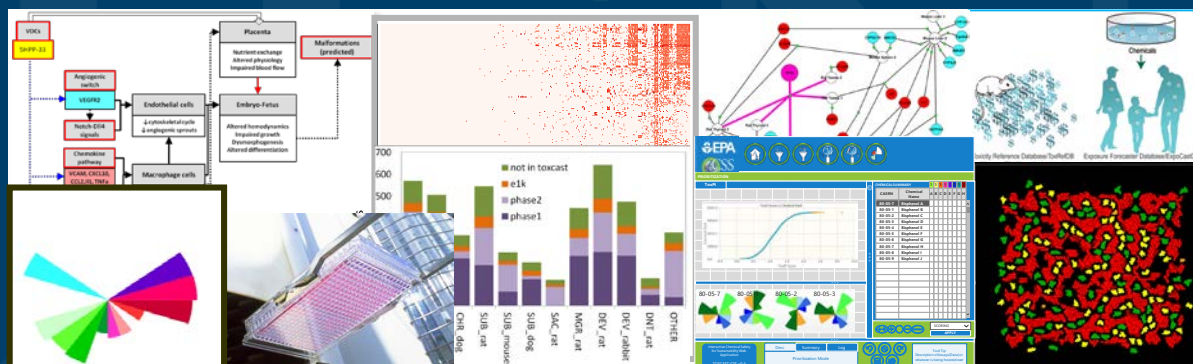


Filling in the Gaps: The Role Functional Genomics Can Play in 21st Century Toxicology



SOT Symposium: Effectively Leveraging Cellular Functional Genomics Strategies for Elucidating Chemical Mechanisms of Action

March 13, 2018

Keith Houck

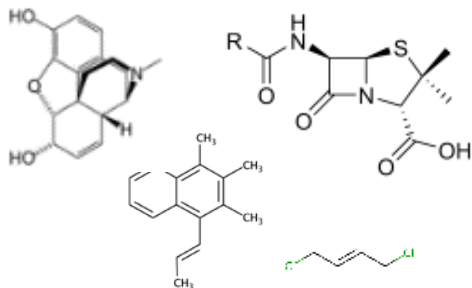
National Center for Computational Toxicology

I have no conflicts of interest to disclose!

The views expressed in this presentation are those of the author and do not necessarily reflect the views or policies of the U.S. EPA

Acknowledged Need to Innovate in Toxicology

Number of Chemicals/Combinations

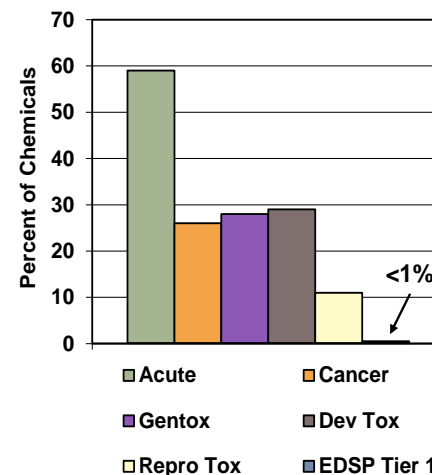


Why?

