Total Number of Interactions: 28

Total time to retrieve/parse file: 8162 ms

Data Retrieval Complete

At the bottom of the main window, a status bar displays "Nodes: 0 (0 selected) Edges: 0 (0 selected)".





Database Search

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

EBI-39933,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
<input type="checkbox"/> Interaction?	Ac: EBI-39933	Name: ga-99	
-	Type: aggregation		
<input type="checkbox"/> rr44 yeast^E , <input type="checkbox"/> cs14 yeast^E , <input type="checkbox"/> rr44 yeast^E , <input type="checkbox"/> mtr3 yeast^E , <input type="checkbox"/> rrp4 yeast^E , <input type="checkbox"/> rr40 yeast^E , <input checked="" type="checkbox"/> rr42 yeast^E , <input type="checkbox"/> rr43 yeast^E , <input type="checkbox"/> rr46 yeast^E , <input type="checkbox"/> rrp6 yeast^E , <input type="checkbox"/> rr41 yeast^E , <input type="checkbox"/> yho1 yeast^E			
<input type="checkbox"/> Interaction?	Ac: EBI-1893	Name: ga-368	
-	Type: aggregation		
<input type="checkbox"/> rr46 yeast^E , <input type="checkbox"/> cs14 yeast^E , <input type="checkbox"/> rr44 yeast^E , <input type="checkbox"/> mtr3 yeast^E , <input type="checkbox"/> rrp4 yeast^E , <input type="checkbox"/> rr40 yeast^E , <input type="checkbox"/> rr42 yeast^E , <input type="checkbox"/> rr43 yeast^E , <input type="checkbox"/> rr45 yeast^E , <input type="checkbox"/> rr46 yeast^E , <input type="checkbox"/> rrp6 yeast^E , <input type="checkbox"/> rr41 yeast^E , <input checked="" type="checkbox"/> q08491^E , <input type="checkbox"/> ima1 yeast^E , <input type="checkbox"/> yg21 yeast^E , <input type="checkbox"/> yho1 yeast^E			

Graph

Path

Reset

Interactor?

Graph?

Clicking on a node of the graph will :

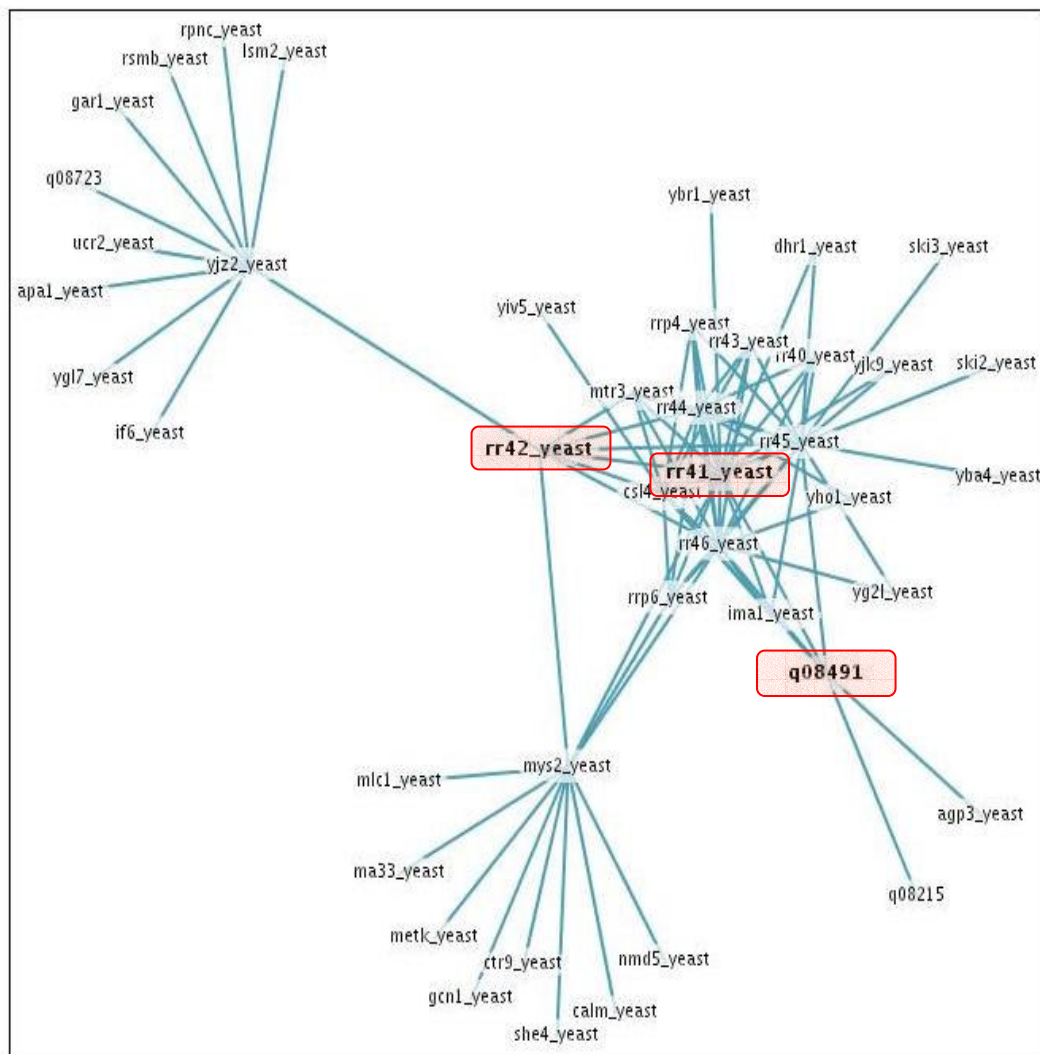
- center the view?
- add a network?

