

NA5



A (Proteome)Binders Exchange Format (NA5.1.4)

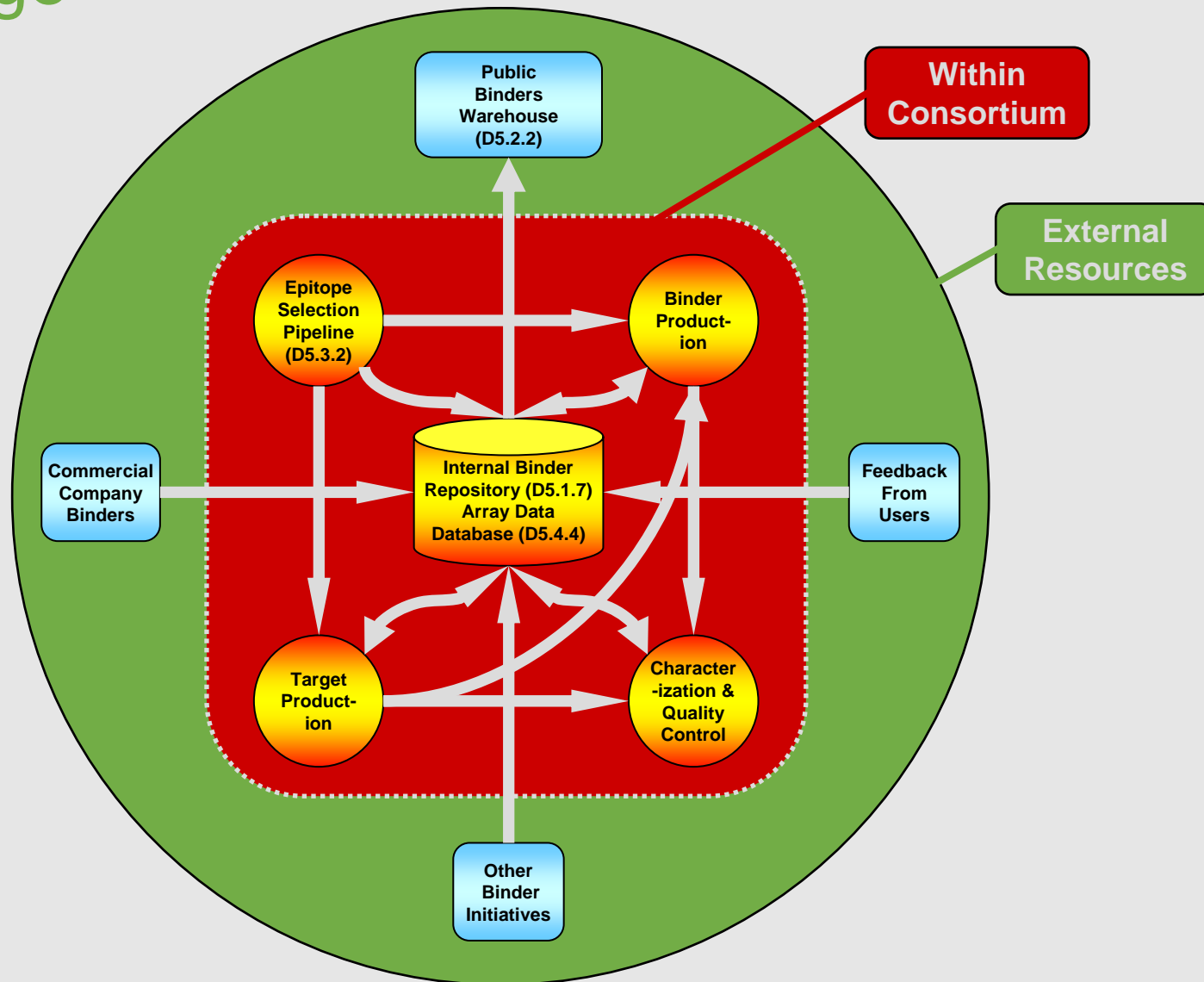
Bringing It All Together

EMBL-EBI



EBI is an Outstation of the European Molecular Biology Laboratory.

Exchange /Share Events



“Where it’s at”, -web page on the PSI site

The screenshot shows the HUPO Proteomics Standards Initiative website. The header includes the PSI logo, navigation tabs for Workgroups, Publications, Documents, Events, Forums, Organisation, and Tutorials, and the HUPO Human Proteome Organisation logo. The main content area is titled 'Antibody-Antigen binding' and includes a search bar, a countdown to the PSI spring meeting 2008, an events calendar for January 2008, a user login form, and a navigation menu. The right sidebar contains a 'List of Contents' with 13 items, an 'Introduction' section, and a paragraph describing the PSI's goals and the specific page's content.