Ethical Concerns

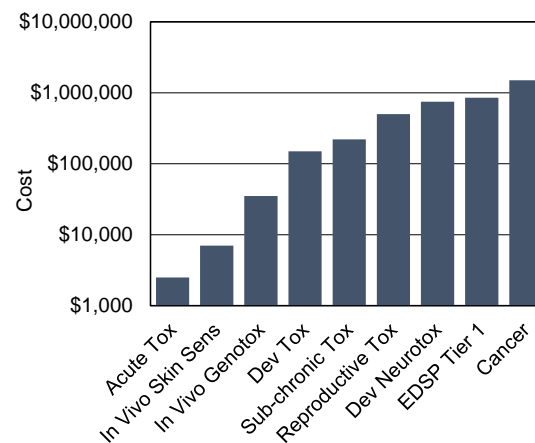


Lack of Data



Modified from Judson *et al.*, EHP 2010

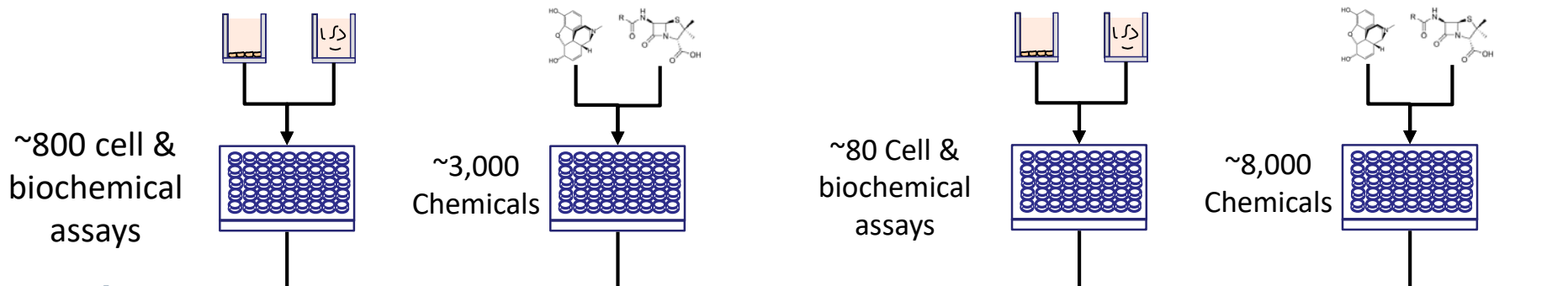
Economics



One Approach: High-Throughput Hazard Screening

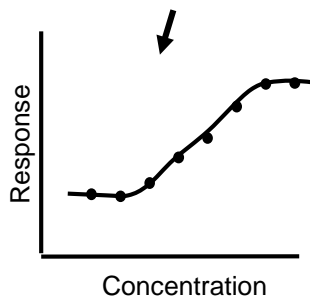
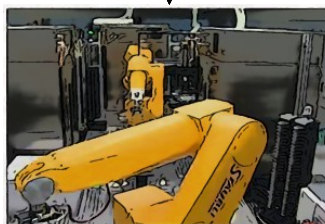
ToxCast

Tox21



MIE's/pathways

Models

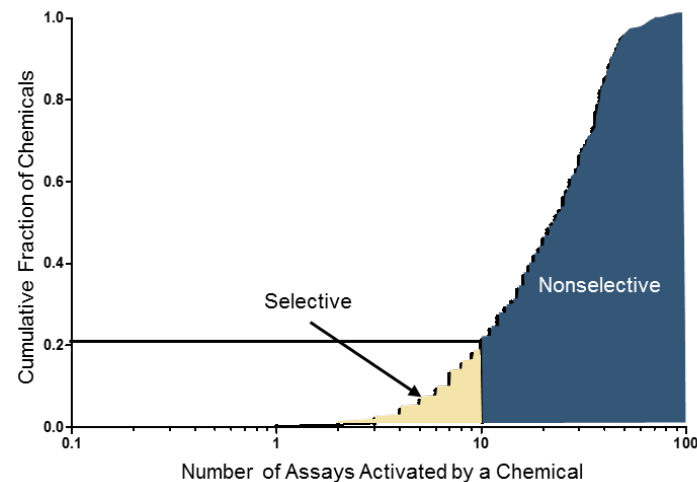
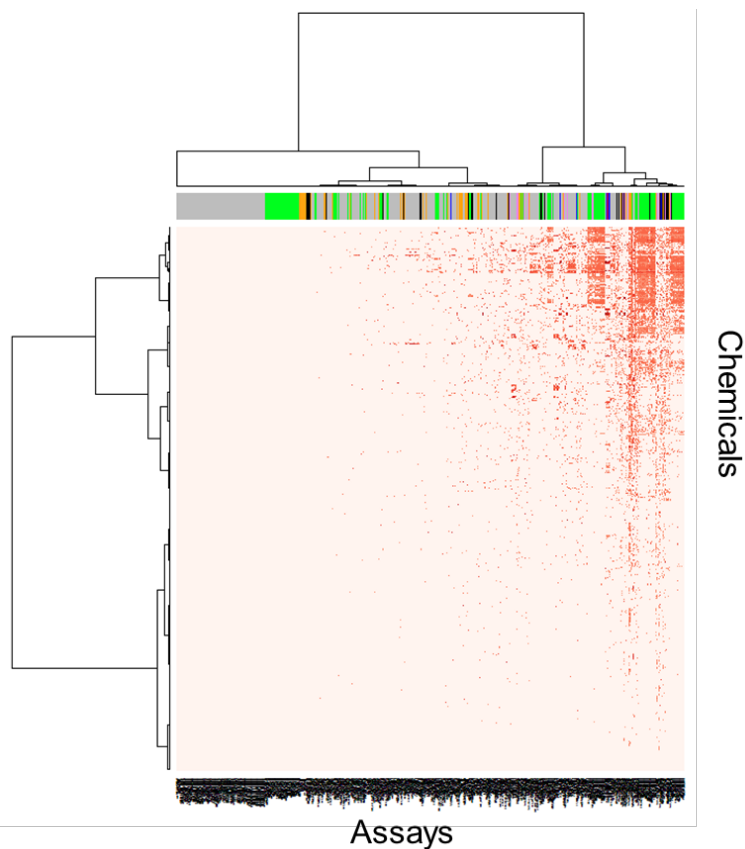


Challenges Encountered

- Promiscuous chemical-target interactions
 - Which are toxicologically relevant?
 - How do we identify assay artifacts?
- Limited biological/toxicological diversity screened
 - Thousands of possible MIE's
 - Hundreds of biological pathways