PSI-XML?

Links

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

Interaction network for 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 type="checkbox"/>
GO:0000176	C:nuclear exosome (RNase compl	<input type="checkbox"/>
GO:0006402	P:mRNA catabolism	<input type="checkbox"/>
GO:0000178	C:exosome (RNase complex)	<input type="checkbox"/>
GO:0005737	C:cytoplasm	<input type="checkbox"/>

Editor - Microsoft Internet Explorer

File Edit View Favorites Tools Help

Back Forward Stop Home Search Favorites Media Print Mail New Tab



[Help Topics](#) [FAQ](#)

Editor - Experiment ¹

Experiment ▼

Search ?

Create ?

[Logout](#)

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 binc

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

Interactions

2 items found, displaying 1 to 2 1

Action	Short Label	Ac	Full Name
<input type="button" value="Edit Interaction"/> <input type="button" value="Delete Interaction"/>	if43yeast-if4eveast	EBI-74705	A novel inhibitor of cap-dependent translation initiation in yeast: p20 competes with eIF4G for binding to eIF4E
<input type="button" value="Edit Interaction"/> <input type="button" value="Delete Interaction"/>	if4yeast-if43eveast	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
<input type="button" value="Recent Interaction"/> <input type="button" value="Search Interaction"/>	<input style="width: 100%;" type="text"/>	<input style="width: 100%;" type="text"/>

Annotations

Action	Topic	Description
<input type="button" value="Add Annotation"/>	--- Select --- ▼	<div style="border: 1px solid #ccc; height: 40px;"></div>

Crossreferences

Action	Database	Primary Id	Secondary Id	Release Number	Reference Qualifier
<input type="button" value="Edit Crossreference"/> <input type="button" value="Delete Crossreference"/>	pubmed	9118949			primary-reference
<input type="button" value="Add Crossreference"/>	--- Select --- ▼	<input style="width: 100%;" type="text"/>	<input style="width: 100%;" type="text"/>	<input style="width: 100%;" type="text"/>	primary-reference ▼

Submit
Save & Continue
Cancel
Delete

Controlled Vocabulary !!!

The screenshot shows the IntAct web interface. The main content area displays a table of interactions with columns for Host Organism, Interaction Detection, and Participant Detection. Three callout boxes highlight specific interaction types:

- gust pull down**: A list of interaction types including ha tag, his pull down, his tag, in silico, interaction detectio, interologs, isothermal titration, lambda phage display, light scattering, mass spectrometry st, molecular sieving, mrna display, myc tag, nuclear magnetic res, other biochemical te, peptide array, phage display, phylogenetic profile, predictive text mini, protein array, protein complementat, protein in situ arra, proteinchip(r) on a pull down, reverse ras recruitm, ribosome display, scintillation proxim, sequence based phylo, and sequence based predi.
- polyclonal antibody**: A list of interaction types including de novo protein sequ, edman degradation, full identification, monoclonal antibody, nucleotide sequence, partial dna sequence, participant detectio, peptide massfingerpr, peptide synthesis, polyclonal antibody, predetermined, primer specific pcr, protein sequence ide, radio-labelled prote, sequence tag identif, southern blot, and western blot.
- primary-reference**: A list of interaction types including cabri, flybase, go, intact, interpro, newt, pdb, psi-mi, pubmed, sgd, and uniprot.

