

# Quick Introduction to the Biological Pathway Exchange (BioPAX) Format

COMBINE  
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BioPAX: [biopax.org](http://biopax.org)

BioPAX Mailing List: [biopax-discuss@googlegroups.com](mailto:biopax-discuss@googlegroups.com)

Paxtools: [biopax.github.io/Paxtools](http://biopax.github.io/Paxtools)

Pathway Commons: [pathwaycommons.org](http://pathwaycommons.org)

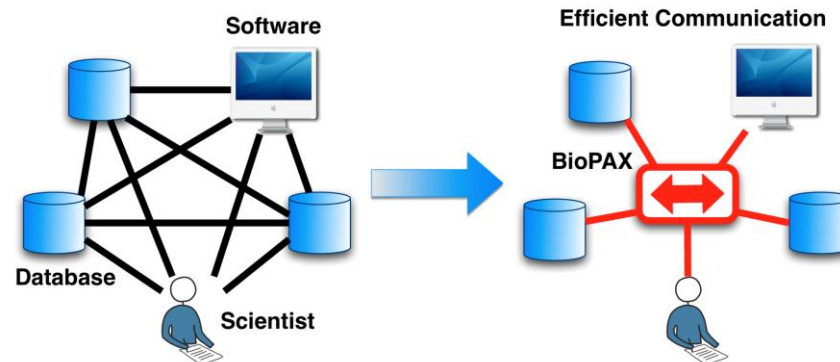
Tutorial Material: [github.com/cannin/biopaxTutorial](https://github.com/cannin/biopaxTutorial)



