

Building the BioAssay Research Database

A Next-Generation Platform for Annotating and Understanding Chemical Biology Datasets

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What is BARD?

A public platform for sharing chemical biology data that uses a standard representation and common language for organizing bioassays and their results.

Goal: To help researchers develop and test hypotheses on the influence of different probes on biological functions.





Precompetitive opportunities with BARD

- Standardized & controlled vocabulary to describe the context of experimental results
- Open source software platform to register assays, and to query and visualize public bioassay data
- An open standard for sharing bioassay annotations and data with the public or between organizations





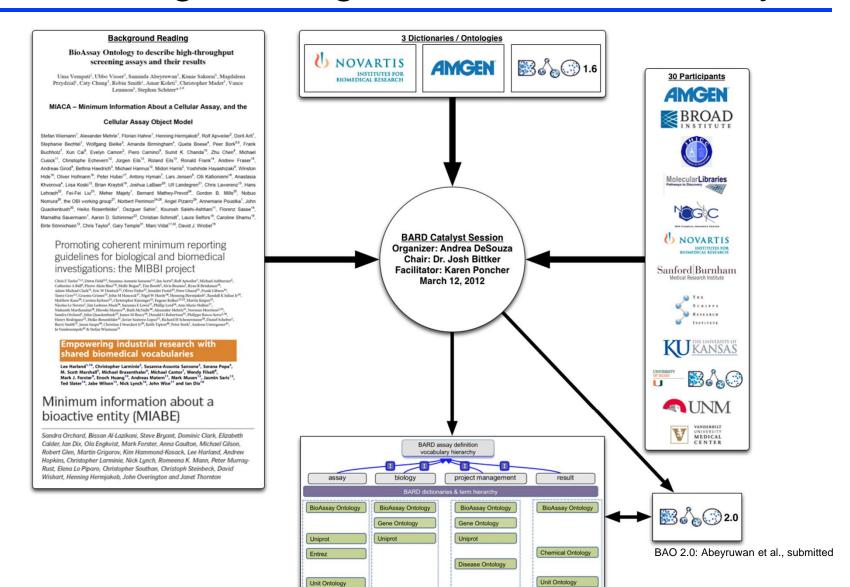
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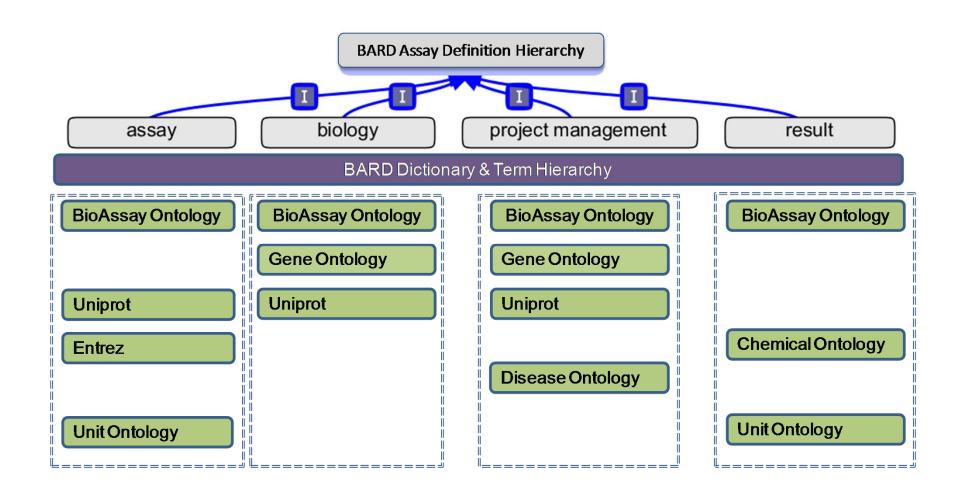
Constructing a biologist-focused vocabulary