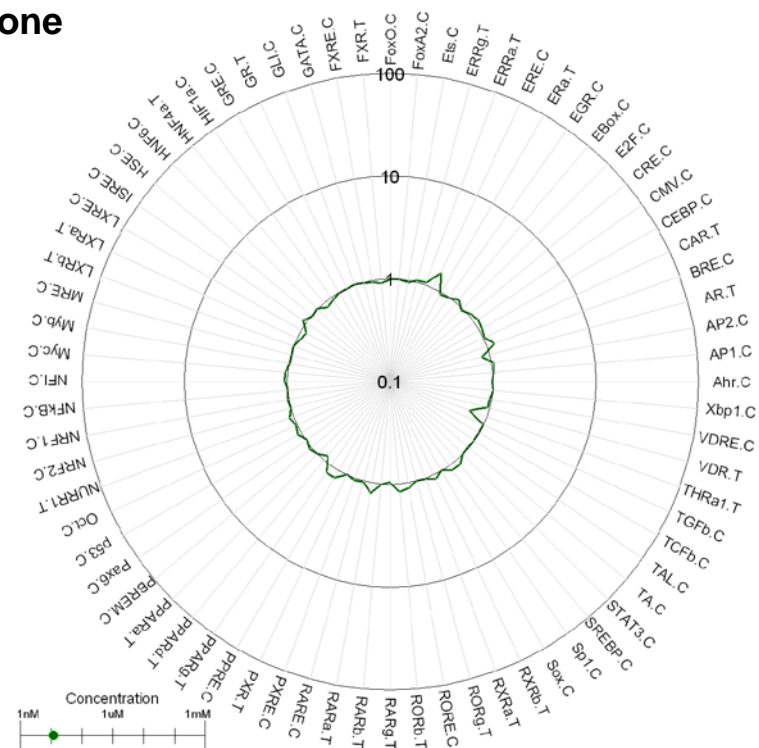
Promiscuous Chemical Response is the Rule

1000 chemicals/
800 assay endpoints



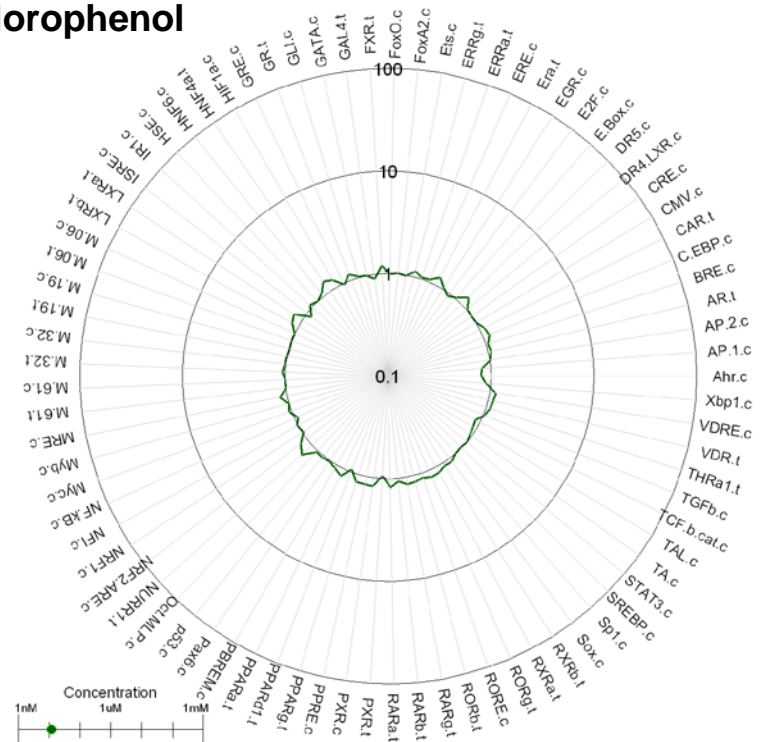
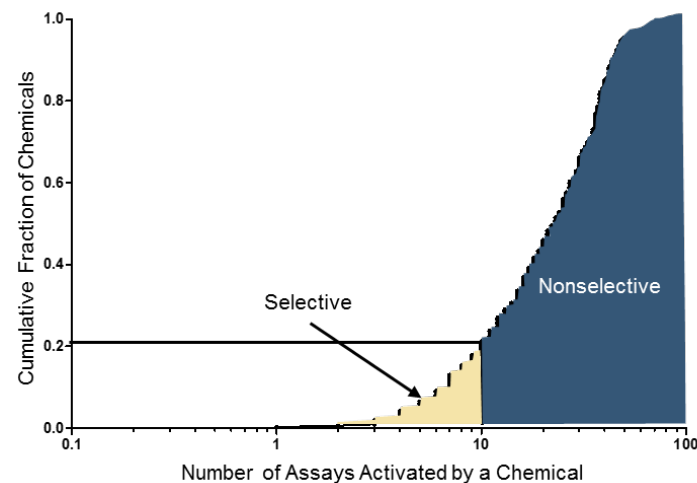
Thomas et al., 2013

Troglitazone



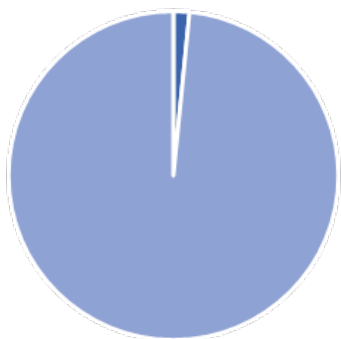
A heatmap visualization of gene expression data. The x-axis is labeled "Assays" and the y-axis is labeled "Genes". A dendrogram on the left side indicates hierarchical clustering of genes, while a dendrogram at the top indicates hierarchical clustering of assays. A color scale at the top of the heatmap ranges from 0 (dark blue) to 100 (dark red), with intermediate values marked at 20, 40, 60, and 80. The heatmap itself is a large grid of colored squares, where the color of each square represents the expression level of a specific gene across a specific assay. The data shows a clear pattern of high expression (red) in the top right corner and low expression (blue) in the bottom left corner.

