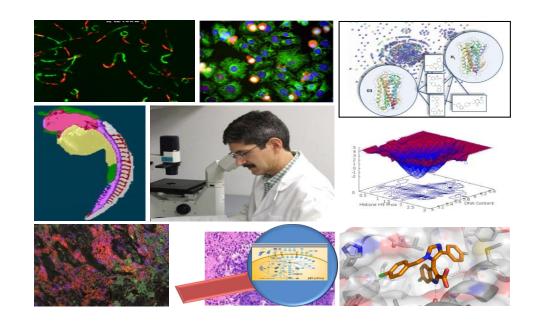
# **University of Pittsburgh Drug Discovery Institute**

The Microphysiology Systems Database (MPS-Db): A platform for aggregating, analyzing, sharing and modeling of in vitro and in vivo safety and efficacy data

https://mps.csb.pitt.edu/

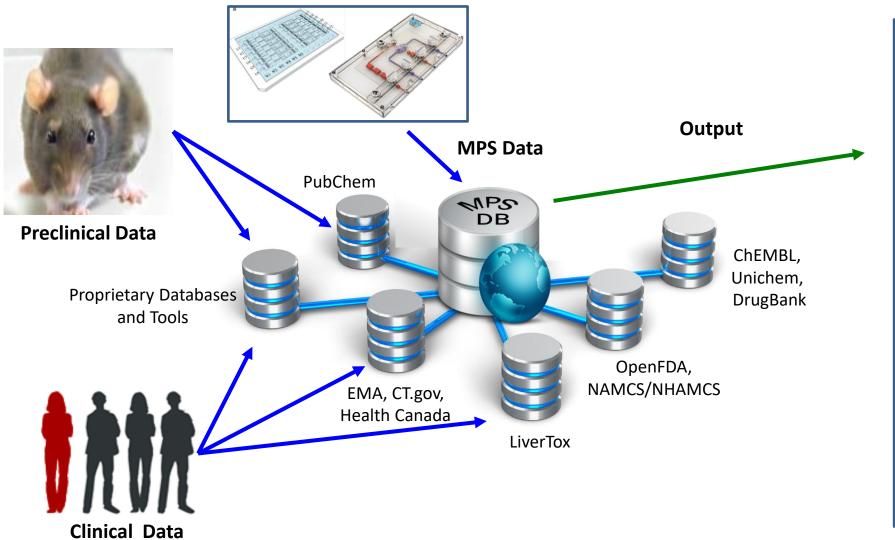


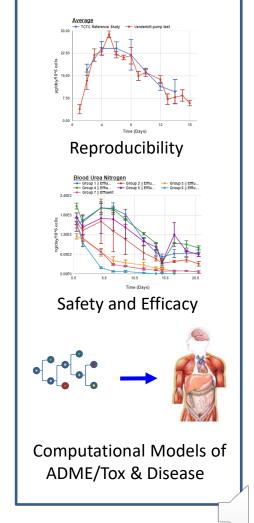


Mark Schurdak, PhD
Director of Operations, University of Pittsburgh Drug Discovery Institute,
Associate Professor, Computational and Systems Biology



# The MPS-Db Is an Internet-Based Platform That Integrates External Databases, to Provide Tools for Data Management, Analysis, and Computational Modeling





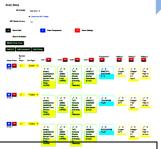
## The MPS-Db Is a Single Entry System Guiding Users Along a Simple, Streamlined Workflow to Design, Create, Implement, Analyze, and Document MPS Studies

**Drug Trials** Adverse Events, ...





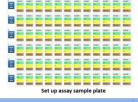
**Study Design** and Creation



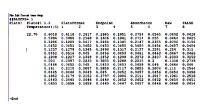
Simple menus facilitate metadata entry for study details

Setting up chips or plates





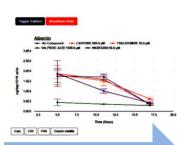
Study Implementation and Data Import



Acquire data and load into MPS-Db

Data import, calibration and review tools

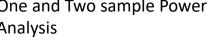
**Graphing and Analysis** 

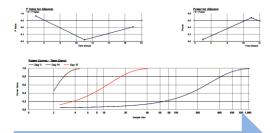


Data Normalization **And Analysis** 

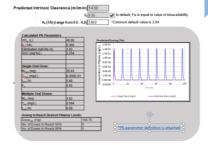


Intra- & Inter-Reproducibility Analysis One and Two sample Power **Analysis** 





#### **Statistics and Data Modeling**



**PBPK Computational** Modeling

Non-Profit sharing options.



#### **Sharing Data**



For-profit sharing options.





# The MPS-Db Development Has Evolved to Serve **Two Types of Data Sharing Applications**

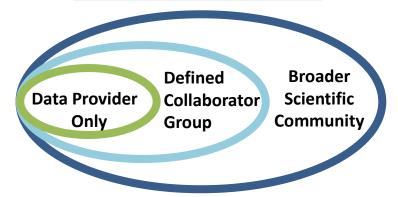
### **Non-Profit: Academic version**

Tissue Chip Consortium, academic institutions, etc.

Provider controls sharing of data & data analyses with:

- Data Provider personnel only
- Defined group(s) of collaborators
- And optionally with the public

### Who can see my data?



### **For-Profit: Commercial version**

Companies using MPS experimental models

For proprietary company projects:

- Installation behind the company firewall
- Integration with **company databases**
- Development of custom features

The company can easily copy selected data to the public MPS-Db for sharing with collaborators or the general public.