Host Organism	Interaction Detection	Participant Detection
s cerevisiae	gust pull down	polyclonal antibody
EBI-74705	A novel inhibitor of cap-dependent translation initiation in yeast: p20 competes with eIF4G for binding to eIF4E	p20 competes with eIF4G for binding to eIF4E
EBI-74709	A novel inhibitor of cap-dependent translation initiation in yeast: p20 competes with eIF4G for binding to eIF4E	p20 competes with eIF4G for binding to eIF4E

Controlled Vocabulary

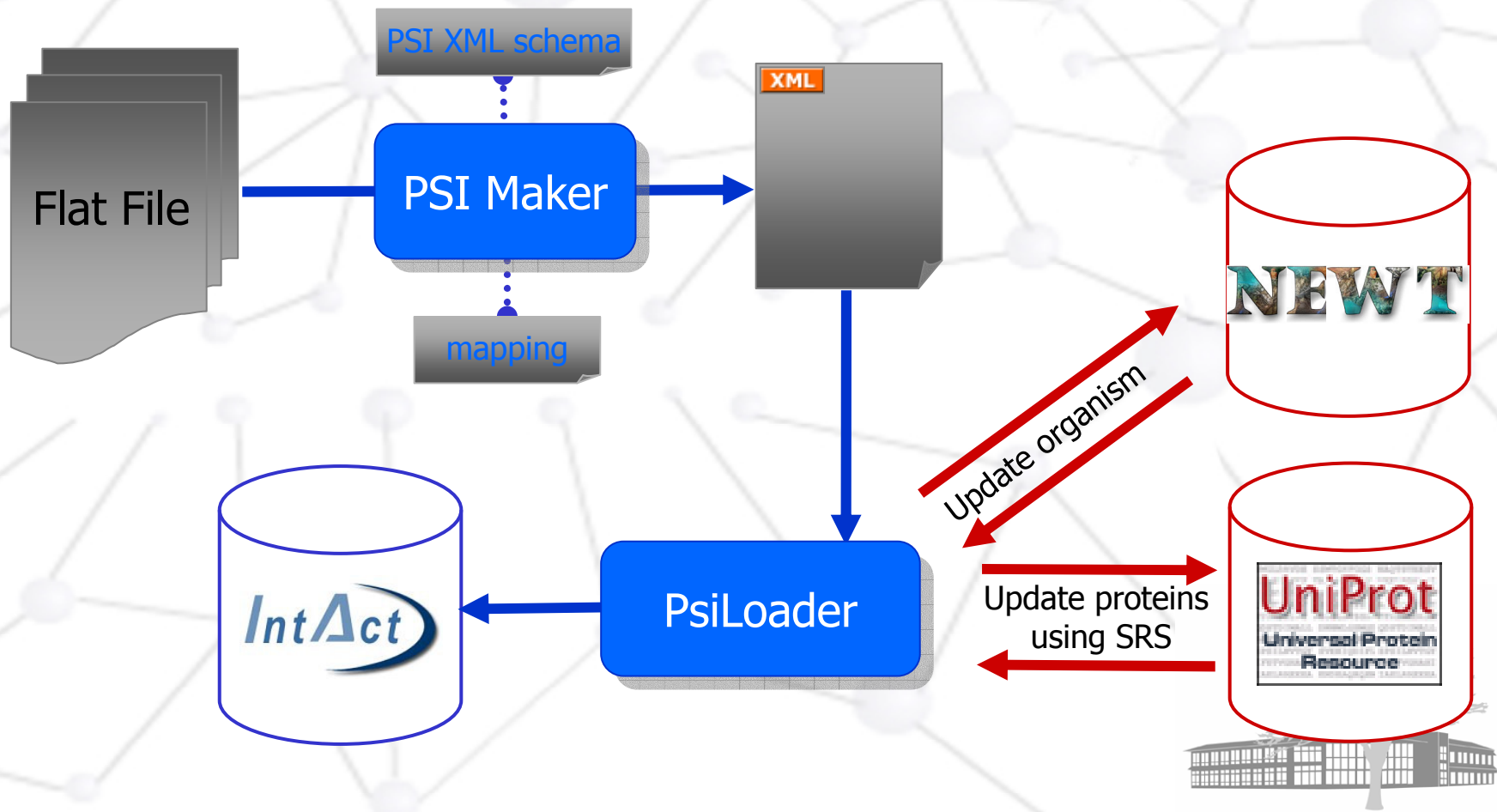
- IntAct has developed CV specific to Molecular Interactions, this is now maintained and extended by PSI.