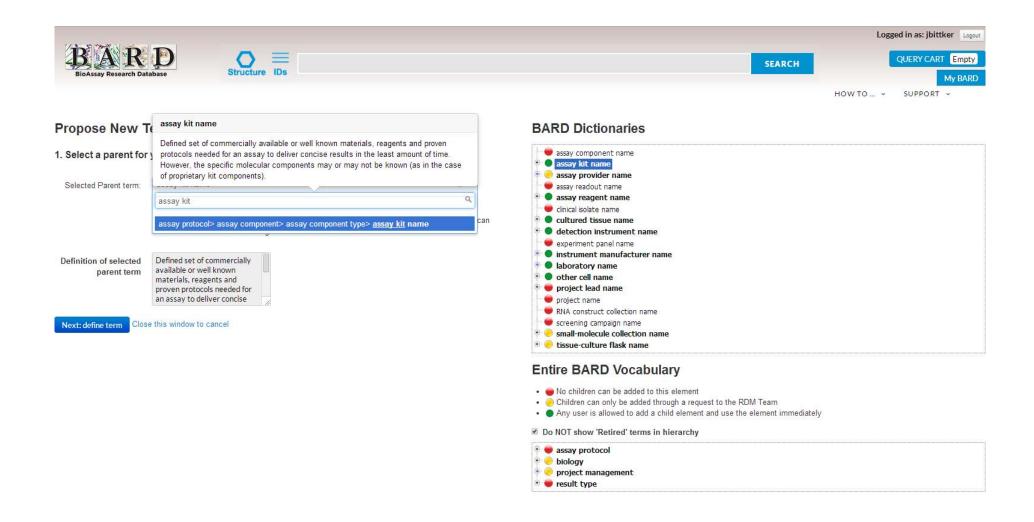
BARD top level concepts & sources







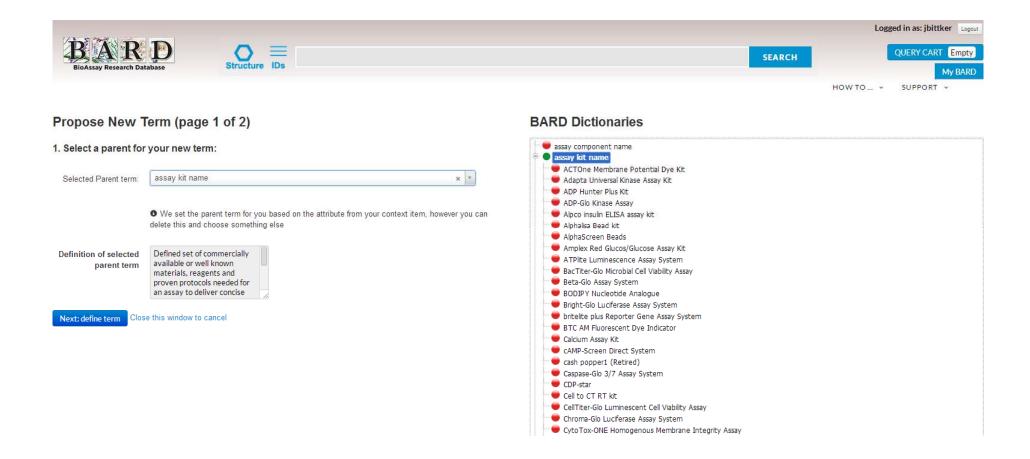
Curation of BARD-managed terms







Curation of BARD-managed terms







Curation of BARD-managed terms

1/1		Logged in as: jbittker Logout		
BARD BioAssay Research Database	Structure IDs		QUERY CART Empty	
DIOASSAY RESEARCH DATABASE		HOW TO •	My BARD SUPPORT ~	
		HOW 10 *	SUPPORT	
Propose New 1	erm (page 2 of 2)			
Selected Parent term	assay kit name			
Definition of selected parent term	Defined set of commercially avai			
2. Enter the name of	your term and a definition for it. (both are required)			
Proposed term *				
Proposed definition *				
3. Enter additional o	otional information about your term.			
Abbreviation				
Synonyms(Comma separated)				
4. Explain why you n	eed to add this term.			
Explanation/Comments				

New terms are provisional but can be used immediately to avoid delays

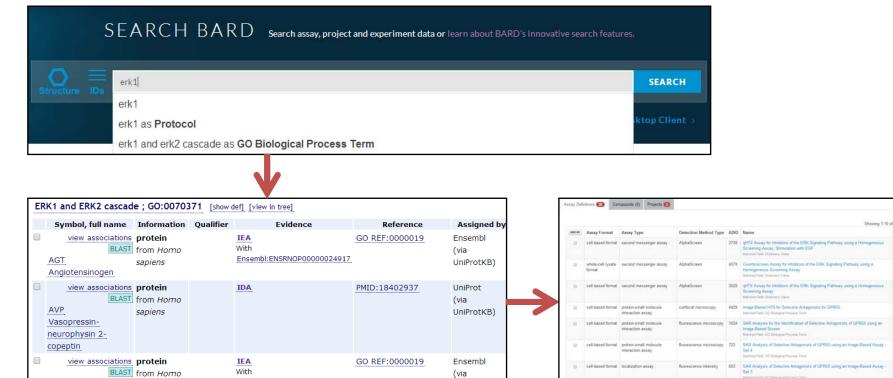




Leveraging of external ontologies

Ensembl:ENSRNOP00000009756

Any updates to a referenced ontology are incorporated into BARD



UniProtKB)

All target-based screens that GO indicates are associated to the queried pathway (and phenotypic assays directly annotated with the pathway)