Pentachlorophenol



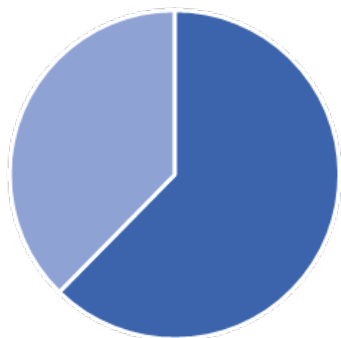
Beginning to Address Concerns for Increased Biological Coverage

Gene Coverage



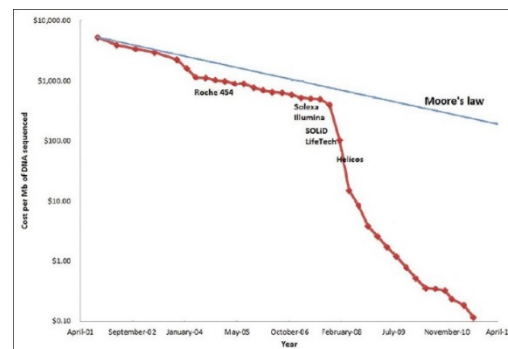
■ ToxCast
■ Not in ToxCast

Pathway Coverage*

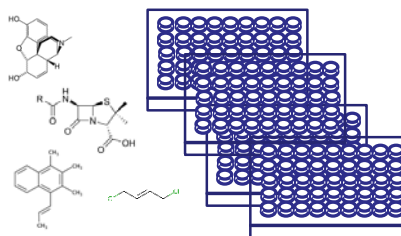


*At least one gene from pathway represented

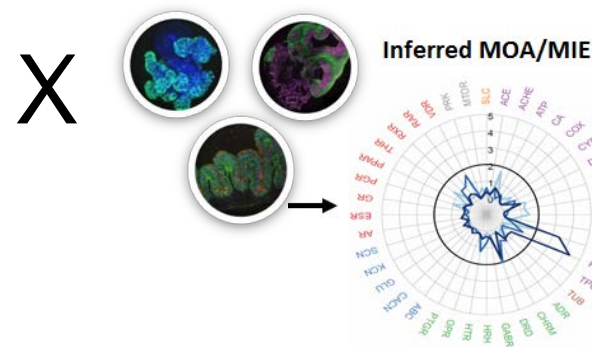
High-throughput transcriptomics (HTTr)



Thousands of chemicals



Multiple Cell Types

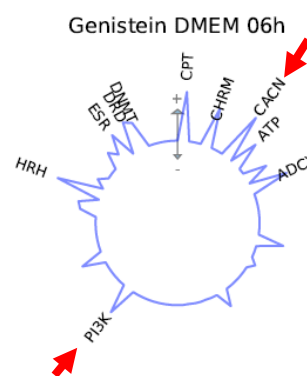
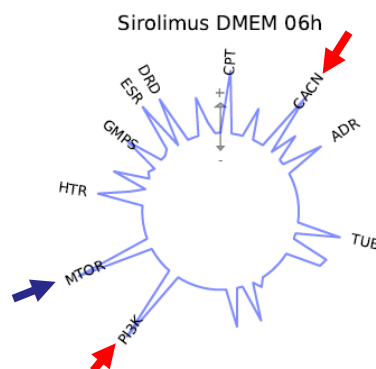
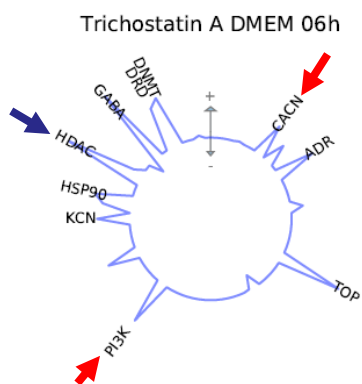
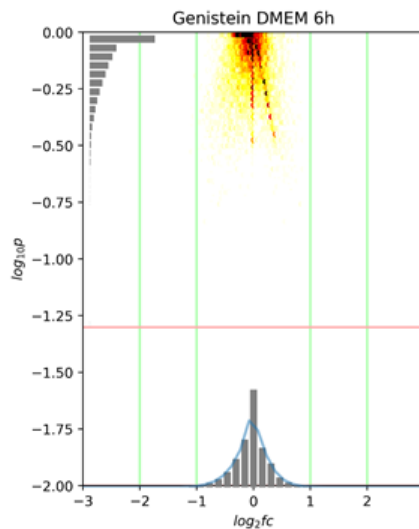
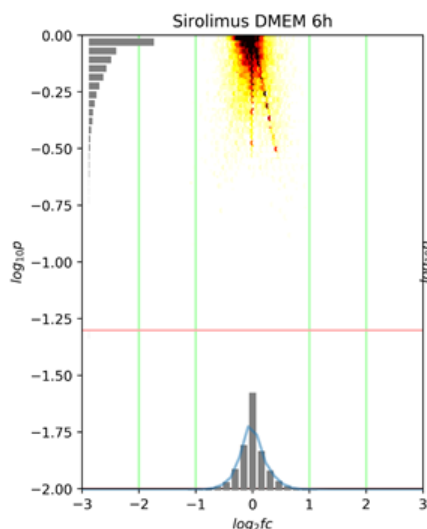
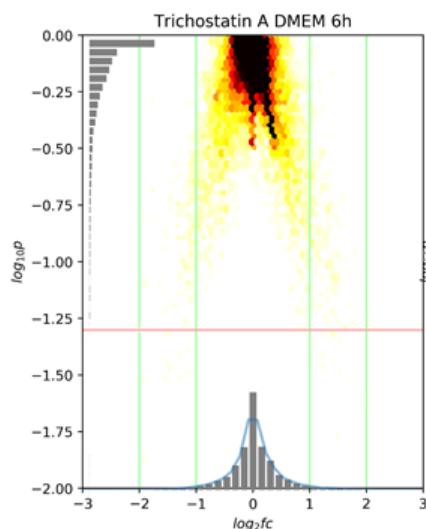