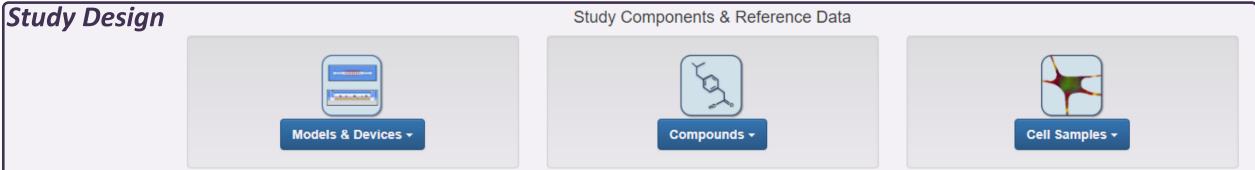
### The MPS-Db Is Organized Based on Workflow

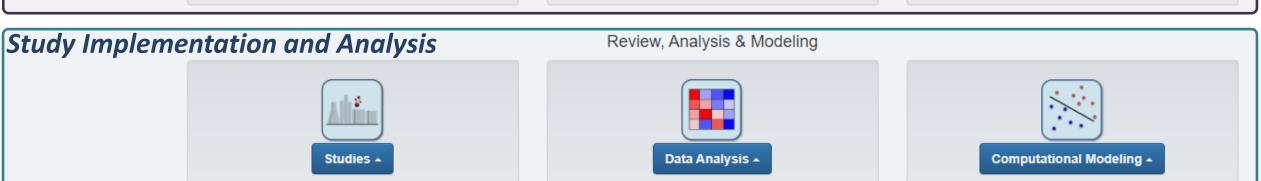


### Microphysiology Systems Database



University of Pittsburgh Drug Discovery Institute

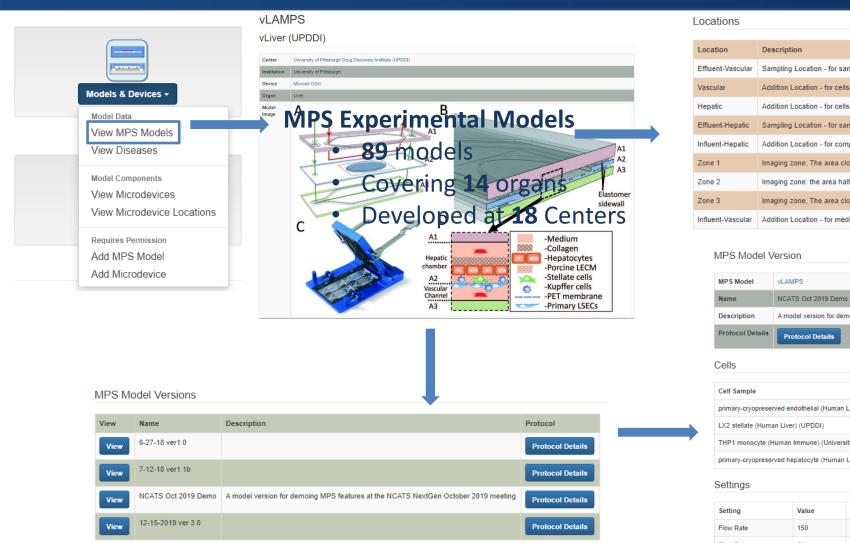








# The MPS-Db Provides Convenient Access to Information on a Variety of MPS Models



Location	Description				
Effluent-Vascular	Sampling Location - for samples from the media flowing out of the vascular chamber.				
Vascular	Addition Location - for cells. Sampling Location - for images.				
Hepatic	Addition Location - for cells. Sampling Location - for images.				
Effluent-Hepatic	Sampling Location - for samples from the media flowing out of the hepatic chamber.				
Influent-Hepatic	Addition Location - for compounds and some settings.				
Zone 1	Imaging zone; The area closest to the influent port with the highest oxygen tension, analogous to Zone 1 in the liver acinus				
Zone 2	Imaging zone: the area halfway between the influent port and effluent port, with reduced oxygen tension analogous to Zone 2 in the liver acinus				
Zone 3	Imaging zone; The area closest to the effluent port with the lowest oxygen tension, analogous to Zone 3 in the liver acinus				
Influent-Vascular	Addition Location - for media, compounds, circulating immune cells, and some settings.				

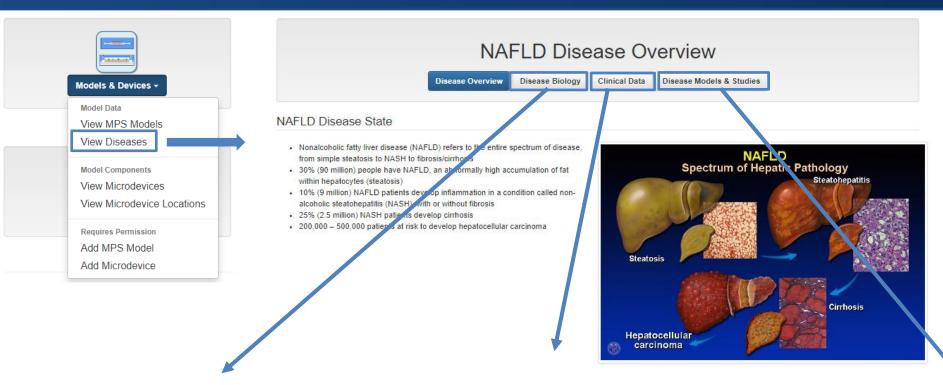
MPS Model	VLAMPS
Name	NCATS Oct 2019 Demo
Description	A model version for demoing MPS features at the NCATS NextGen October 2019 meeting
Protocol Details	Protocol Details