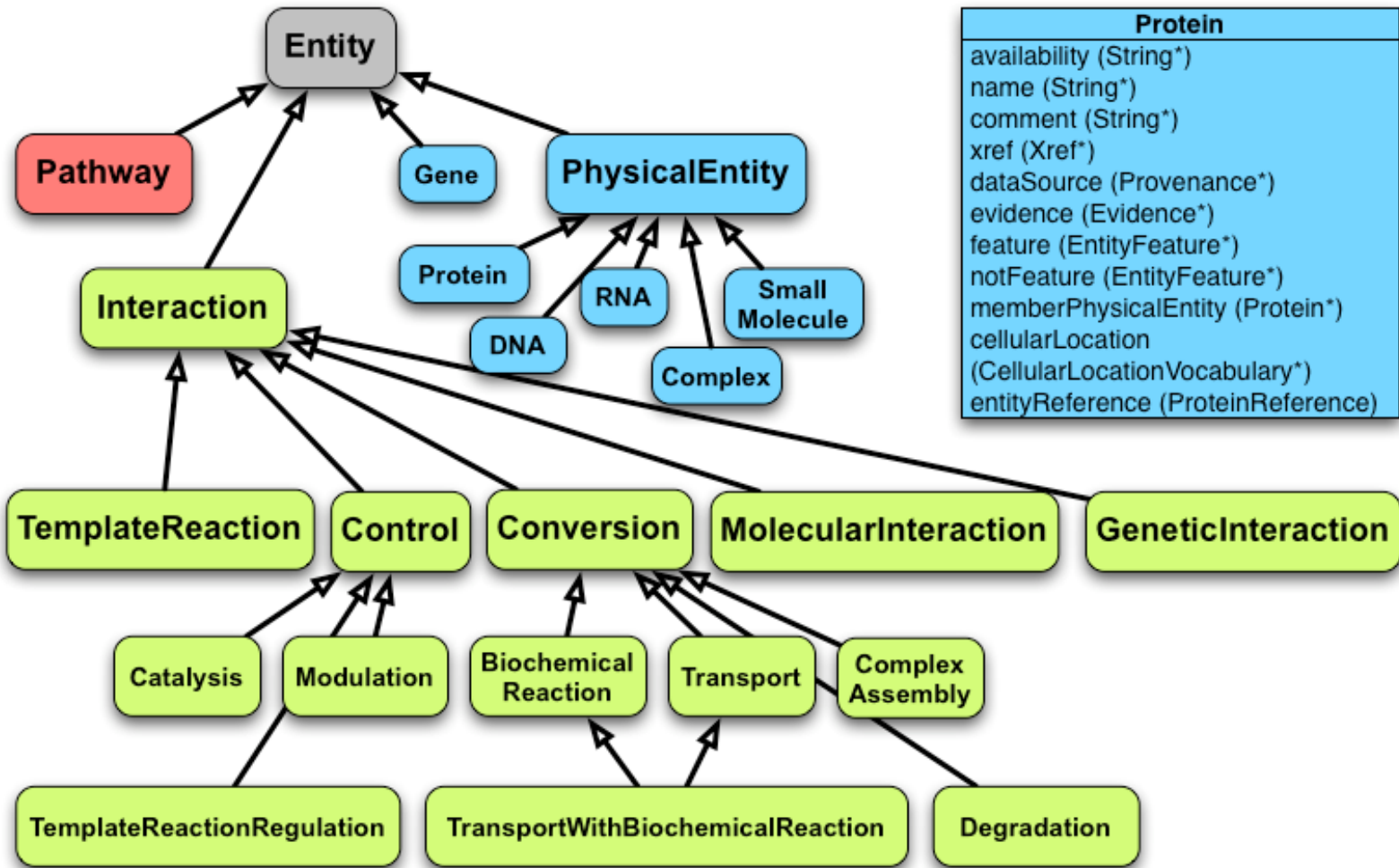
**DANA-FARBER**  
CANCER INSTITUTE

# BioPAX Scope/Goals

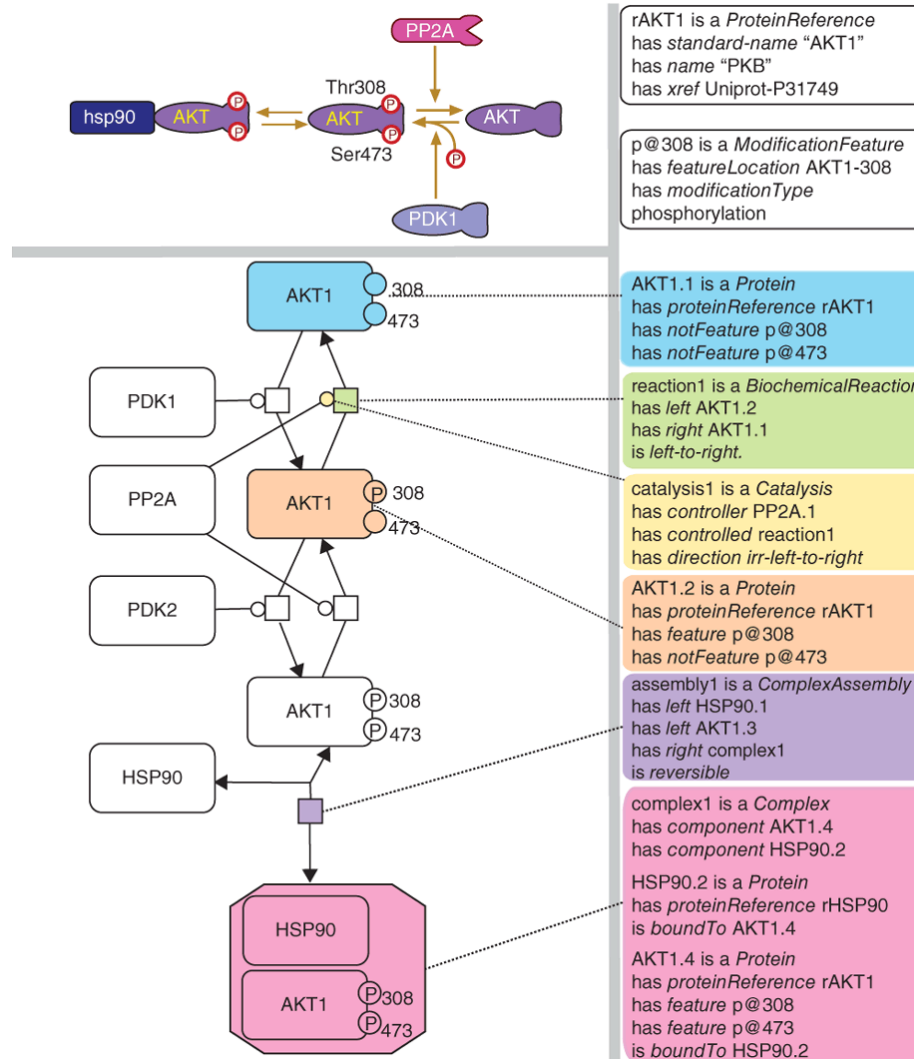
- To represent biological interactions and pathways
  - Pathways are collections of interactions that biologists have found useful to group together for organizational, historic, biophysical or other reasons
  - Types
    - Metabolic pathways
    - Signaling pathways
    - Protein-protein, molecular interactions
    - Gene regulatory pathways
- Encourage a community-wide effort to distribute pathway data in standard format; over 500 databases listed on pathguide.org