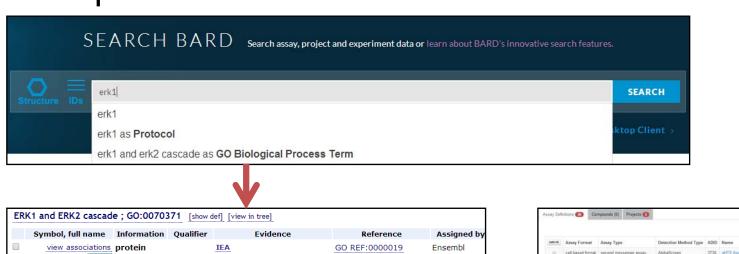
CCL11

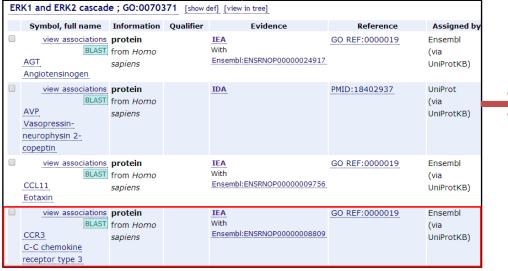
Eotaxin

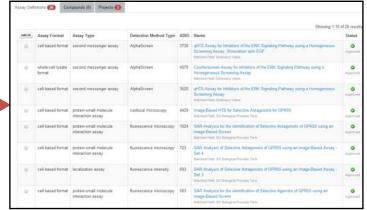
sapiens

Leveraging of external ontologies

Any updates to a referenced ontology are incorporated into BARD







New evidence added to GO is reflected in BARD search results





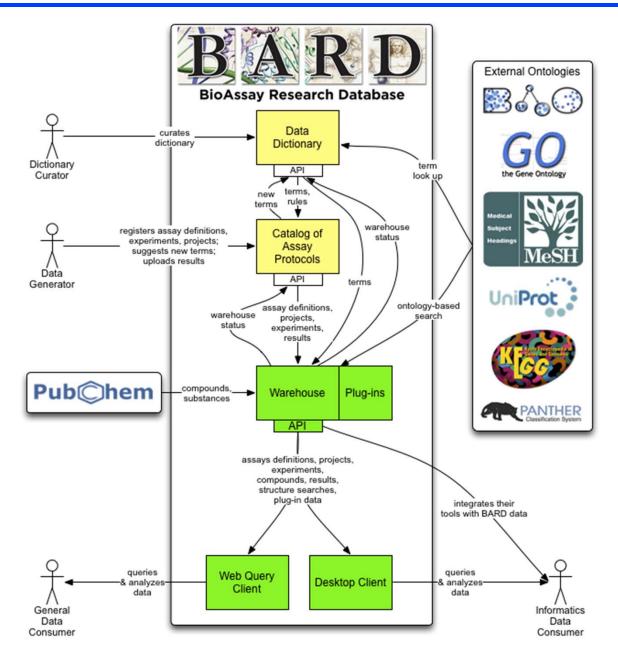
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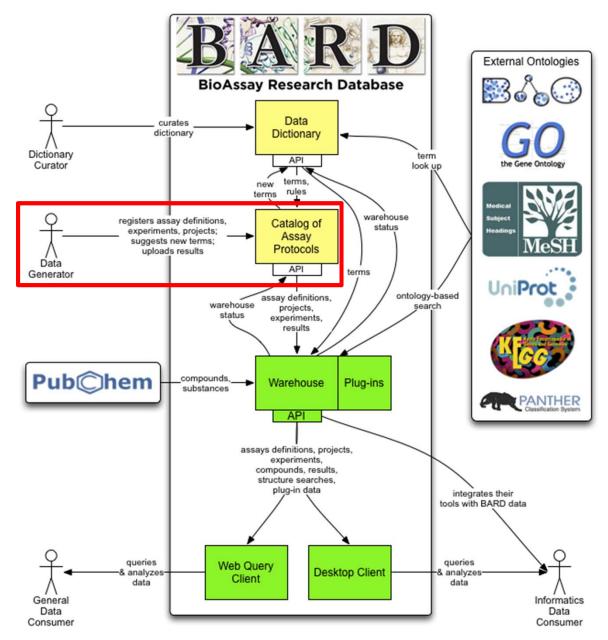
Build using component-based architecture







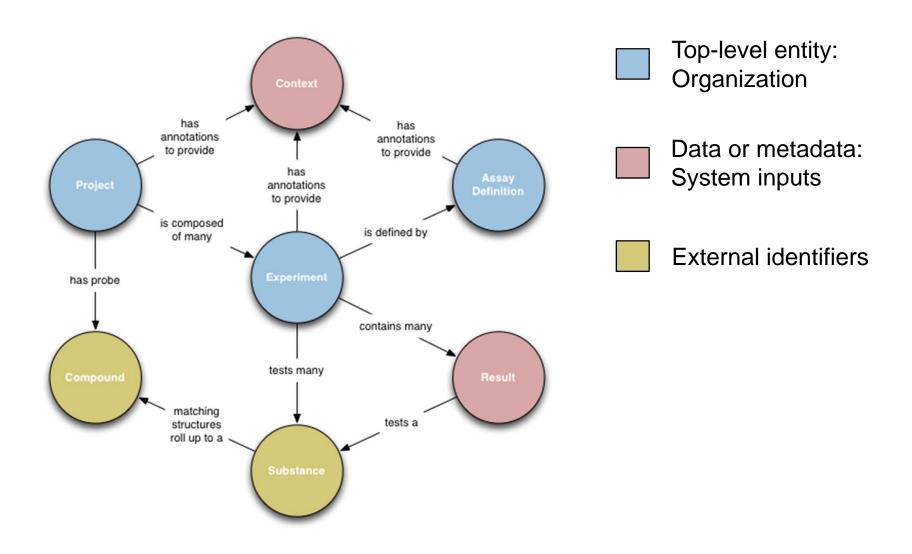
Build using component-based architecture