CvInteraction	Ac: EBI-94	Name: <i>classical two hybrid</i>	classical two hybrid
definition	<p>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.</p>		
psi-mi	MI:0018	-	Type: identity
pubmed	10967325	-	Type: go-definition-ref



PSI Loader

Example of use:
Insertion of large scale experiment



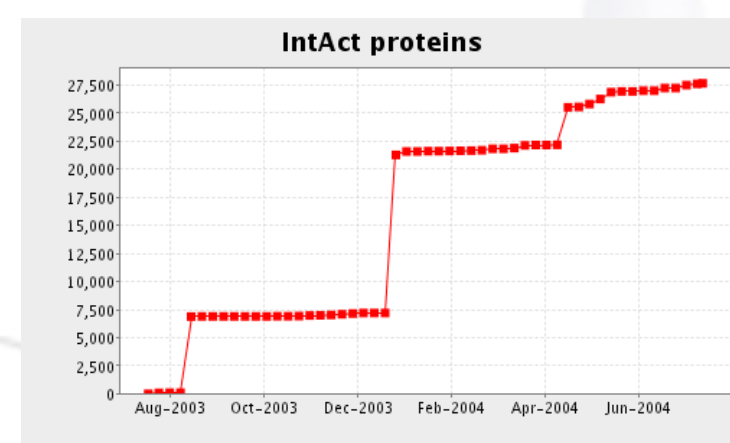
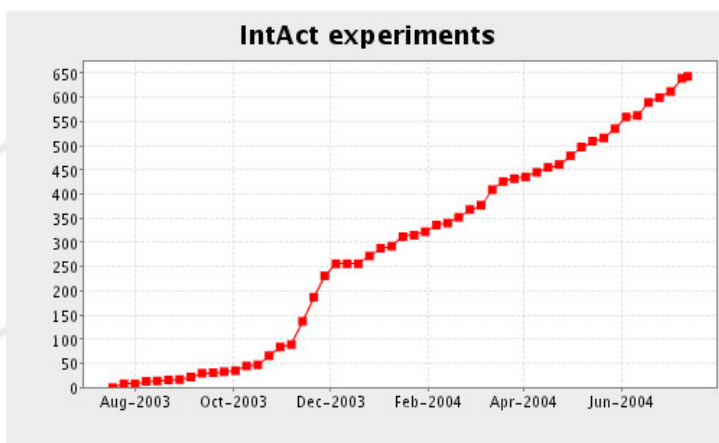
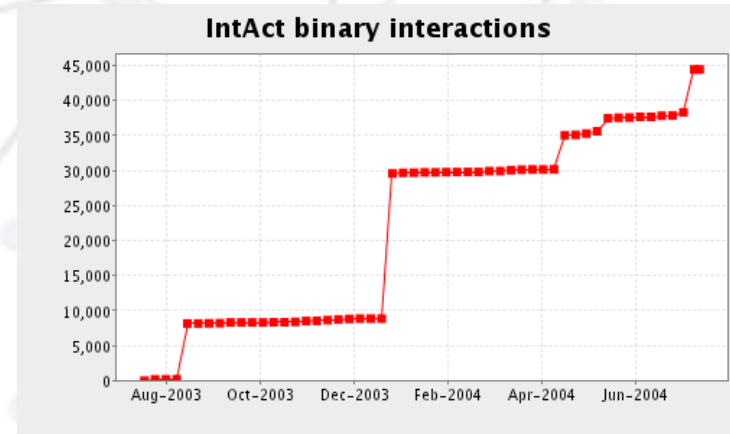
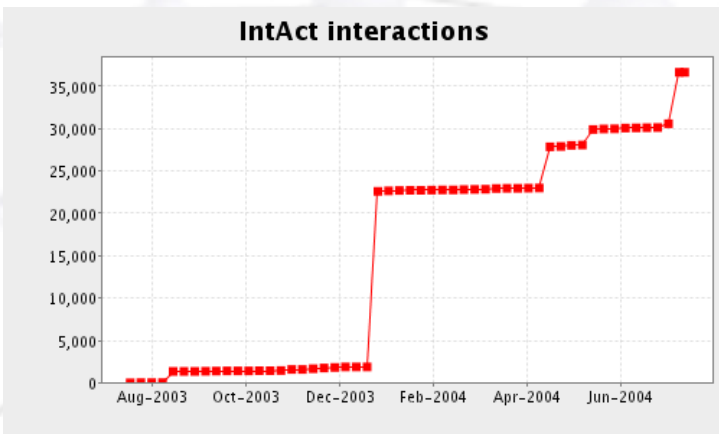
Data

All data publicly available, released monthly

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



Data statistics



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>



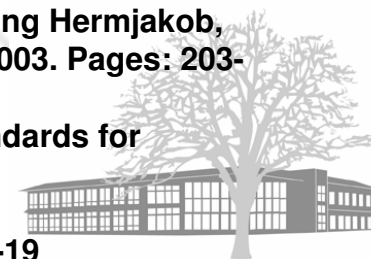
The IMEx consortium

- *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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- EBI Industry Group
- HUPO

• Misc.

- Rolf Apweiler
- GO curators

YOU!

<http://psidev.sf.net>