Requirements:

- Low cost
- Whole genome
- 384 well
- Automatable

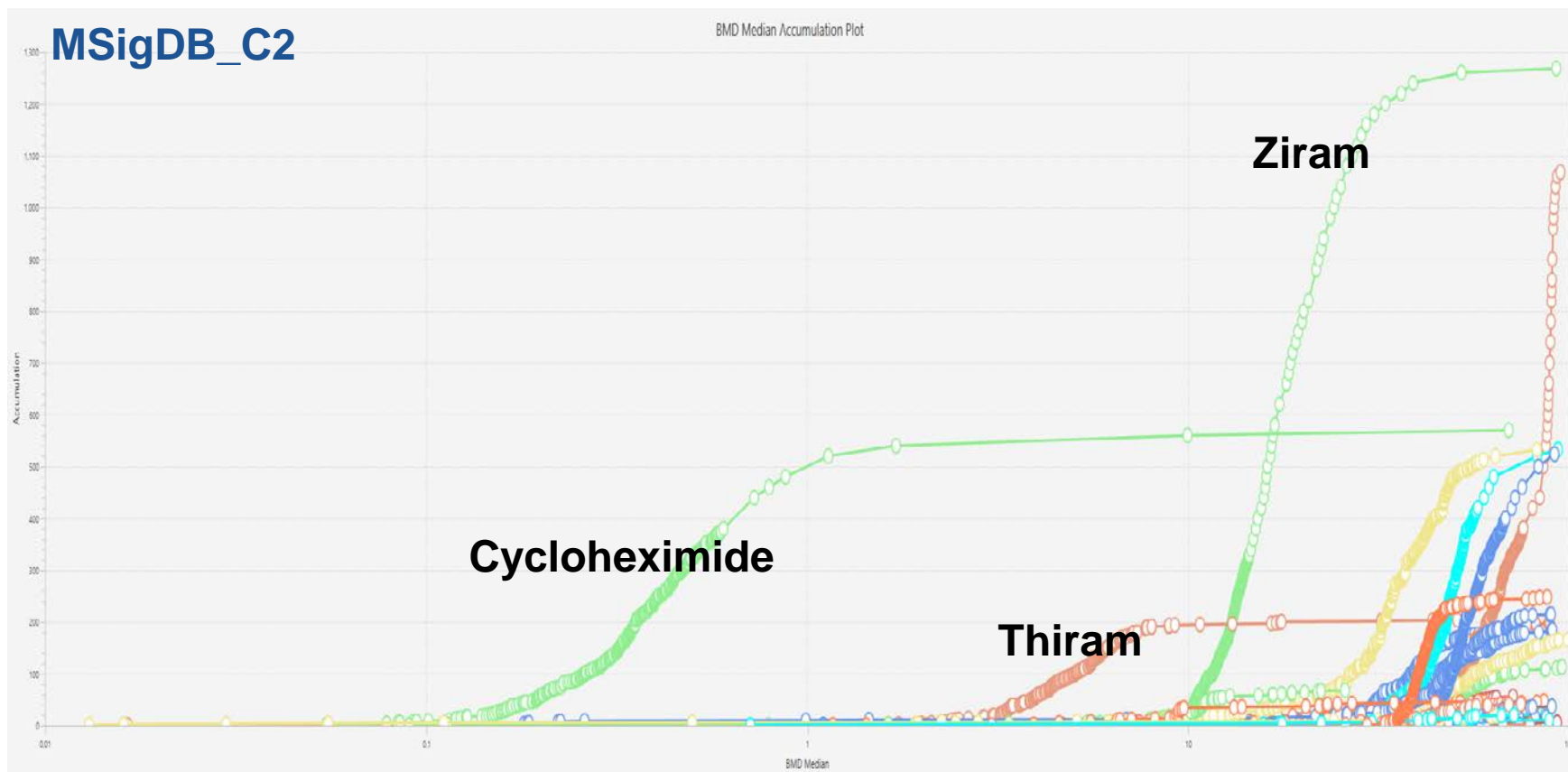
Connectivity Mapping (CMAP) Demonstrates Multiple Pathway Matches