Structure for capturing bioassay relationships

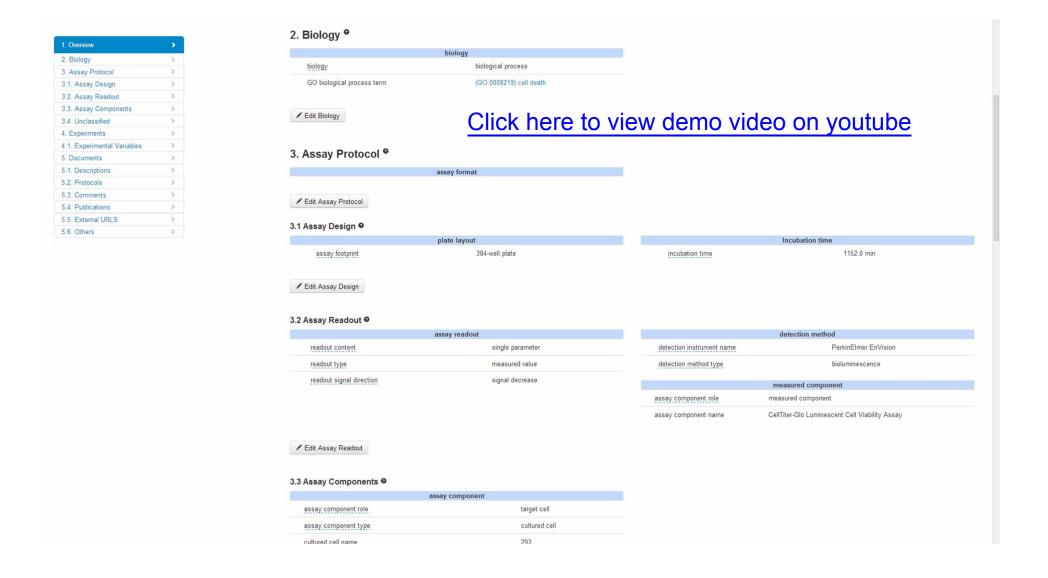




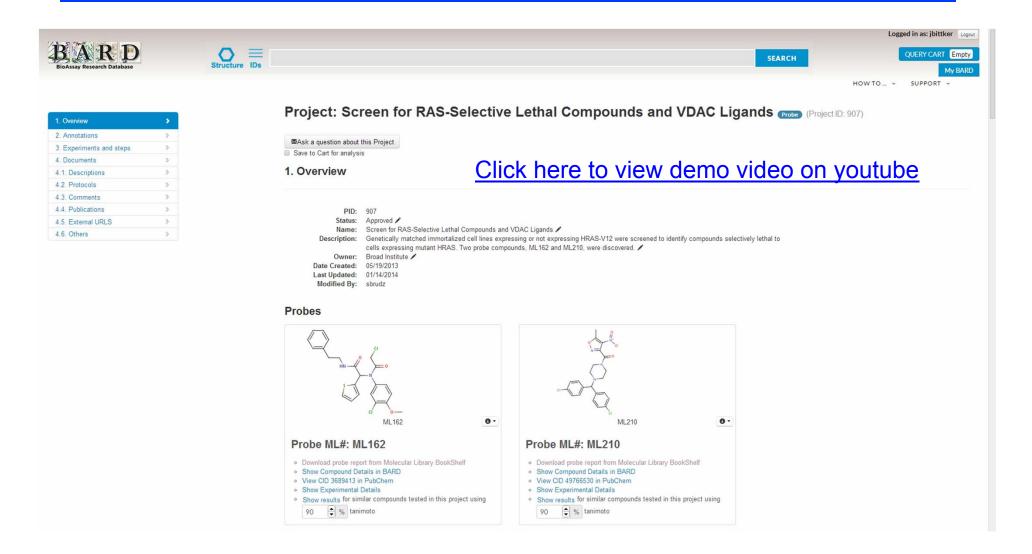


Interactive tools: assay definition

Autocomplete & definitions for controlled terms



Interactive tools: projects

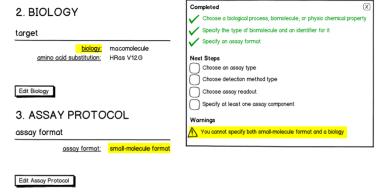




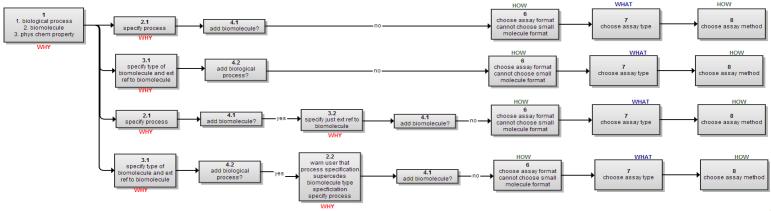


Guided process for defining bioassays

 Suggests path for providing minimum information necessary to define an assay; Allows cloning & editing of existing public protocols



