NCATS BioPlanet of Pathways

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DPI/NCATS

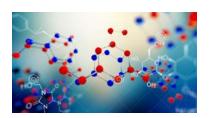
October 24, 2019



Background – Toxicity Prediction



In vitro assays



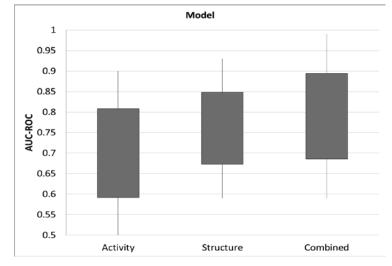
Chemical Structure







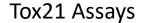
In vivo toxicity

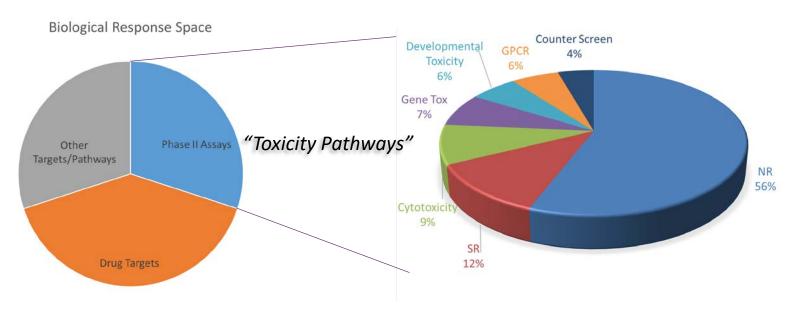


Tox21 Assays



Biological Response Space Coverage





- Problem Disruption of any pathway could potentially result in toxicity
- Question How many assays and what types of assays should be screened to cover enough toxicity mechanisms to effectively predict in vivo toxicity?
- Solution A comprehensive pathway resource that represents the entire biological response space



A Comprehensive Pathway Resource

- Issues with existing pathway databases
 - Focus on particular areas of biology, e.g., metabolism vs. signaling
 - Data are computationally generated without direct experimental evidence
 - Simple data integration of individual resources without further curation or validation
 - Different types of data mixed together with no distinctions made between, e.g., pathways and protein—protein interactions
 - No additional annotations provided beyond gene-pathway memberships
 - Restricted access commercial databases with high cost
- Need a complete, non-redundant, open-source solution for integrated data analysis

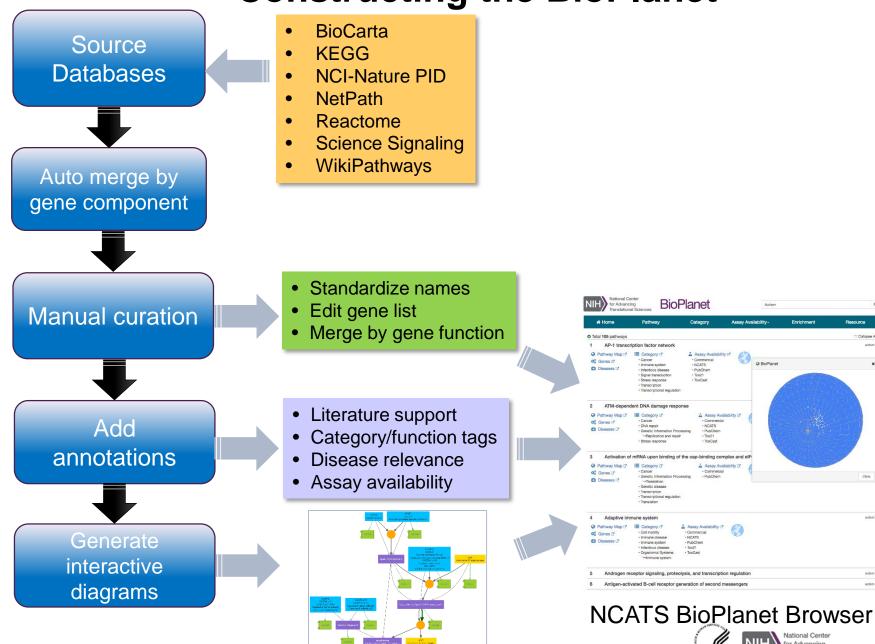


NCATS BioPlanet of Pathways

- A comprehensive resource for
 - Assay selection/prioritization for toxicity prediction
 - Gene expression data analysis
 - Integrated data analysis
- Data from all public sources
- Manual curation to ensure data quality
- Detailed annotations on source, species, biological function/process, disease/toxicity relevance, assay availability
- Currently:1658 curated human pathways (~10,000 genes)
- Public web browser for easy data visualization and analysis
 - http://tripod.nih.gov/bioplanet/