Cell Sample	Cell Biosensor	Density	Unit	Passage#	Addition Time	Addition Location
primary-cryopreserved endothelial (Human Liver) (Samsara-HL160019)	naive (none)	100,000.0	cells / chip		D-3 H00 M00	Vascular
LX2 stellate (Human Liver) (UPDDI)	naive (none)	36,000.0	cells / chip		D-2 H00 M00	Hepatic
THP1 monocyte (Human Immune) (University of Pittsburgh)	naive (none)	15,000.0	cells / chip		D-2 H00 M00	Hepatic
primary-cryopreserved hepatocyte (Human Liver) (Thermo Fisher-Hu1838)	naive (none)	100,000.0	cells / chip		D00 H-22 M00	Hepatic

Setting	Value	Unit	Addition Time	Duration	Addition Location	
Flow Rate	150	μL/hour	D00 H00 M00	D21 H00 M00	Influent-Vascular	1
Flow Rate	50	μL/hour	D00 H00 M00	D21 H00 M00	Influent-Hepatic	)



# MPS Disease Model Development Is Assisted With Information Obtained Through the Disease Portal



#### **Pre-Queried links to databases:**

- Genomic data
- KEGG
- Proteomic data
- Metabolomic data
- DrugBank

#### Clinical data:

- Manually curated clinical data
- Pre-Queried links to Clinical Trials.gov
  - Completed studies with results