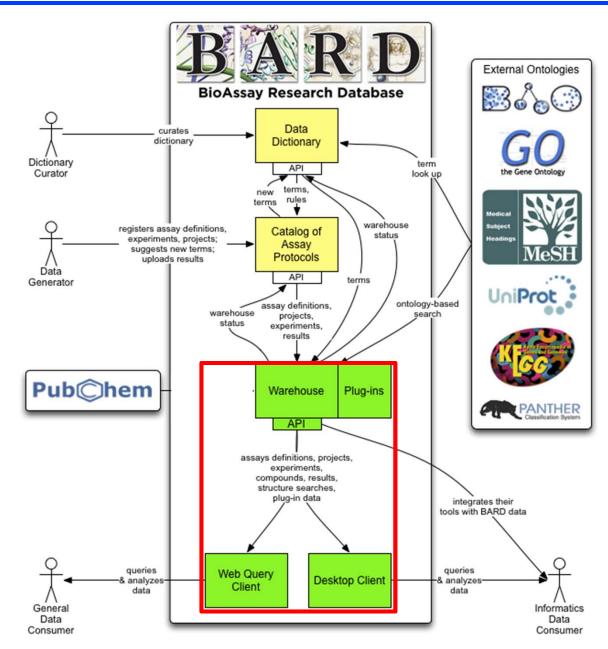
Logic checks for consistency







Using annotations: Finding & understanding bioassay data

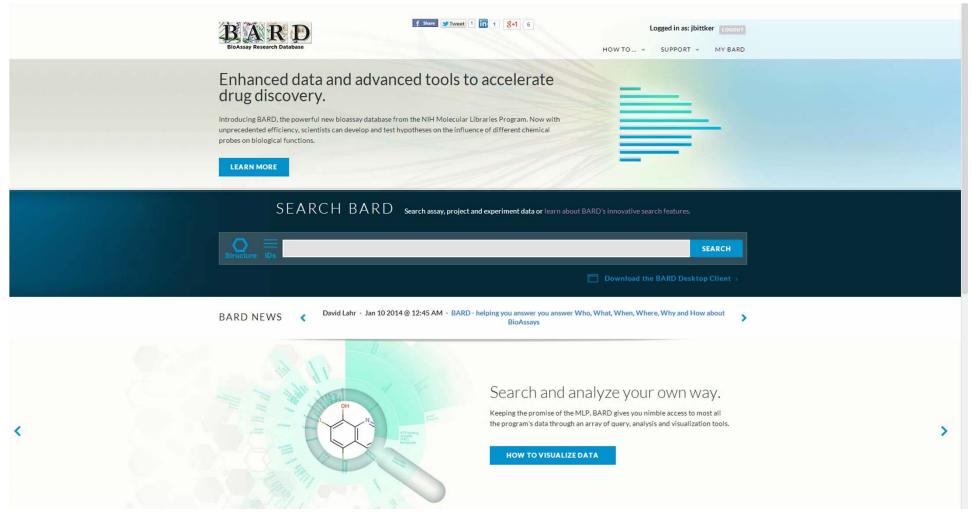






Using annotations: Finding & understanding bioassay data

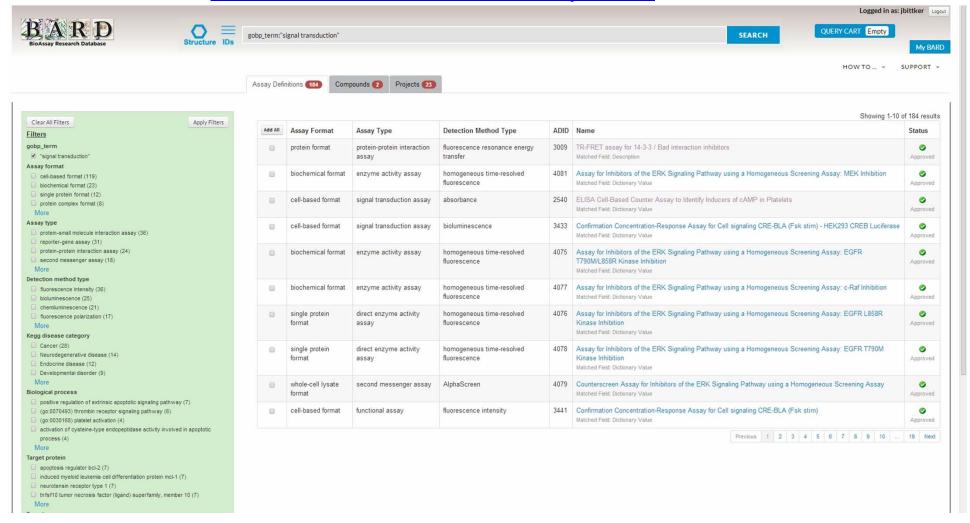
 Simple autocomplete interface allows basic searching by free text or specific annotation; searching by IDs or structures
 Click here to view demo video on youtube