Constructing the BioPlanet



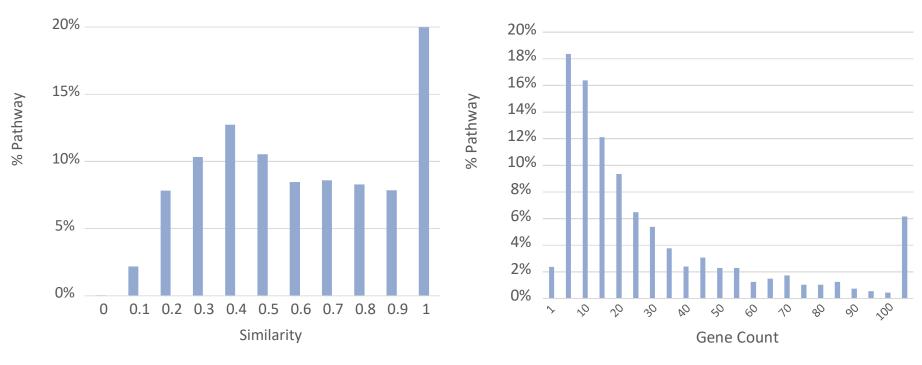
Pathway data sources

| | Number of | Number | |
|-----------------------|----------------|----------|---|
| Database | human pathways | of genes | URL |
| | 214 | 5520 | http://www.genome.jp/kegg/pathway.html |
| KEGG | | | |
| BioCarta* | 314 | 1494 | https://cgap.nci.nih.gov/Pathways/BioCarta_Pathways |
| | 1283 | 6125 | http://www.reactome.org/ |
| Reactome | | | |
| WikiPathways | 204 | 4064 | http://www.wikipathways.org/ |
| NCI-Nature - Pathway | 722 | 3725 | http://pid.nci.nih.gov/ |
| Interaction Database* | | | |
| Science Signaling* | 58 | 1234 | http://stke.sciencemag.org/about/help/cm |
| NetPath | 35 | 2877 | http://www.netpath.org/ |

^{*}Original database site is no longer supported.



Overview of source pathways – Data redundancy



Manual curation

- Remove redundancy merge pathways by gene function
- Pathways with too few genes remove or merge into larger pathways

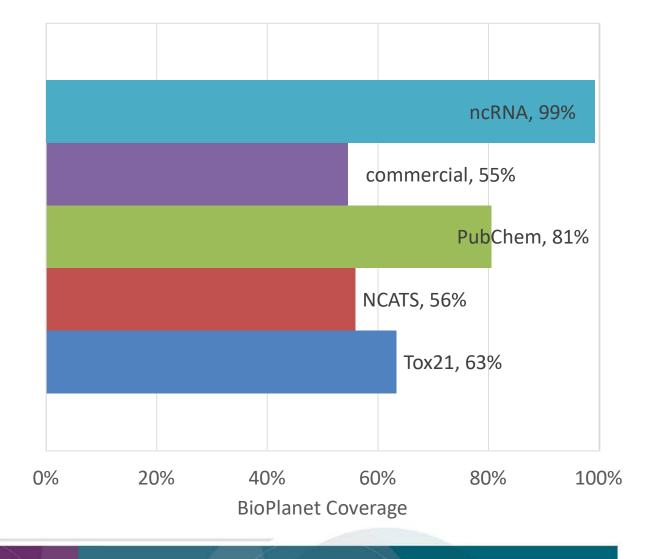


Pathway tags

| Major Systems | Metabolism | Signalling |
|------------------------|------------------------------|----------------------------|
| Circulatory system | Nucleic acid metabolism | Cell signalling |
| • • | | G-protein coupled |
| Digestive system | Carbohydrate metabolism | receptor |
| Endocrine system | Protein metabolism | Nuclear receptor |
| Excretory system | Lipid metabolism | Transcriptional regulation |
| | Vitamin and cofactor | |
| Immune system | metabolism | Stress response |
| Musculoskeletal system | Small molecule metabolism | Environmental adaptation |
| Nervous system | Xenobiotic metabolism | Chronology |
| Sensory system | Energy metabolism | Transport |
| | _ | |
| Genetic Information | Protein folding, sorting and | |
| Processing | degradation | |
| DNA replication | Protein modification | Disease |
| DNA repair | | Cancer |
| Transcription | | Cardiovascular disease |
| RNA processing | Cell Cycle | Genetic disease |
| Translation | Cell cycle | Immune disease |
| | Cell growth | Infectious disease |
| Development | Cell death | Neurological disease |
| Development | Cell division | Physical disorder |
| - | | Endocrine and metabolic |
| Adhesion | Cell proliferation | disease |
| Cell differentiation | Reproduction | Sepsis |
| Cell motility | | Substance dependence |