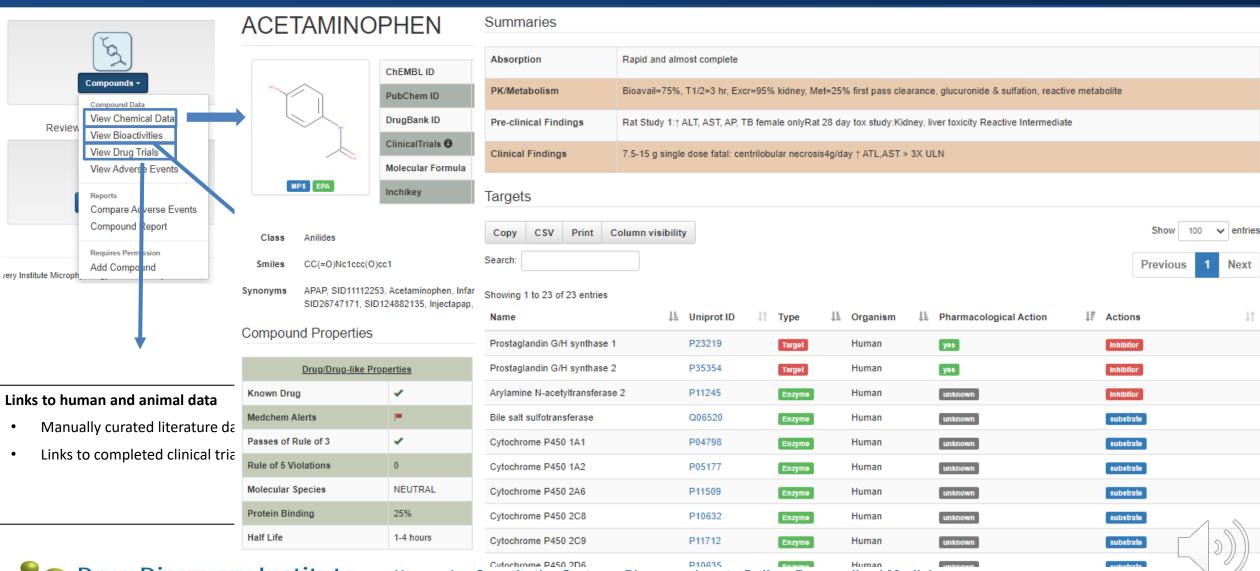
#### **Direct links to**

- Other models of the disease
- Studies using these models

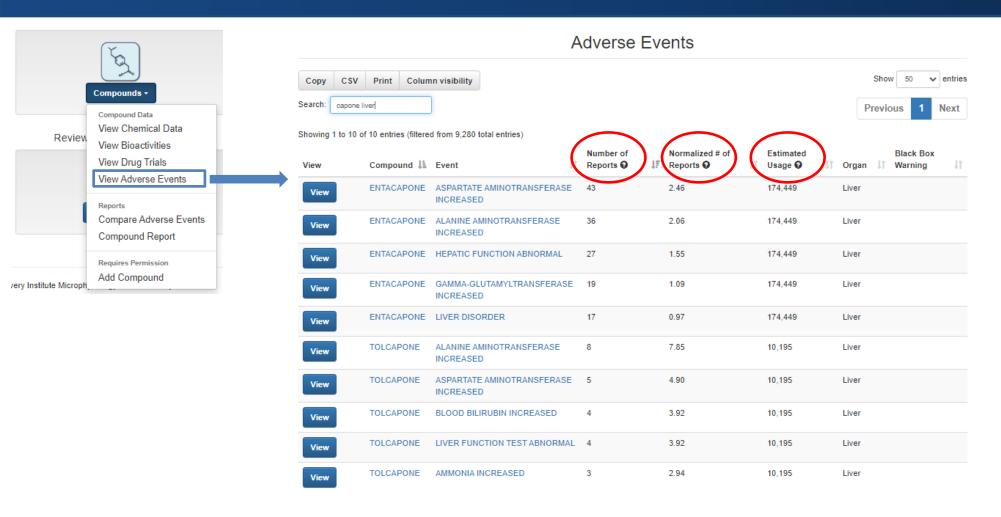




# The MPS-Db Links to Information to Aid in the Identification of Compounds for Model Validation

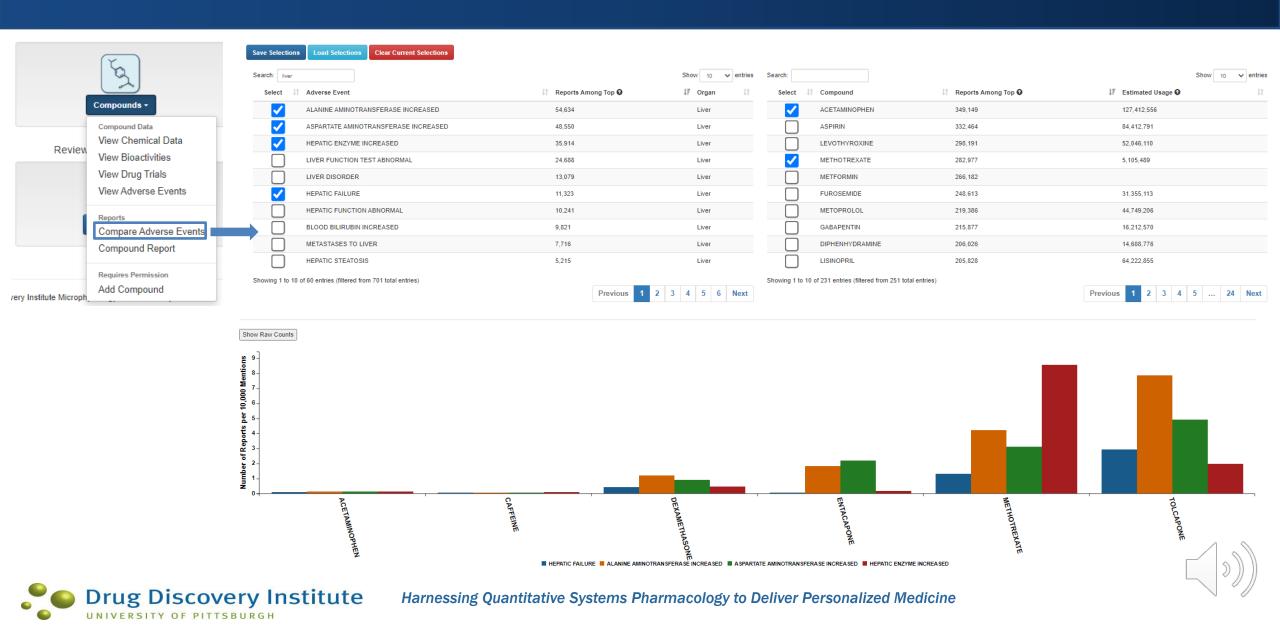


# Linking to FAERS and CDC Databases Enables Identification of Test Compounds Based on Normalized Reported Adverse Events