Using annotations: Finding & understanding bioassay data

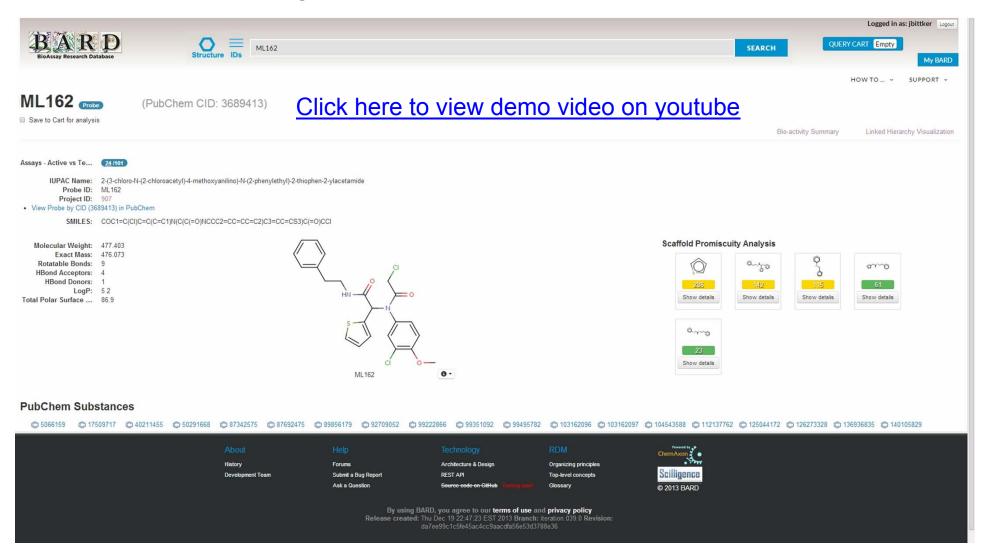
 Filtering results allows a focus on the desired understanding: By target, assay details, reagent, etc.

Click here to view demo video on youtube



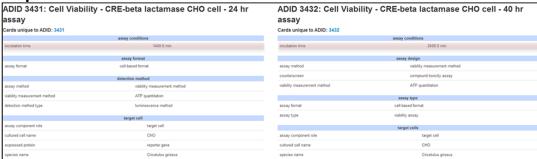
Visualizing data using structured annotations

Filtering and visualizing activity allows rapid understanding of multiple datasets

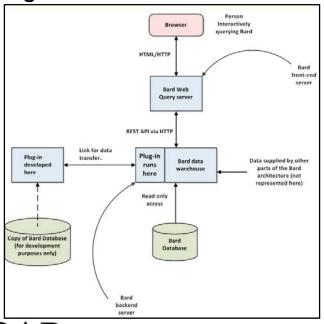


Additional uses of annotations

Establishing a measure of similarity between assays to enable clustering of protocols



Plugin architecture allows direct calls to warehouse API for metadata



Name	Lead Author[s]	Institution	Brief Description	Status
Badapple	Jeremy Yang	UNM	Evidence-based promiscuity scores	released Oct 2012
SmartCyp	Rajarshi Guha	NCGC	Prediction of which sites in a molecule that are most liable to metabolism by Cytochrome P450	released March 2013
WhichCyp	Rajarshi Guha	NCGC	Prediction of which Cytochrome P450 isoform(s) is(are) likely to bind a drug-like molecule	released June 2013
HScaf	Jeremy Yang	UNM	Scaffold analysis	In development
TBE (kNN)	Oleg Ursu	UNM	kNN, nearest neighbors bioactivity profiler	In development
TBE (Filtering)	Jeremy Yang	UNM	Druglike/leadlike/probelike suitability filtering	In development
Assay based similarity	Vlado Dancik	Broad	Compound similarity based on bioactivity	In development
TBE (SVM)	Lars Carlssong	AstraZeneca & UNM	SVM classifier	Planned
ALOGPS	Igor Tetko	HZM & UNM	LogP prediction	Planned
TBE (QSAR)	Alex Tropsha	UNC & UNM	QSAR modeling	Planned





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Sharing bioassays using a common language