Assay Coverage of BioPlanet

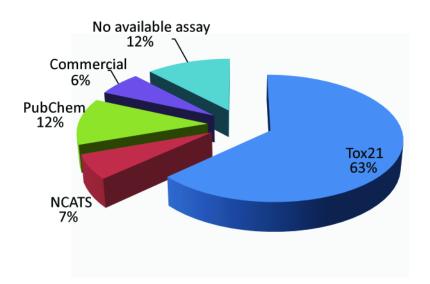


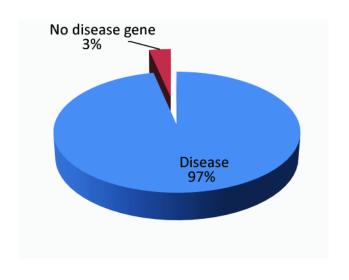


Assay Coverage of BioPlanet: Disease

D

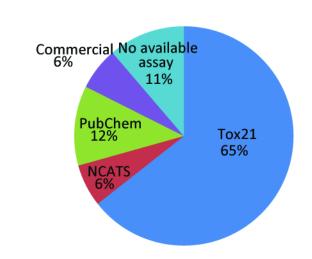
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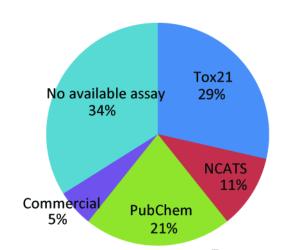


Disease Pathways

Other Pathways

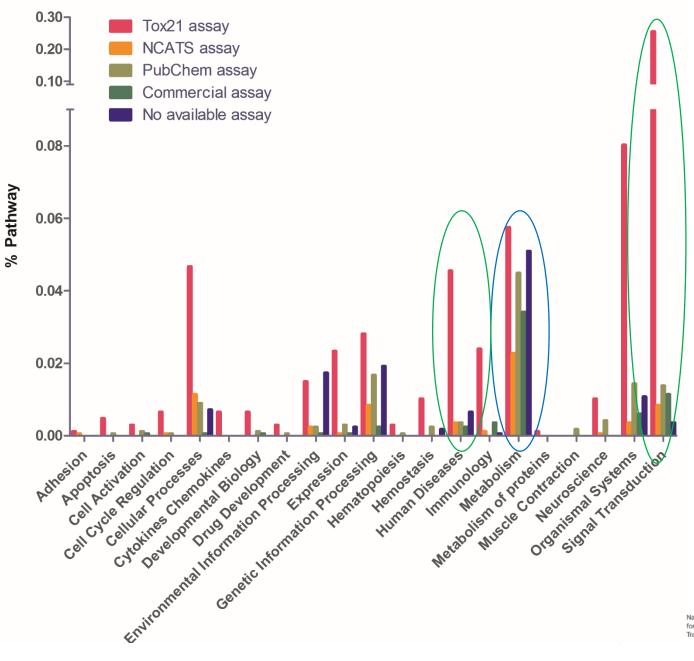


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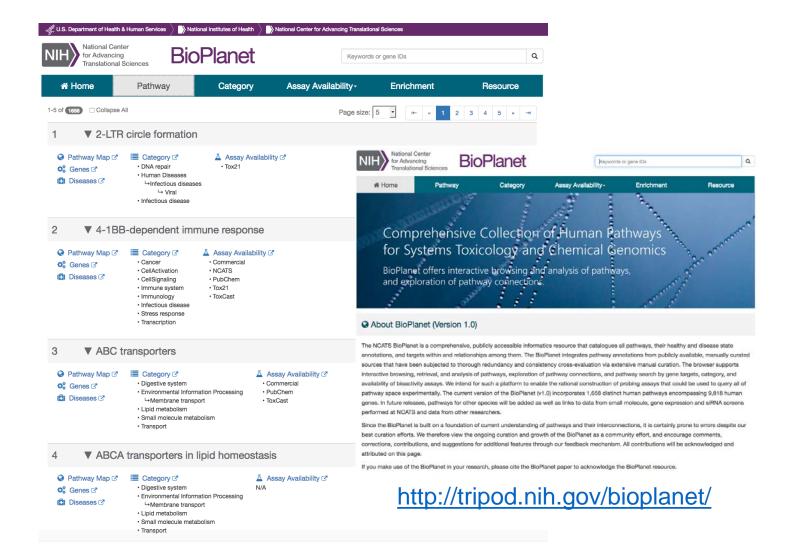