Search

Search

Countdown

105 days until PSI spring meeting 2008 in Toledo, Spain.

Events

January 2008						
Sun	Mon	Tue	Wed	Thu	Fri	Sat
		1	2	3	4	5
6	7	8	9	10	11	12
13	14	15	16	17	18	19
20	21	22	23	24	25	26
27	28	29	30	31		

User login

Username: *

Password: *

Log in

- Create new account
- Request new password

Navigation

- create content
- Meeting minutes
- PSI Mailing Lists
- groups

Who's online

Home

Antibody-Antigen binding

Submitted by dgloriam on Mon, 2007-05-14 14:02.

Proteomics Standards Initiative

Protein-Binder Exchange Documentation

List of Contents

- Introduction
- Purpose of the exchange format
- Purpose of this web page
- XML schema documentation
- Controlled vocabularies
- Minimum requirements for binder and protein target representation
- Annotation manual
- Example files
- Release schedule
- List of planned features
- How to comment
- Tools
- Further information and relevant links

Introduction

The Proteomics Standards Initiative (PSI) aims to define community standards for data representation in proteomics to facilitate data comparison, exchange and verification. For detailed information on all PSI activities, please see [PSI Home Page](#).


This page describes the application of the PSI **molecular interactions** data exchange format, PSI-MI XML2.5, to the transfer of binding molecule (protein-binder), e.g. antibody, data. The utilization of an existing format and its associated tools is time- and cost-efficient and provides a more reliable product. The molecular interactions exchange format is suitable because it has an appropriate scope and is one of the most mature proteomic standards available. While the exchange format (XML schema) in itself has been conserved the representation has been extended by adding terms to the associated controlled vocabulary. Moreover, a separate annotation manual and several example XML files have been produced.

The work on mapping protein-binder data to the exchange format for molecular interactions, extending the associated controlled vocabularies and producing documentation was carried out by **EMBL-EBI** in collaboration with the University of Bordeaux and the PSI-MI work group as part of the

- <http://www.psidev.info/index.php?q=node/281>

Merged CV loaded into the IntAct editor

- DRAFT PROTEIN BINDER CV
 - ☒ ← [?] alias type
 - ☒ ← [?] attribute name
 - ☒ ← [?] experiment attribute name
 - ☒ ← [?] feature attribute name
 - ☒ ← [?] interaction attribute name
 - ☒ ← [?] organism attribute name
 - ☒ ← [?] participant attribute name
 - ☒ ← [?] biological role
 - ☒ ← [?] cross-reference type
 - ☒ ← [?] database citation
 - ☒ ← [?] experimental material type
 - ☒ ← [?] experimental method
 - ☒ ← [?] experimental preparation
 - ☒ ← [?] experimental role
 - ☒ ← [?] experimental scope
 - ☒ ← [?] feature detection method
 - ☒ ← [?] feature range status
 - ☒ ← [?] feature type
 - ☒ ← [?] interaction type
 - ☒ ← [?] characterization experiment
 - ☒ ← [?] colocalization
 - ☒ ← [?] molecule production experiment
 - ☒ ← [?] physical interaction
 - ☒ ← [?] interactor type
 - ☒ ← [?] parameter type
 - ☒ ← [?] parameter unit
 - ☒ ← [?] participant identification method



[Show Users](#)
[Logout](#)

Editor - Interaction ¹³

Intact AC	Short Label	Full Name
EBI-35580	10c9_11g9-specific	Test of 10c9-hsa and 11g9-haptoglobin binding
Created 2007-DEC-30 by POSTGRES.		Last updated 2007-DEC-30 by POSTGRES.

Kd	Interaction Type	Organism
0.0	cross-reactivity ass	in vitro

Experiments

Action	Short Label	Pubmed Id	Intact AC	Full Name
Delete Experiment	weiler-2003-g		EBI-35566	Characterization of monoclonal antibodies to human group B rotavirus: enzyme-linked immunosorbent assay.

Experiments not yet added to the Interaction

Action	
Recent Experiment	Search Experiment <input type="text"/>

Interactors

Action	Short Label	SP AC	Intact AC
Search Interactor	<input type="text"/>	<input type="text"/>	<input type="text"/>

Action		
Delete Feature	Link Features	Unlink Features

Annotations

Action	Topic	Description
Edit Annotation	Delete Annotation	figure legend
		4a

Action	Topic	Description
Add Annotation	<input type="text" value="-- Select --"/>	<input type="text"/>