Controlled vocabulary with public references

230	high-signal control	BAILO: saxpy protocols askey component askey component rare-saxpy option rates askey control rates high-sayal control. Contains the substrate litration without inhibitor to reflect the maximum enzyme activity at each substrate concentration. Depending on the composition of the inhibitor stocks, DMSO might be needed in the control wells to assure consistency across all the experiments.	BioAssay Ontology : http://www.bioassayontology.org/bao#BAO_0000156
231	low-signal control	BAID- Basing protocol- basing component raise basing component raise basing central raises have signal control. Contains the substrate triation without enzyme or substrate and without inhibitor. The low controls should reflect the signal expected for no enzyme activity at each substrate concentration. Depending on the composition of the inhibitor stocks, DMSO registed be needed in the control wells to assure consistency across all the experiments.	BioAssay Ontology : http://www.bioassayontology.org/bao#BAO_0000168
232	negative control	IDATIC- assay protoco- assay component- assay component rise- assay certificate negative control. Used to determine the baseline against which the effect of the test perturbagen is compared. Often the negative control is the solvent (e.g., DMSO) in which the perturbagen was dissolved.	BioAssay Ontology : http://www.bioassayontology.org/bao#BAO_0000079
233	positive control	BARD- assay protocol- assay component- assay component rise- assay cellination rise- assay control roles positive control. A chemical compound or reagent used in each plate of an assay to normalize the response of the test perturbagens (by plate). The positive control is known from previous experiments or is a previously established standard. It is usually highly active, resulting in a strong response of the intended effect. In an inhibition assay, the positive control would usually result in the complete inhibition, which measurement is then used for normalization. In an activation assay it would result in high activation, which measurement is then used for normalization. Using controls provides an external reference and reduces the number of false negatives and false positives.	BioAssay Ontology : http://www.bioassayontology.org/bao#BAO_0000000
151	cell-culture role	BARCh assay protocol- assay component- assay component role- assay definition role- cell-culture role	
249	antibiotic	BARC+ assay protocol- assay component- assay component role+ assay definition nole+ cell-culture role+ artificitio	Open Biemedical Ontologies - CHEBI : http://purl.obolibrary.org/obo/CHEBI_22582
250	differentiation agent	BARD- assay protocol- assay component- assay component role- assay defiction role- cell-culture role- differentiation agent	BioAssay Ontology : http://www.bioassayontology.org/bao#BAO_0002087
251	fixative	SARD- assay protocol- assay component- assay component role- assay definition role- cell-culture role- fixative	Open Biomedical Ontologies - CHEBI : http://purl.obolibrary.org/obo/CHEBI_50913

Business rules: what is required to minimally define an assay?
 2. Biology **

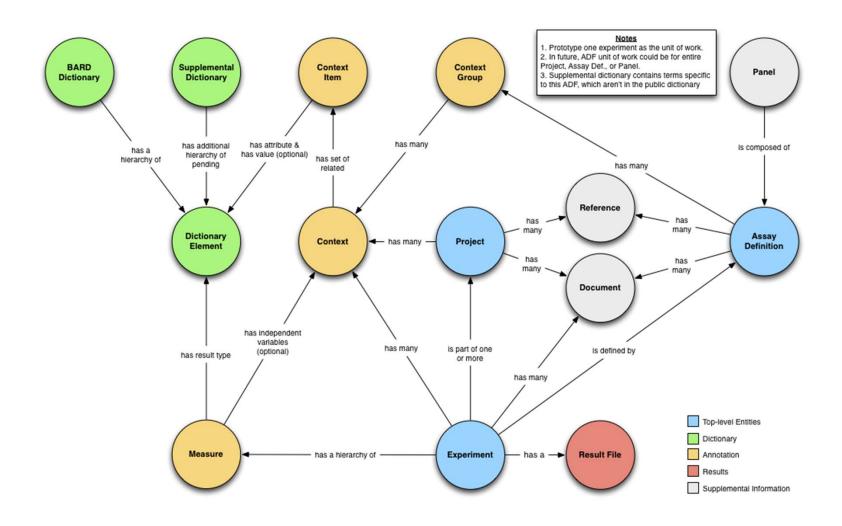
biology				
biology	macromolecule			
target, there should one	ogy defined as a something that can be considered a molecular other item that references one of the following terms (GO gene-NCBI accession number, UniProt accession number, gene Entrez			