Assay Coverage of BioPlanet: Pathway Category

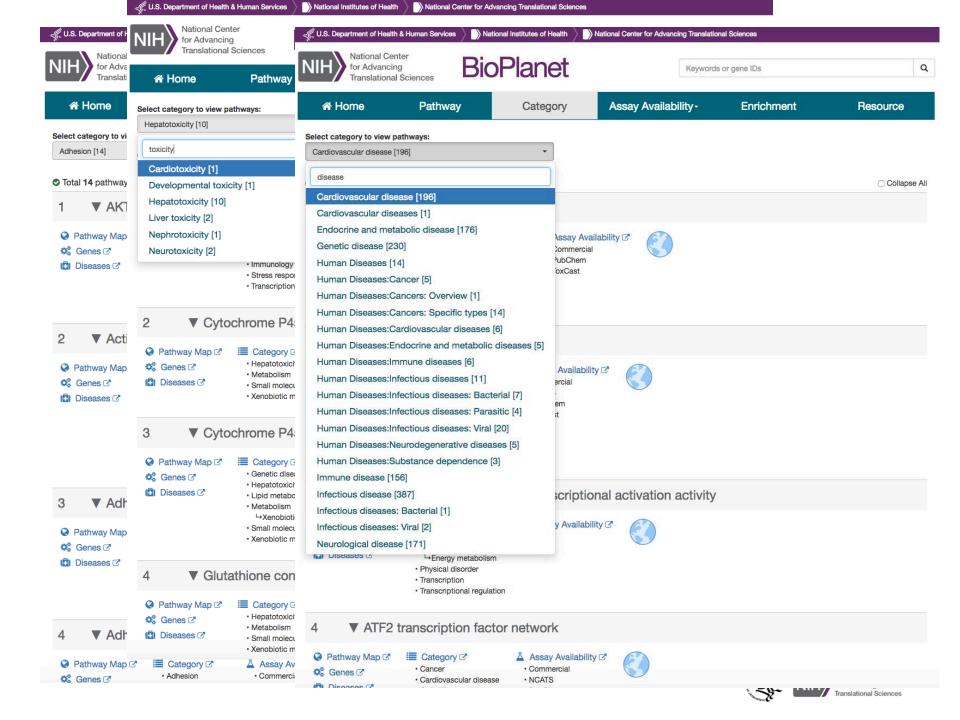


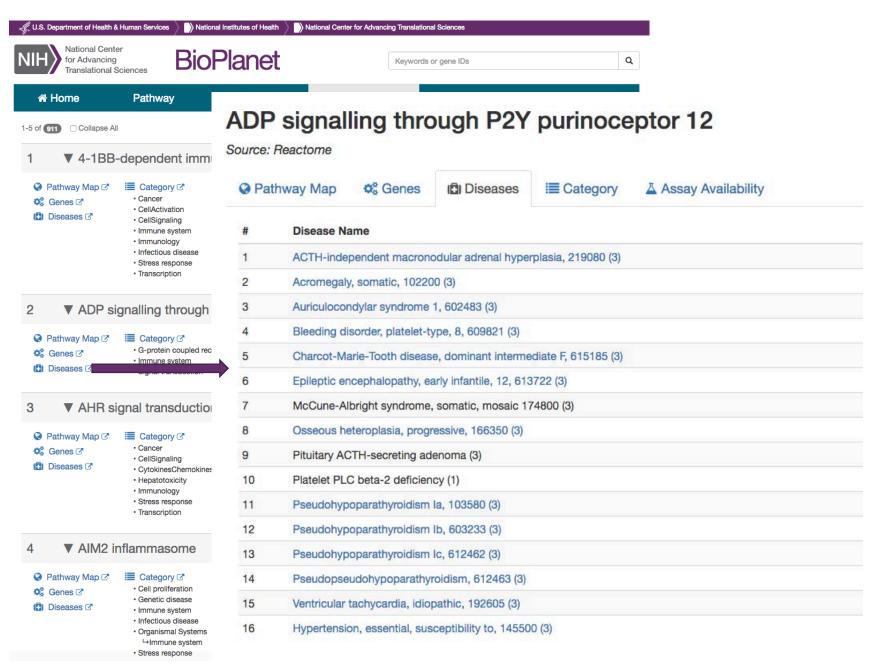
The BioPlanet Browser















Pathway





1-5 of 527 Collapse All

Pathway Map

😋 Genes 🗷

Diseases ☑

LncRNA ☑

☆ Home



Category

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TOX21 PUBLIC DATA

REPLICATE AGGREGATED

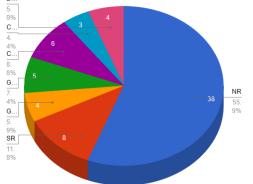
UPDATE

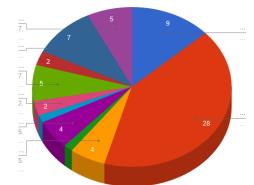
DOWNLOAD SUBSCRIBE HELP

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■ Category <</p>

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☆ Used in Tox21 Challenge

| Protocol Name | Assay Target | Target Category | Cell Line | Cell Type | | |
|-----------------------------------|----------------------------------|-----------------|------------|-----------------|--|--|
| tox21-ahr-p1 ☆ | AhR | NR | HepG2 | Liver | | |