- Differential gene expression observed with reference chemicals
- Putative targets identified using Connectivity Mapping
- Large degree of promiscuity of predicted targets observed
- Currently evaluating additional methods for MIE prediction



Putative target
 Promiscuous Target Mapping

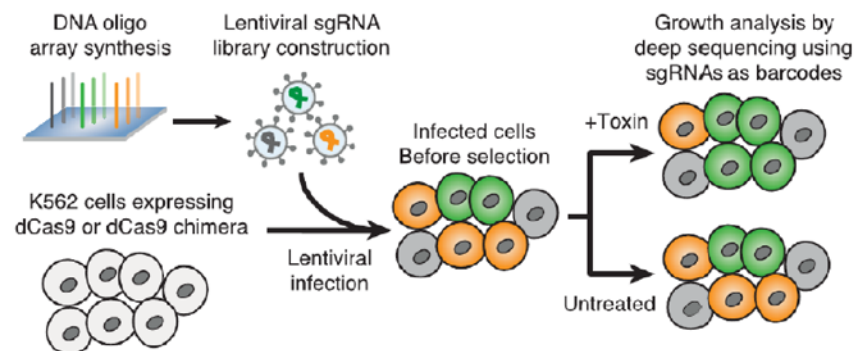
Pathway Potencies by Benchmark Dose (BMD) Analysis: Similar Issues



- Broad range of pathway level potency estimates and number of pathways affected across chemicals.

Functional genomics: Help with Defining Mechanistic Relevancy?

- Most chemicals have apparent polypharmacology—what is the critical/relevant MOA?
 - Could use potency to define but this may not be linked to adversity
 - Transcriptomics is high content but function is generally inferred
- **Functional genomics** allows for bridging between genotype and phenotype
- Previously mostly used in prokaryotic systems such as *S. cerevisiae*
- Advent of **CRISPR-Cas9** opens door for higher throughput applications in mammalian cells