### **Compare Adverse Event Tool Shows Relative Clinical Activity of Compounds**



### The MPS-Db Is Organized Based on Workflow

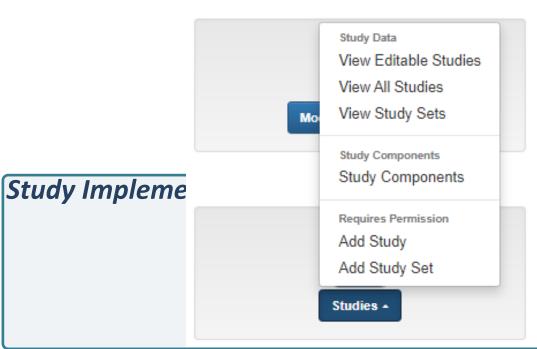


### Microphysiology Systems Database



University of Pittsburgh Drug Discovery Institute

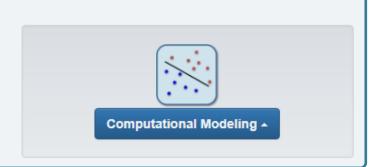
#### Study Components & Reference Data





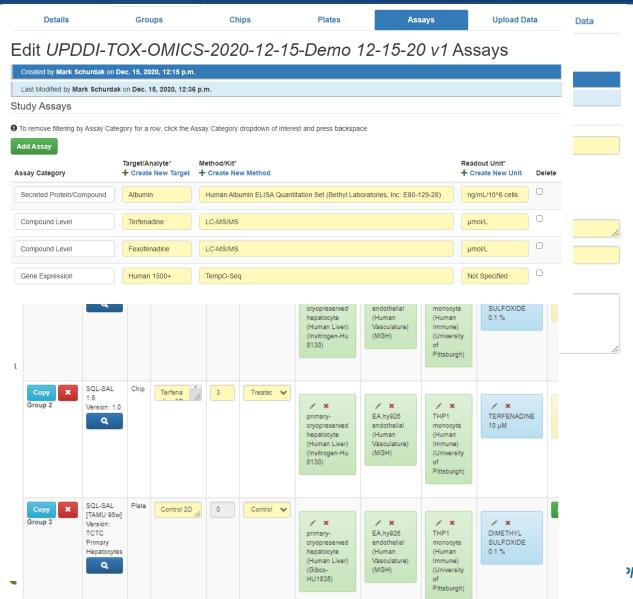








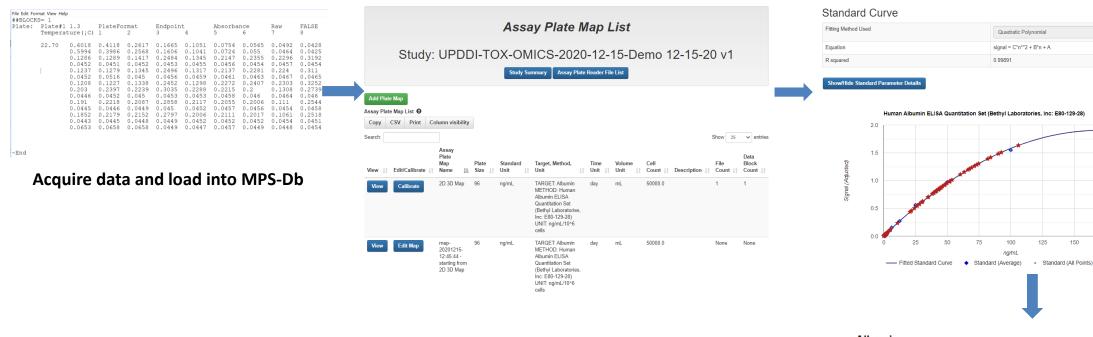
# A Streamlined Workflow Facilitates Study Creation Directly in the MPS-Db



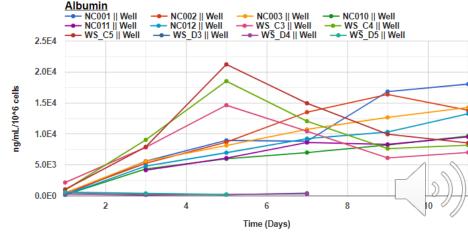
- Simple menus facilitate metadata entry for study details
- MPS model component information is automatically entered when setting up a study
- Entering in information as groups facilitates Study Setup
- Assay category dropdowns expedite selection of Target/Analyte and Method Kits used in the study



# Study Data Are Easily Imported Into the MPS-Db



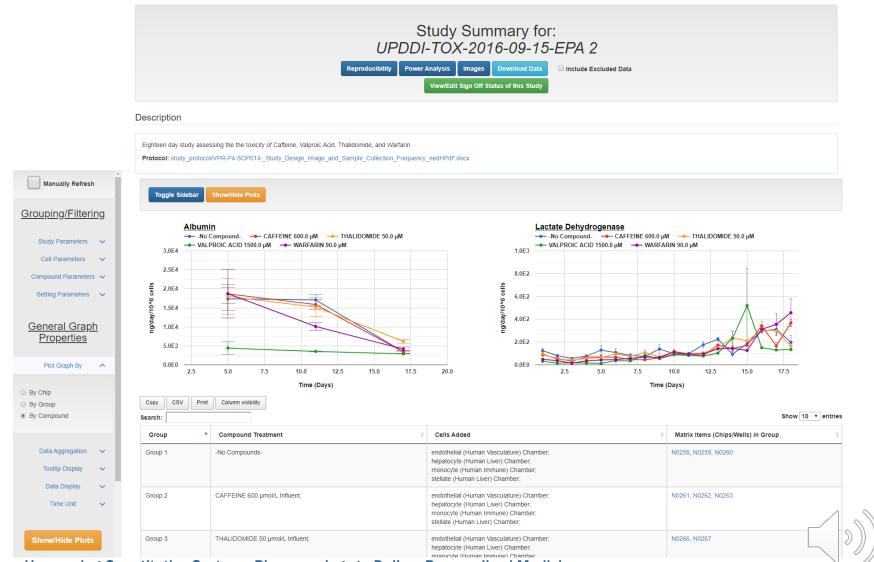
- Integrated tools allow for importing raw data directly from a variety of plate readers.
- Sample data are calibrated and normalized against standards in the MSP-Db
- Results are reviewed prior to submitting to the Db