| tox21-ap1-agonist-p1 | AP-1 agonist | SR | ME-180 | Cervical Cancer | | |
| tox21-ar-bla-agonist-p1 ☆ | AR-BLA agonist | NR | HEK293 | Kidney | | |
| tox21-ar-bla-antagonist-p1 | AR-BLA antagonist | NR | HEK293 | Kidney | | |
| tox21-are-bla-p1 ☆ | ARE | SR | HepG2 | Liver | | |
| tox21-ar-mda-kb2-luc-agonist-p1 ☆ | AR-MDA agonist | NR | MDA-MB-453 | Breast Cancer | | |
| tox21-ar-mda-kb2-luc-agonist-p3 | AR-MDA agonist (with antagonist) | NR | MDA-MB-453 | Breast Cancer | | |
| | | | | | | |

▼ AHR signal tra

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Genes 🗷 CellSi Diseases ☑ Cytok

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Source Name **Assay Name**

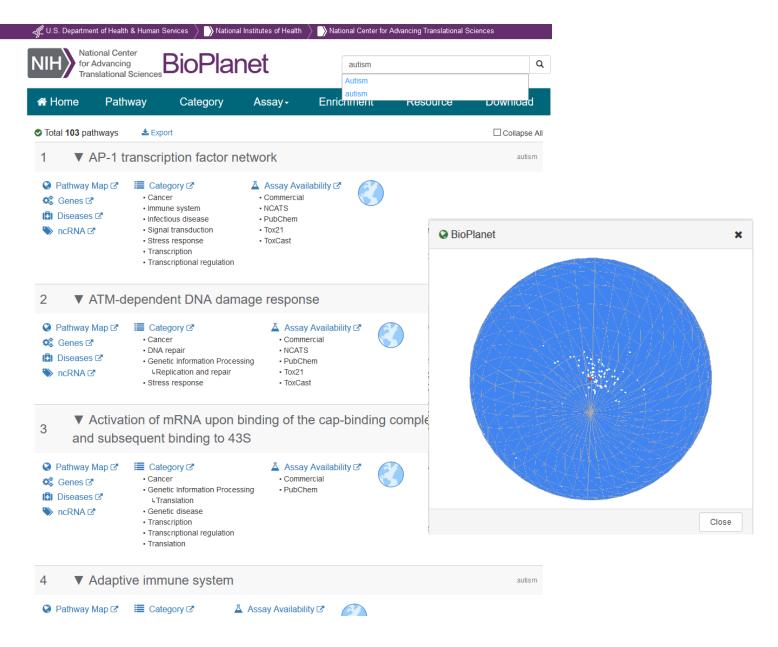
Tox21 tox21-ahr-p1

qHTS assay to identify small molecule that activate the aryl hydrocarbon receptor (AhR) signaling pathway