# BioPAX Ontology Classes



# From Pathway Diagrams to BioPAX



rAKT1 is a *ProteinReference*  
 has *standard-name* "AKT1"  
 has *name* "PKB"  
 has *xref* Uniprot-P31749

p@308 is a *ModificationFeature*  
 has *featureLocation* AKT1-308  
 has *modificationType*  
 phosphorylation

AKT1.1 is a *Protein*  
 has *proteinReference* rAKT1  
 has *notFeature* p@308  
 has *notFeature* p@473

reaction1 is a *BiochemicalReaction*  
 has *left* AKT1.2  
 has *right* AKT1.1  
 is *left-to-right*.

catalysis1 is a *Catalysis*  
 has *controller* PP2A.1  
 has *controlled* reaction1  
 has *direction* irr-left-to-right

AKT1.2 is a *Protein*  
 has *proteinReference* rAKT1  
 has *feature* p@308  
 has *notFeature* p@473

assembly1 is a *ComplexAssembly*  
 has *left* HSP90.1  
 has *left* AKT1.3  
 has *right* complex1  
 is *reversible*

complex1 is a *Complex*  
 has *component* AKT1.4  
 has *component* HSP90.2

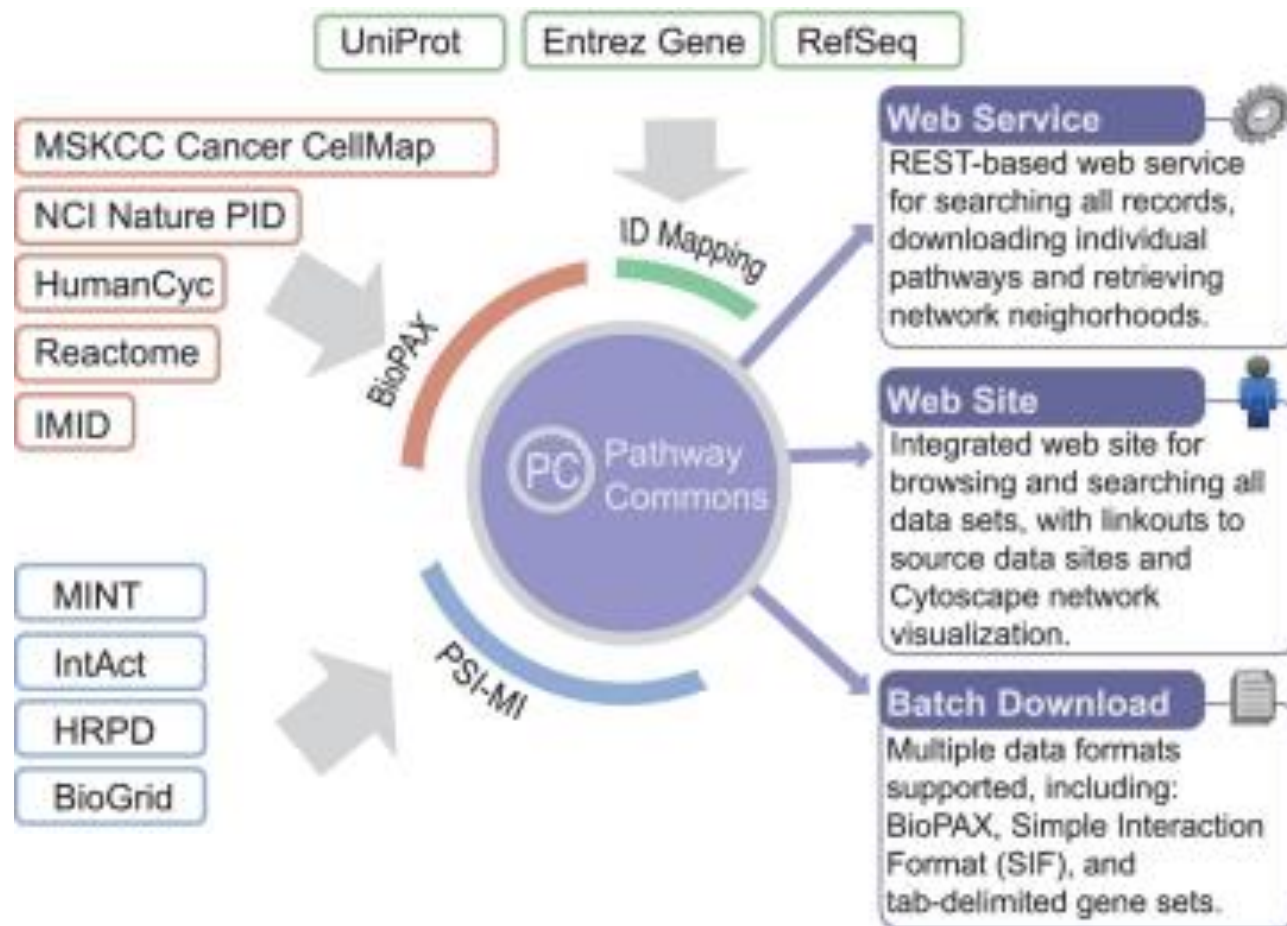
HSP90.2 is a *Protein*  
 has *proteinReference* rHSP90  
 is *boundTo* AKT1.4

AKT1.4 is a *Protein*  
 has *proteinReference* rAKT1  
 has *feature* p@308  
 has *feature* p@473  
 is *boundTo* HSP90.2

# Latest Activities

- BioPAX Java Paxtools API 5.1.0 released late Sept. 2018
  - Major changes related to sbgn-converter
- Major update for paxtoolsr R package with next Bioconductor release
- Facilitate web development using JSON-LD
- Greater support with SBGN to visualize and automatically layout BioPAX content as SBGN-PD diagrams
  - [apps.pathwaycommons.org/search](https://apps.pathwaycommons.org/search)
  - [web.newteditor.org](https://web.newteditor.org)