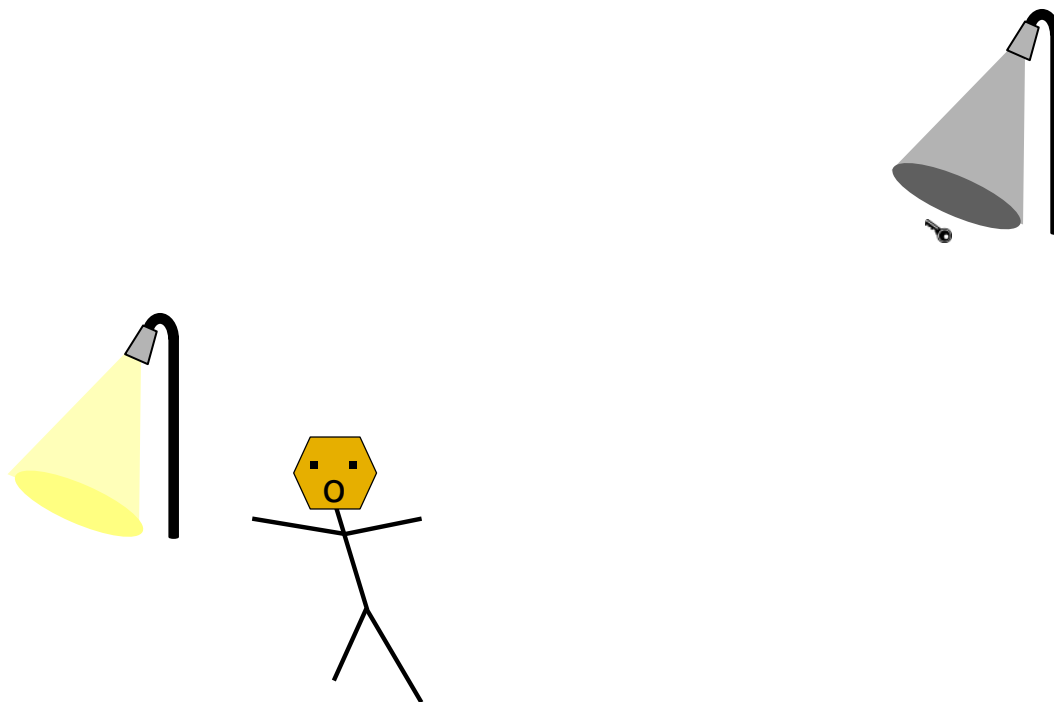


Gilbert et al., Cell, 2014

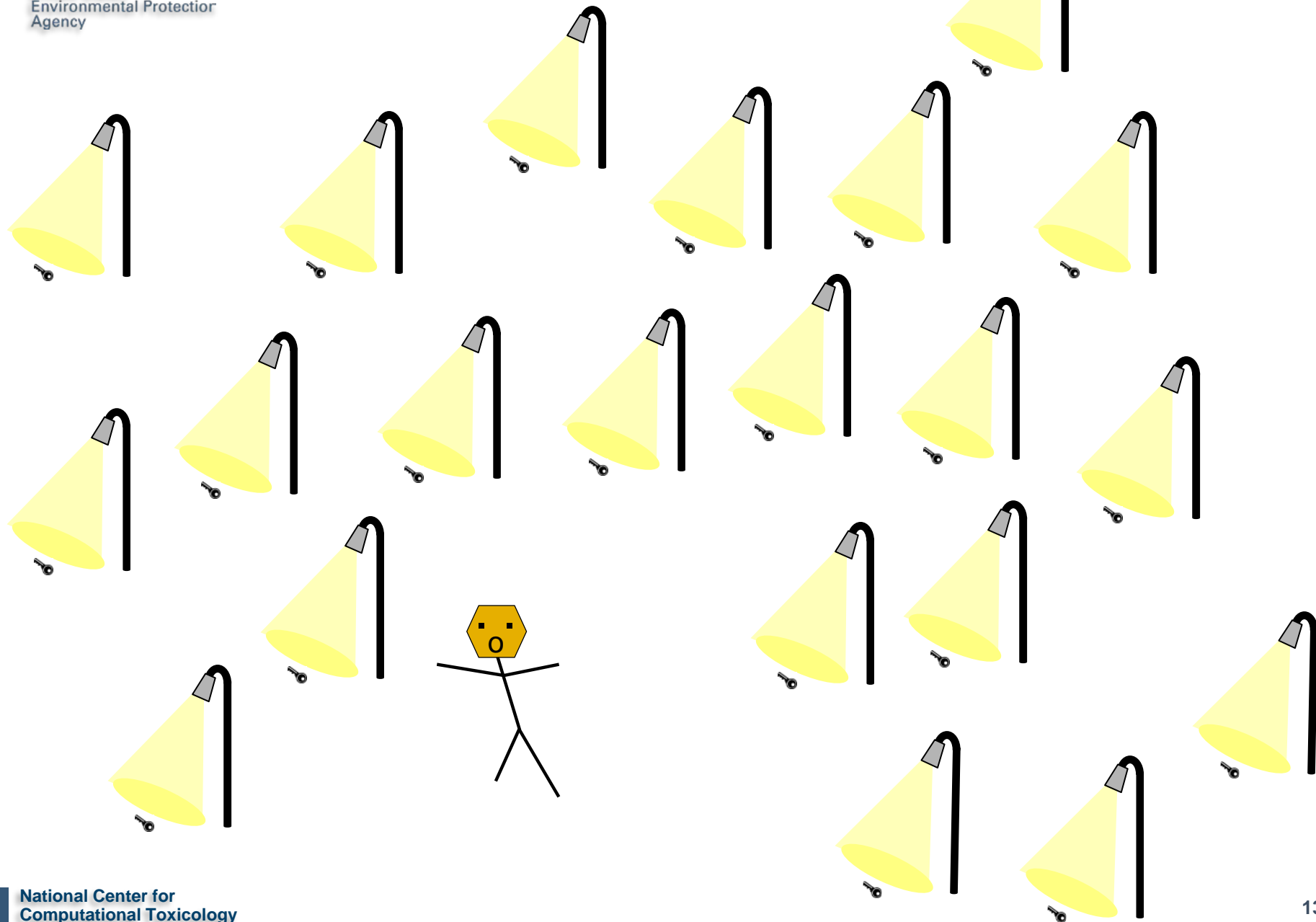
Advantages of Functional Assays

- Non-targeted approach--unbiased (*relatively*)
- Genomics
 - Full genome/proteome
 - Critical interactions drive functionality measured
 - Pathway mapping may be necessary (one-to-many problem)
- Chemical Proteomics
 - Full proteome
 - Direct chemical:target interaction
 - Measured in context of cell milieu
 - Identification of MIEs