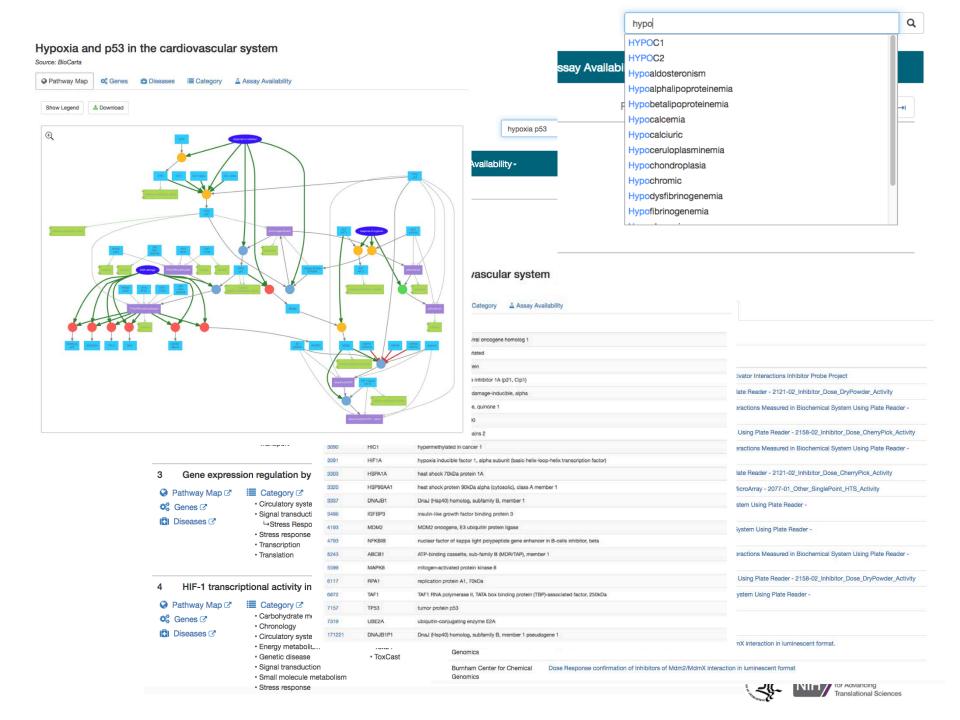
tox21-ahr-p1 Tox21

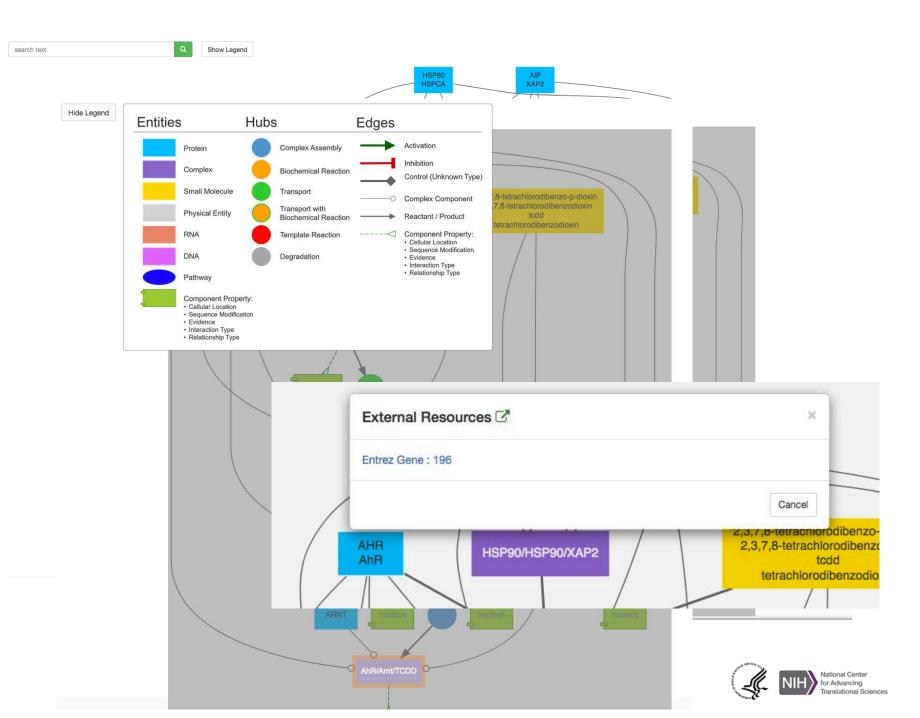
qHTS assay to identify small molecule that activate the aryl hydrocarbon receptor (AhR) signaling pathway: Summary