# Pathway Commons Database ([pathwaycommons.org](http://pathwaycommons.org))



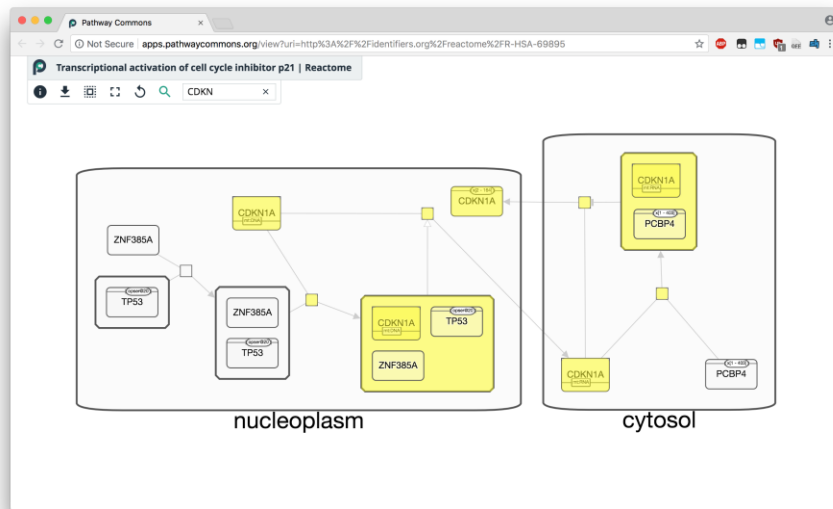
Includes signaling, drug/target, metabolic, regulatory, etc DBs

Reactome	11924
NCI PID	16017
PhosphoSitePlus	13642
HumanCyc	7024
HPRD	40618
PantherDB	5282
DIP	7102
BioGRID	244843
InAct	98347
BIND	35566
TRANSFAC	261624
mirTarBase	51214
DrugBank	19159
Recon X	10910
CTD	313174
KEGG	4472
WikiPathways	9756
Total Interactions	1150674

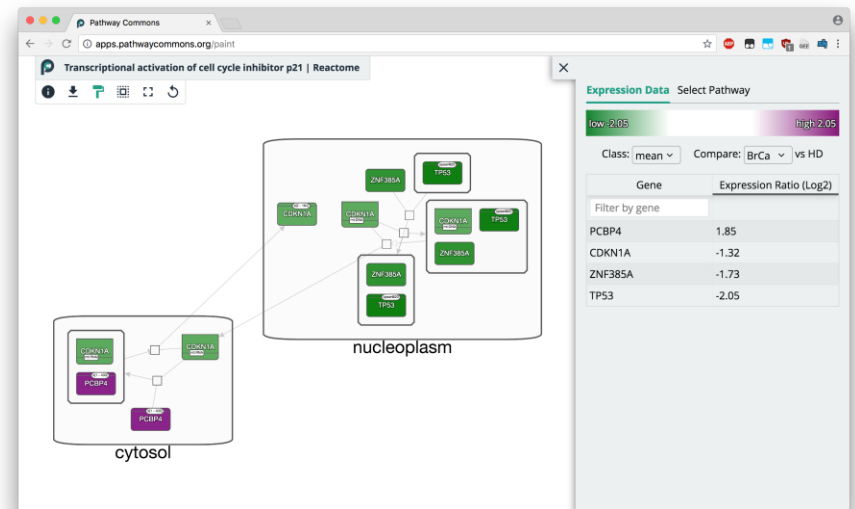
Cerami et al (2011)

# Pathway Commons Apps

- SBGN-based views of Pathway Commons queries
- Automated layout of query results



[apps.pathwaycommons.org/search](https://apps.pathwaycommons.org/search)



[apps.pathwaycommons.org/paint](https://apps.pathwaycommons.org/paint)  
(prototype)

# Acknowledgements: Main Team

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  - Augustin Luna
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- University of Toronto
  - Jeffrey Wong
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  - Emek Demir
- Previous Members
  - Arman Aksoy (Mount Sinai), Onur Sumer (MSKCC)



# Acknowledgements (2)

## Current Participants

- SRI Bioinformatics Research Group: P. Karp, S. Paley, J. Pick
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- Vassar College: K. Dahlquist
- Columbia: A. Rzhetsky

## Collaborating Organizations

- Proteomics Standards Initiative (PSI)
- Systems Biology Markup Language (SBML)
- CellML
- Chemical Markup Language (CML)

## Additional Projects

- Gene Ontology
- CHEBI
- SwissProt
- UniChem
- Protégé, U. Manchester, Stanford