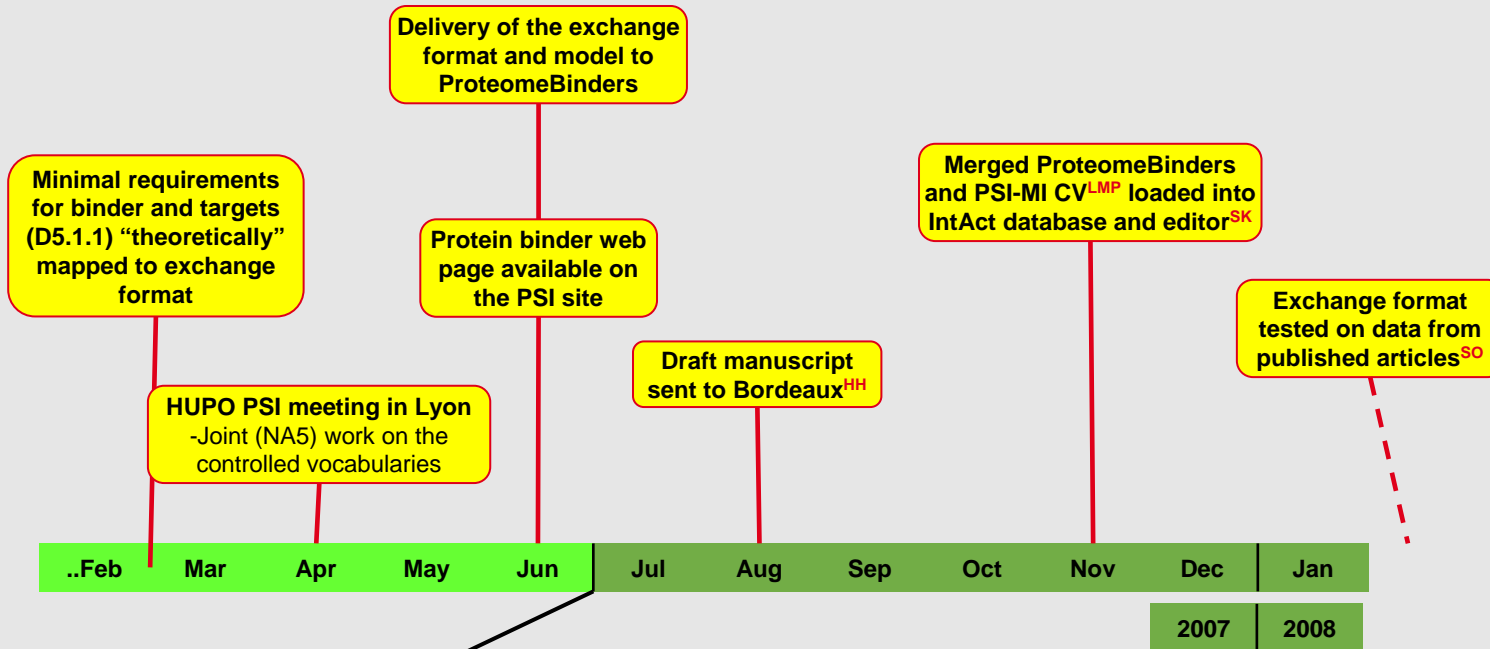
IntAct kickstart: http://www.ebi.ac.uk/~intact/devsite/local_install.html

Up to date

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W
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DG Full-time, ProteomeBinders

DG ~25% time, ESF funding



HH: Henning Hermjakob (coordination, writing)
LMP: Luisa Montecchi Palazzi (CV)
SK: Samuel (Sam) Kerrien (IntAct database)
SO: Sandra Orchard (Annotation)



Annotation of binder and target data

JOURNAL OF CLINICAL MICROBIOLOGY, Feb. 1989, p. 245-250
0095-1137/89/020245-06\$02.00/0
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Vol. 27, No. 2

Characterization of Monoclonal Antibodies to Human Group B Rotavirus and Their Use in an Antigen Detection Enzyme-Linked Immunosorbent Assay

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ELSEVIER Analytical Biochemistry 321 (2003) 217-225
www.elsevier.com/locate/yabio

A proteomics-based approach for monoclonal antibody characterization

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JMB Available online at www.sciencedirect.com
ScienceDirect

A Designed Ankyrin Repeat Protein Evolved to Picomolar Affinity to Her2

Christian Zahnd^{1,†}, Emanuel Wyler^{1,†}, Jochen M. Schwenk²
Daniel Steiner¹, Michael C. Lawrence³, Neil M. McKern³
Frédéric Pecorari¹, Colin W. Ward³, Thomas O. Joos²
and Andreas Plückthun^{1,*}

Annotation of binder and target data

- Experimental scopes:

- Purification from sample and extracts, immunization, generation of hybridoma, epitope mapping, affinity determination, cross-reactivity assessment, validation of binders for experimental techniques (WB & ELISA)...