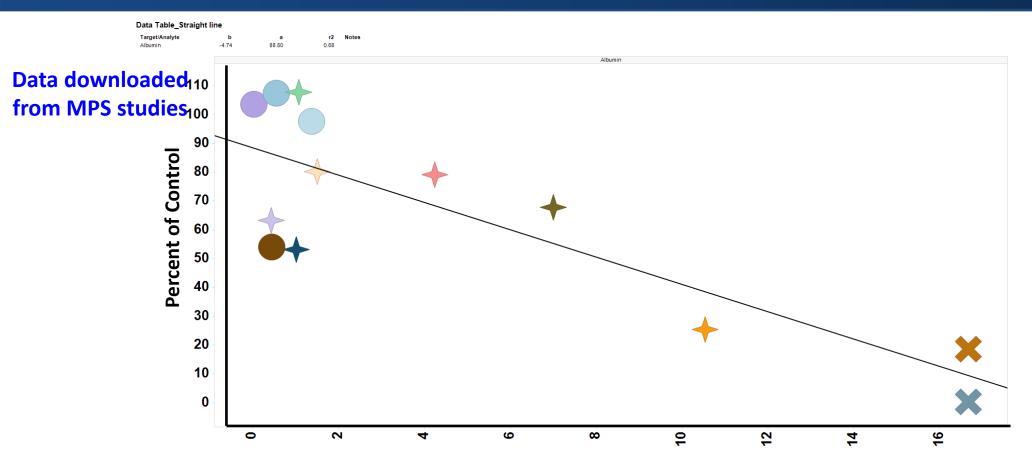
# Visualization Tools Enable Flexible Analysis of Study Data

- A Grouping/Filtering sidebar menu provides filters to select and group samples by specific study parameters to narrow down or expand the results set for analysis.
- A General Graph Properties
  menu provides options for
  customization of plots and selection
  of plots to display.
- Functionality is enabled to convert individual plots to show percent control, and convert from time series to dose response





# Data Can Be Easily Exported From the MPS-Db for Analysis in Other Software



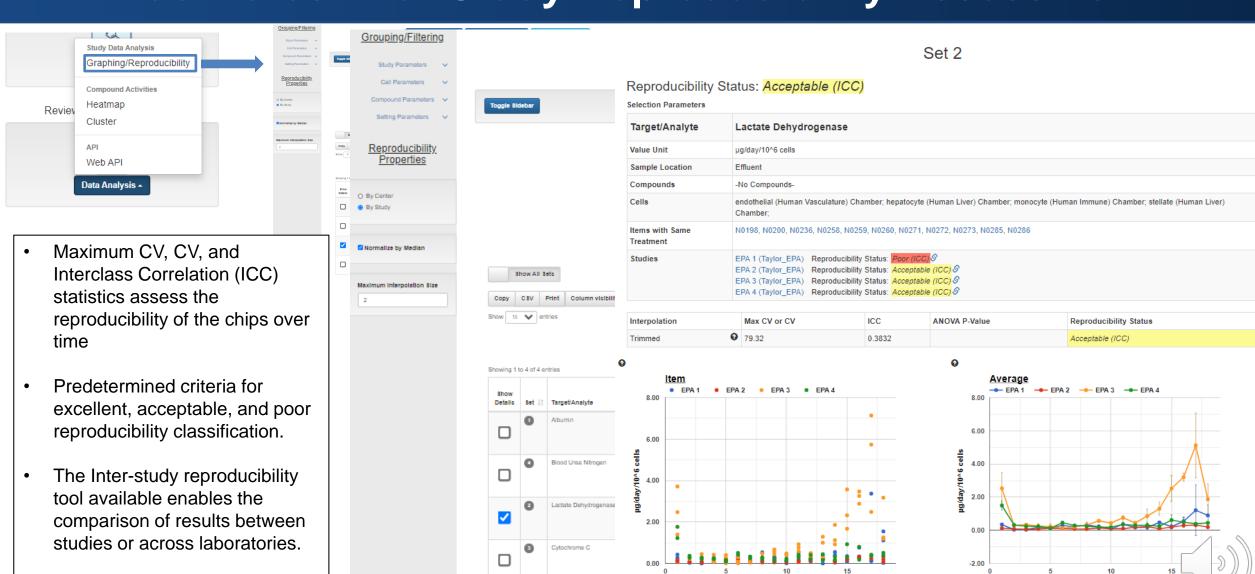
No. of Normalized Reports of Major Liver Adverse Events