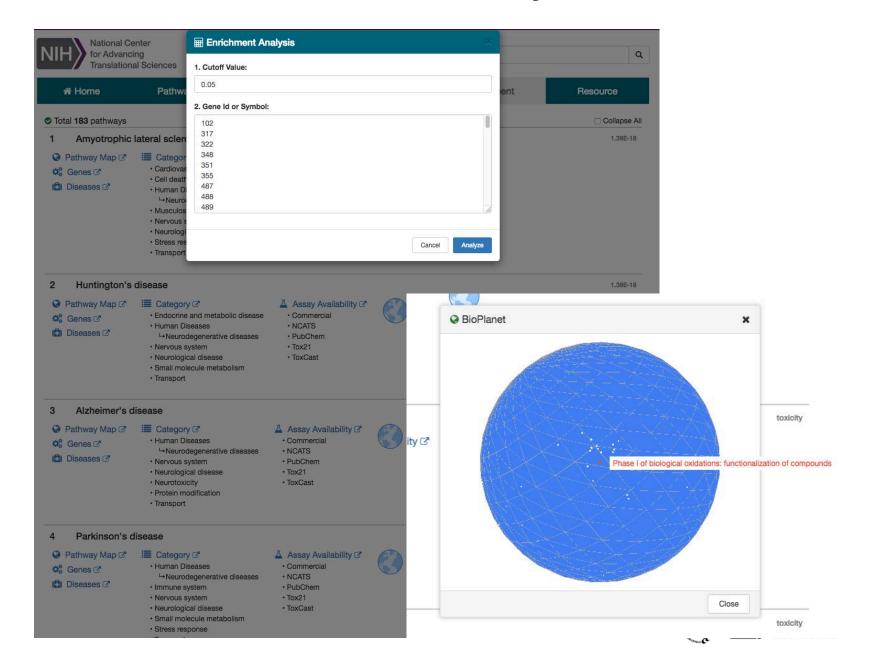




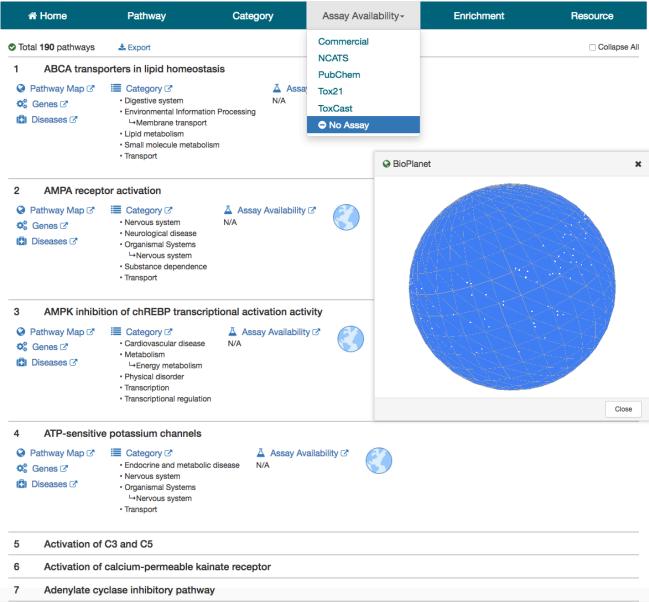




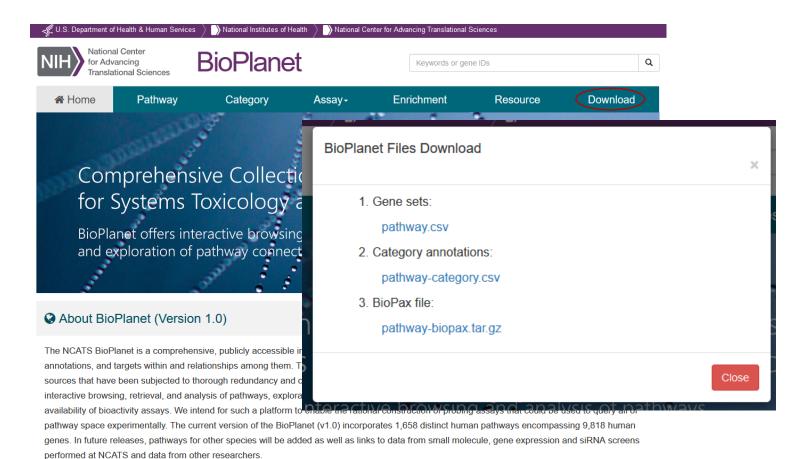
Gene Enrichment Analysis



A Tool to Guide Assay Development







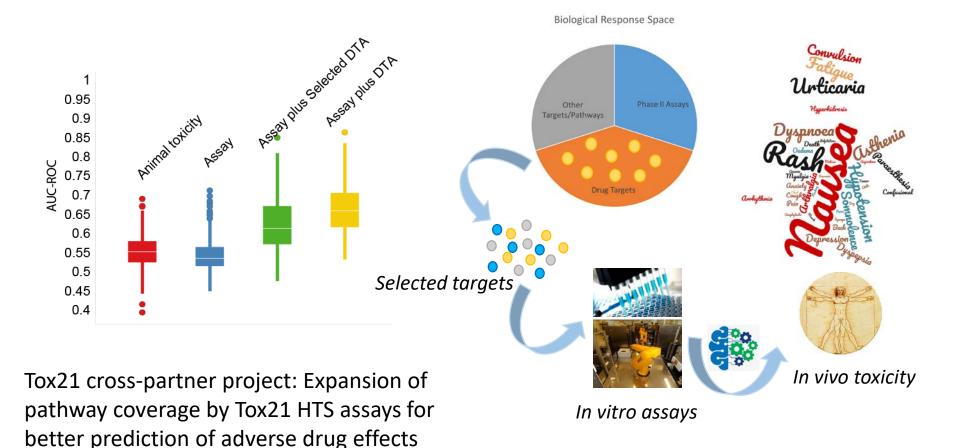
BioPlanet Tutorial provides a thorough, yet succinct description of all aspects of the BioPlanet resource, including navigation, key controls, and data structure.