- Experimental techniques:

- ELISA, WB, extraction, HPLC, immunization, pull down, MS,

- Molecule/Material types (“interactor types”):

- Proteins, mAbs, viruses, serum, lysates, cell lines, hybridoma, media..

Data from different sources (e.g. articles or labs) can be merged when viewed giving more information about binder and targets.



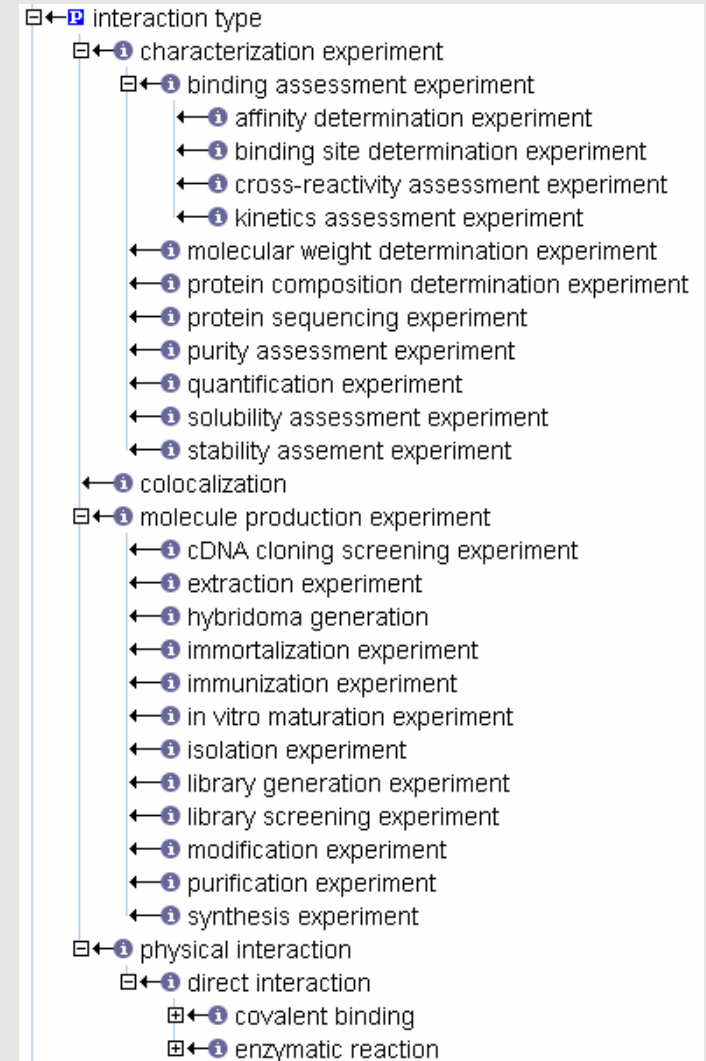
Annotation, -the good news

- The exchange format can capture the data minimum requirements data in the annotated articles.
- The CV and the representation is now more “IntAct-like” than before which should ease the compatibility with the various IntAct tools.



Annotation, -the bad news

- Different concepts for molecular interactions and binder-target data results in suboptimal semantics:
 - For example the –"interaction types" CV corresponds to the experimental scopes of binder and target production and characterization



Current compatibility issues with IntAct

- **Functionality not implemented in the editor:**
 - Parameters (numeric values with an unit e.g. molecular weight, kinetics, affinity, temperature..)
 - New interactor types such as “antibody”, “virus” etc.
 - Experimental preparation terms
 - Annotation of data without an article. For ProteomeBinders internal data there will be no publication.
- **Non-“PSI-MI CV terms” that have not been loaded:**
 - Cell lines for elements: “source”, “expressed in” and “hostOrganism”
 - The “negative” annotation topic for labelling non-occurring interactions
- **PSI-MI CV terms that fail to load into the editor:**
 - Many but not all CV terms for experimental roles. The reason to why just some terms are not imported is unknown.
- **Modifications are needed to export data in XML format**



Controlled Vocabulary

- To what extent will the Bordeaux “ligand binder ontology” be useful also for the exchange format CV?
- There is much work on writing the definitions for the new CV terms. Can this be a shared effort?
- (Question for EBI primarily: Should the ProteomeBinders CV and PSI-MI CVs be maintained as 1 joint CV?)



Minimum requirements

- The minimum requirements are not “minimum” enough
 - PSI minimum requirements documents for other types of data have been made less extensive in the refinement process.
 - Examples of info that might be excluded are:
 - Structural characteristics and biophysical properties (are often available via referenced databases)
 - The location of binding sites (e.g. epitopes and paratopes) (this information is often not available)
 - Could/Should ProteomeBinders have more extensive minimum requirements than PSI does?



What's next

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