Data downloaded from Adverse Events tables



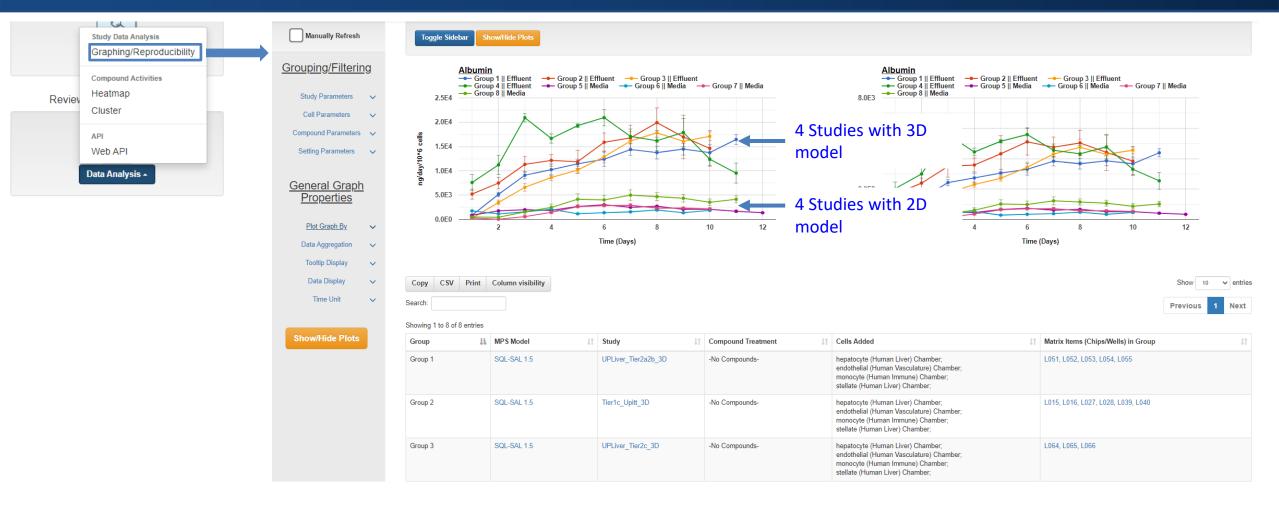


# Integrated Reproducibility Analysis Statistics Facilitates Inter-Study Reproducibility Assessment



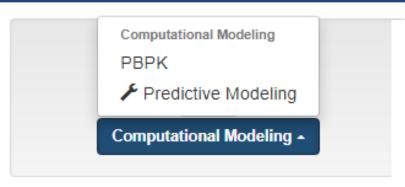
Time (Davs)

# Graphing/Reproducibility Feature Allows Easy Comparison of Study Sets

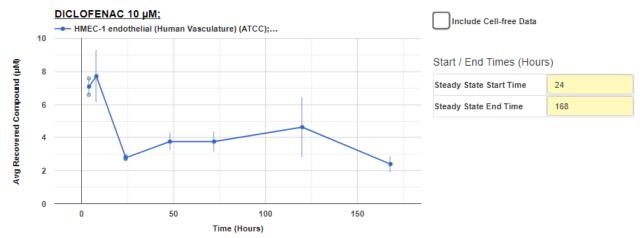




# Integration of Computational Modeling Tools

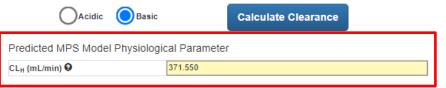


 Physiologically-based PK tools estimate blood levels based on hepatic clearance calculated from liver MPS experimental models.



# No. of Cells in Chip (for Calculations) 80,000 Compound Physicochemical Parameters Compound DICLOFENAC MW 296.15 logD 2 1.44 pKa 4.18 fu 0.01 Fa 0 0.927 Ka (1/h) 3.84

Model Parameters



#### Species Parameters

Species	Human
Species	
Organ	Liver
Body Mass (kg)	70
Total Organ Weight (g)	1,400
Organ Tissue (Cells/g)	130,000,000
Blood Volume (L)	5
V <sub>p</sub> (L/kg) ❷	0.0436
V <sub>E</sub> (L/kg) ❷	0.151
R <sub>E/I</sub> <b>②</b>	1.4
V <sub>R</sub> (L/kg) ❷	0.38
Absorptive Surface Area (m²) @	200
K <sub>I</sub> (1/h) <b>Q</b>	0.302

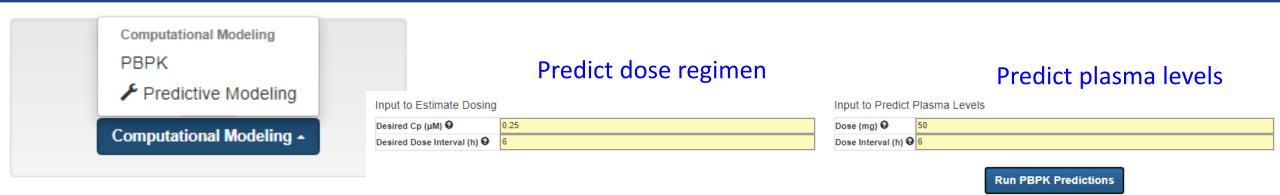
#### References:

Lombardo F, Obach RS, Shalaeva MY, Gao F. Prediction of human volume of distribution values for neutral and basic drugs. 2. Extended data set and leave-class-out statistics.. J Med Chem.. 2004. doi:10.1021/jp/04081.

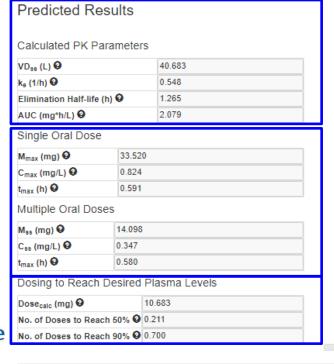
Usansky HH, Sinko PJ. Estimating human drug oral absorption kinetics from Caco-2 permeability ush an absorption-disposition model: model development and evaluation and derivation of analytical solutions for k(a) and F(a).. J Pharmacol Exp Ther.. 2005. doi:10.1124/jpet.104.076182. PMID:15833900

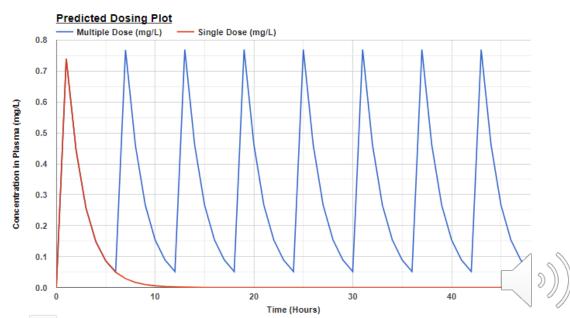


# **Integration of Computational Modeling Tools**



- Physiologically-based PK tools estimate blood levels based on hepatic clearance calculated from liver MPS experimental models.
- Computational models are being integrated into the MPS-Db that will utilize omics data to understand disease pathways and networks, and drug mechanism of action.