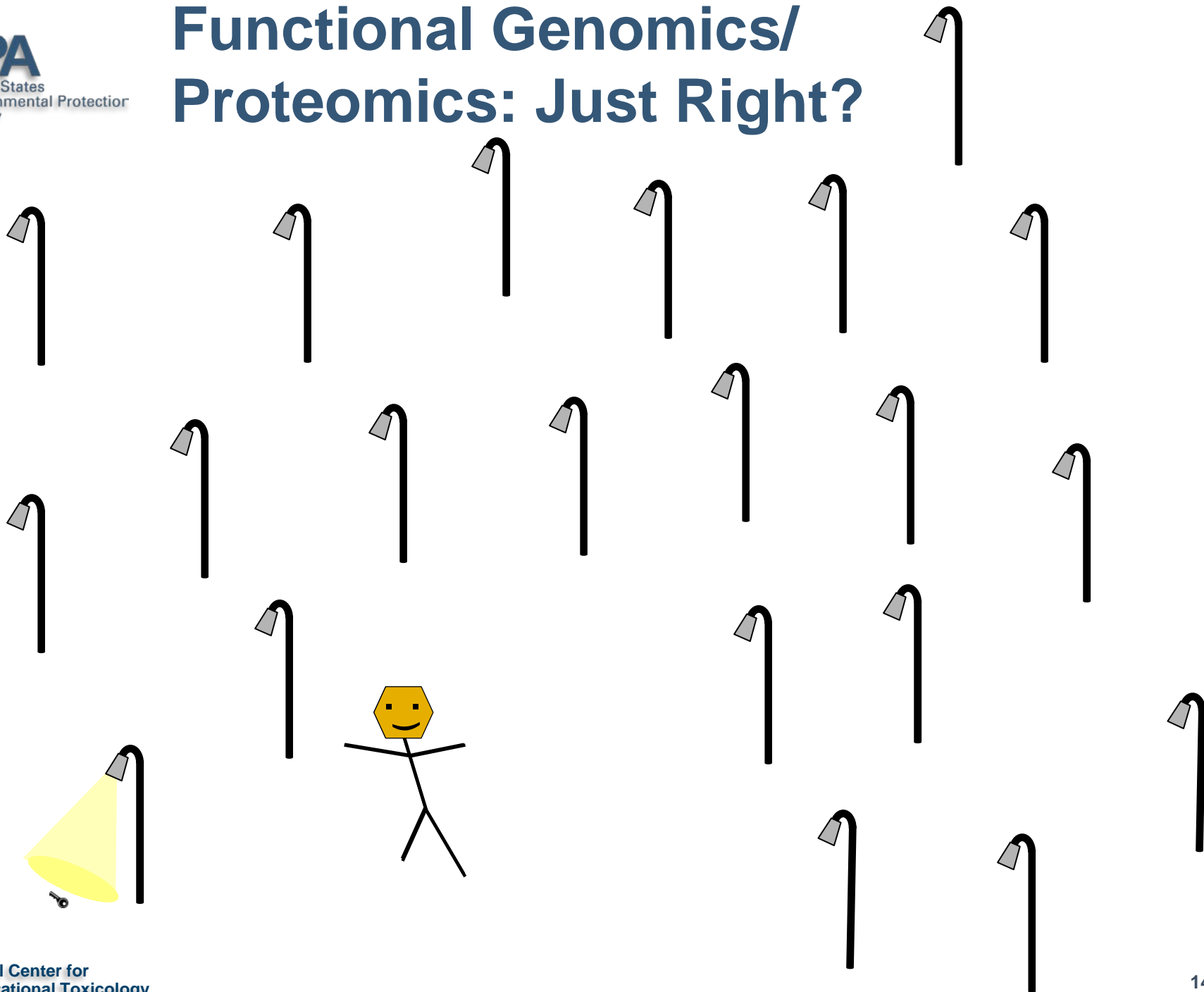
Focused Toxicology: Limited Scope



HTT: Promiscuity



Functional Genomics/ Proteomics: Just Right?



Pathway to Integration of Functional Genomics into Environmental Risk Assessment

- More proof-of-concept and validation studies with well-characterized toxicants
- Development of assay technology that facilitates expansion of functional endpoints beyond cell viability
 - *cell line engineering of pathway reporter lethality assays, sorting on reporter gene expression, sorting/single cell RNA sequencing, etc.*
 - *in vivo* assays in organisms suited to HTT such as *C. elegans* or *Danio rerio*
- Use of physiologically relevant cells and cell systems

Thank You for Your Attention and Now on to the Show!

- **The Use of CRISPR-Cas9 Technology for Validation and De-Validation of Targets from Functional Genomics** Peter Newham, AstraZeneca, Cambridge, United Kingdom.
- **CRISPR Genetic Screens on Cellular Stress Response to Proteo-Toxicants.** Quan Lu, Harvard T.H. Chan School of Public Health, Boston, MA.
- **Genome-Wide CRISPR-Cas9 Screens in Human Cell Lines Provide Novel Mechanistic Insights into Toxic Responses to Arsenic and Acetaldehyde** Amin Sobh, University of California Berkeley, Berkeley, CA.
- **Pooled Genome-Wide Screens as a Powerful Tool for Studying Drug Mechanism of Action in Cancer.** Federica Piccioni, Broad Institute of MIT and Harvard, Cambridge, MA.
- **Development of a Hybrid Chemical Proteomics Platform for Proteome-Wide Identification of Protein Targets of Environmental Chemicals.** David Ross Hall, University of Toronto, Toronto, ON, Canada.
- **Panel Discussion**