Object relational structure





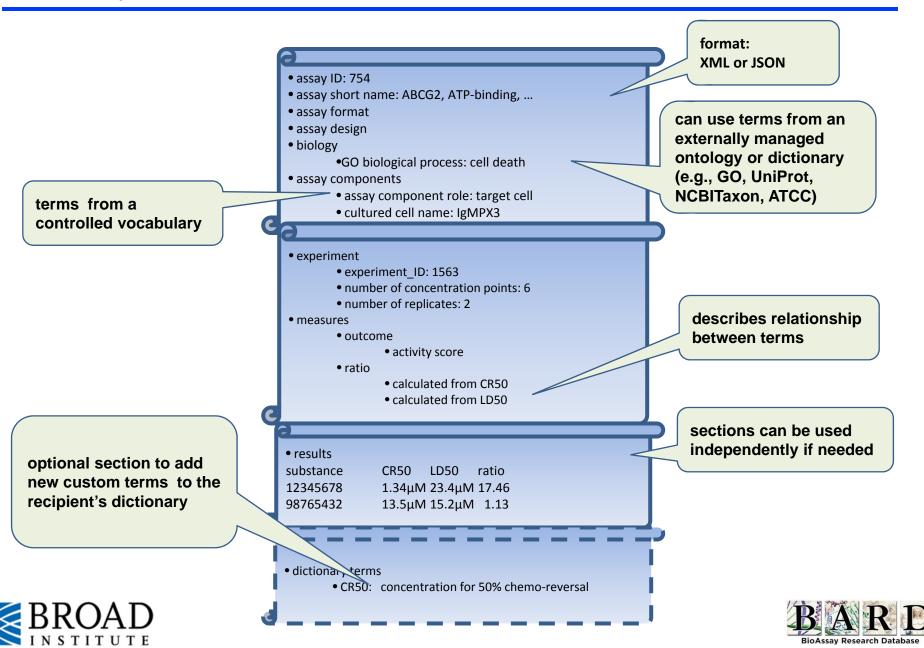
Formalizing object relationships







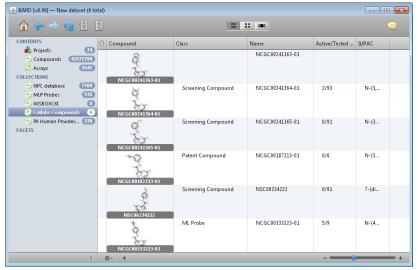
Assay Definition Format



Using with private data

- User ID: Currently Atlassian Crowd, changing to Mozilla Persona
- Objects owned by teams, editable by users on team

 Desktop client allows direct import of private structures and assays, including encrypted structure transfer for comparison to public data store



 Private deployments- open source code and documentation for creating internal build. 3rd party licenses required: Oracle, ChemAxon





Upcoming improvements

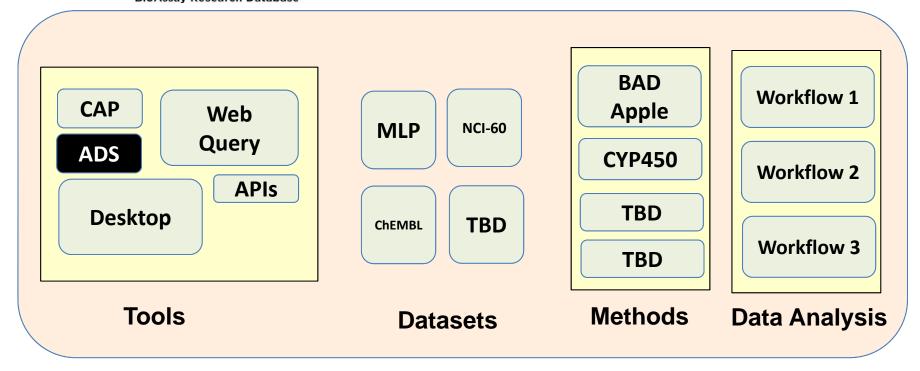
- Query tools public, demonstrations on BioAssay Research Database YouTube channel
- Annotation tool release Feb 2014
- Addition of public datasets beyond MLP including signature-based data e.g. LINCS
- Release of additional plugins
- Normalization of chemical names and structures to further standardize data





Long-Term Path Forward





Sustained Community Engagement

http://bard.nih.gov





Direct Contributors



NIH Molecular Libraries - Glenn McFadden, Mike North, Ajay Pillai

National Center for Advancing Translational Sciences – Chris Austin (PI), John Braisted, Marc Ferrer, Rajarshi Guha, Ajit Jadhav, Dac-Trung Nguyen, Tyler Peryea, Noel Southall, Cordelle Tanega, Henrike Veith



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University of Miami – Saminda Abeyruwan, Hande Küküc, Vance Lemmon, Ahsan Mir, Magdalena Przydzial, Kunie Sakurai, *Stephan Schürer (PI)*, Uma Vempati, Ubbo Visser



Vanderbilt University – *Eric Dawson (PI)*, Bill Graham, Craig Lindsley, Shaun Stauffer



Sanford-Burnham Medical Research Institute – "T.C." Chung, Jena Diwan, Michael Hedrick, Gavin Magnuson, Siobhan Malany, Ian Pass, Anthony Pinkerton, *Michael Jackson (PI)*, Sumeet Salaniwal, Derek Stonich



Scripps Research Institute - Yasel Cruz, Jill Ferguson, Mark Southern (PI)