# We Continue to Develop the MPS-Db

### **Currently in development**

- Integration of Genomic data and tools for visualization (Phase II)
- Enhancements to the Coronavirus Covid-19 Disease Portal

#### **Next up in development**

- Enhance preclinical and clinical reference data, and optimize data concordance analysis
  - Integrate in vivo data
- Computational pathway modeling using Genomic data

### **Developing commercialized version**

- Enable full MPS-Db functionality behind data provider's firewall
- Enable interfacing with private company databases for their proprietary use
- Provide links to MPS device, cell, and reagent vendors.





### **Summary: The MPS-Db Provides Value for All MPS Developers and Users**

### **MPS-Developers**

### **MPS-Users**

- Aggregated biological information for model design
- Track model performance during development
  - Aggregated reference data for establishing clinical relevance
    - Biomarker identification

- Ease of secure data sharing in a standardized format
- Quick access to experimental protocols and key references
- Flexible graphing capabilities for comprehensive data analysis
- Statistical analyses for reproducibility analysis and DOE
- Easy comparison of performance across models

- Rapid selection of diseased/healthy
   MPS models
  - Access to existing model data to evaluate performance and identify context of use
  - Integration with proprietary databases/
- Integrated computational modeling





# **Webinar Series in Progress**

- ✓ Introduction to the Microphysiology Systems Database (MPS-Db) A Critical Tool for Managing, Analyzing, and Modeling MPS Experimental Data (October 6, 2020)
  - ✓ A video recording of the webinar is available on the MPS-Db help page <a href="https://mps.csb.pitt.edu/help/">https://mps.csb.pitt.edu/help/</a>
- ✓ **Designing studies and choosing test compounds in the MPS-Db** (November 10, 2020)
  - ✓ A video recording of the webinar is available on the MPS-Db help page <a href="https://mps.csb.pitt.edu/help/">https://mps.csb.pitt.edu/help/</a>
- ✓ Study workflow and data entry (December 8, 2020)-(December 15,2020)
  - ✓ A video recording of the webinar is available on the MPS-Db help page <a href="https://mps.csb.pitt.edu/help/">https://mps.csb.pitt.edu/help/</a>

• Data analysis in the MPS-Db (January 26, 2021)- registration link coming soon





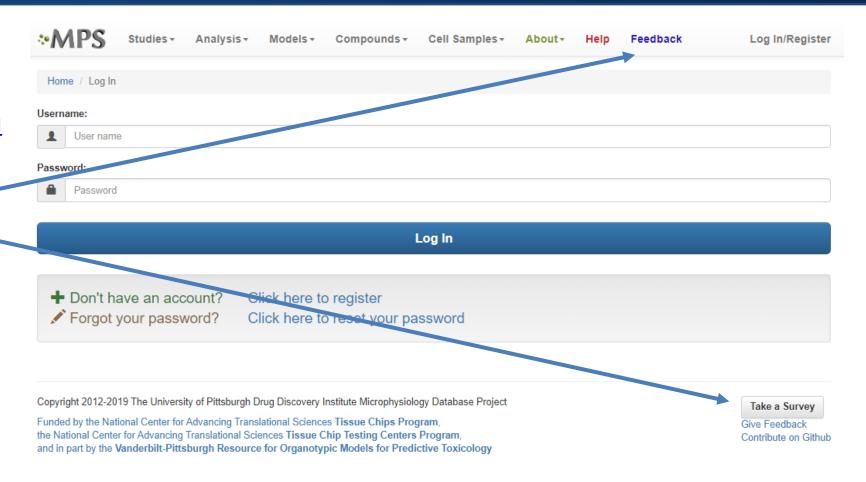
# Login, Explore, and Provide Feedback on the MPS-Db

### Login/Register

https://mps.csb.pitt.edu

#### Please provide feedback,

- Feedback function
- email to
  - MPSHELP@pitt.edu
  - gough@pitt.edu





# Schedule an Individual Interactive Online Training:

- Feedback function
- •email to

MPSHELP@pitt.edu

gough@pitt.edu







### The MPS-Db Team

### **Core Development Team**

Mark Schurdak – Multi-Pl Bert Gough – Multi-Pl Lans Taylor- Multi-Pl

Celeste Reese -Project Manager
Luke Bergenthal - Database Developer
Quinn Wolter- Database Developer
Sandra Karcher - Data Analyst/Modeler
Mike Castiglione - Data Analyst
Dillon Gavlock - Data Analyst
Tongying Shun - Lead Statistician, DBA

# Applications Development and Support Team

Lawrence Vernetti – Toxicologist, Database Applications

Jan Beumer – Collaborating Toxicologist

Joe Maggiore – Clinical and Commercialization

Harold Takyi – Information Systems Manager

Amanda Maleski – Administration Manager

### **Database Publications**

- 1. Gough A et al. Appl In Vitro Toxicol. 2016;2(2):103-17. PMID: 28781990.
- 2. Schurdak M et al. Lab Chip. 2020;20(8):1472-92. PMID: 32211684
- 3. Sakolish C et al., Toxicology, 2020:152651. PMID: 33307106





### **Thank You for Your Attention**

Questions??

https://mps.csb.pitt.edu/