Since the BioPlanet is built on a foundation of current understanding of pathways and their interconnections, it is certainly prone to errors despite our best curation efforts. We therefore view the ongoing curation and growth of the BioPlanet as a community effort, and encourage comments, corrections, contributions, and suggestions for additional features through our feedback mechanism. All contributions will be acknowledged and attributed on this page.

If you make use of the BioPlanet in your research, please cite the BioPlanet paper to acknowledge the BioPlanet resource.



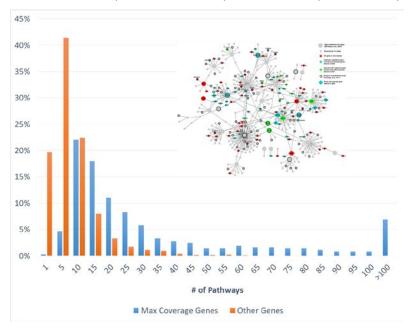
Application – Design an optimal set of assays for human in vivo toxicity prediction

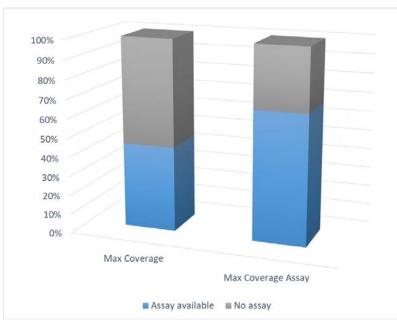




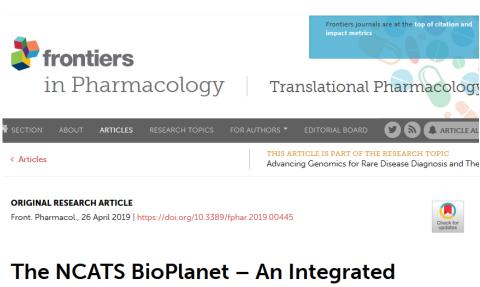
Max Coverage Genes (Hub Genes)

- Minimum set of genes (362) that covers all pathways
 - 411 with preference given to targets with existing assays
- The figure shows that genes in this set each on average covers more pathways than other genes – right shift of "blue" distribution compared to "yellow" distribution
- Genes that each covers >100 pathways: AKT1, MAPK3, MAPK1, HRAS, MAP2K1, MAPK8, GRB2, MAPK14, JUN









The NCATS BioPlanet – An Integrated Platform for Exploring the Universe of Cellular Signaling Pathways for Toxicology, Systems Biology, and Chemical Genomics

| E Ruili Huang¹*, E Ivan Grishagin², E Yuhong Wang¹, E Tongan Zhao¹, E Jon Greene², E John C. Obenauer², E Deborah Ngan¹, E Dac-Trung Nguyen¹, E Rajarshi Guha¹, E Ajit Jadhav¹, E Noel Southall¹, E Anton Simeonov⁴ and E Christopher P. Austin¹ | |
|--|--|
| ¹ Division of Pre-Clinical Innovation, National Center for Advancing Translational Sciences, National Institutes of Health, Rockville, MD, United States ² Rancho BioSciences, San Diego, CA, United States | |
| Chemical genomics aims to comprehensively define, and ultimately predict, the effects of small molecule compounds on biological systems. Chemical activity profiling approaches must consider chemical effects on all pathways operative in mammalian cells. To enable a strategic | |

Huang R, et al. (2019) The NCATS BioPlanet – An Integrated Platform for Exploring the Universe of Cellular Signaling Pathways for Toxicology, Systems Biology, and Chemical Genomics. *Front. Pharmacol.* 10:445. doi: 10.3389/fphar.2019.00445



Moving Forward – A tool for chemical genomics

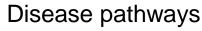
Normal Disease/Toxicity





Gene/protein expression, RaslSeq, RNAi, SNP, etc.

Disease mechanism









In vitro assays Small molecule probes



Potency, efficacy, selectivity, toxicity...





An Ongoing Project

- Periodical update of pathway content
- Additional annotations
 - Toxicity: liver, kidney, heart, skin, etc.
 - Drug-target
- Linking small molecule and gene/protein expression data
 - qHTS, raslSeq, RNAi, SNP, proteomics, etc.
- Adding pathways for other species
 - Rat, mouse, zebra fish, drosophila, c. elegans, etc.



BioPlanet Team

- NCATS
 - Tongan Zhao
 - Yuhong Wang
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 - Noel Southall
 - Anton Simeonov
 - Christopher P. Austin

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 - Ivan Grishagin
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