



# *Leveraging New Approach Methodologies to Complement Aquatic Life Criteria Derivation*

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*The views expressed in this presentation are those of the author alone and do not necessarily reflect the views of the USEPA*





# Project Background

- Aquatic Life Criteria (ALC) are “concentrations of pollutants in ambient water that—if not exceeded—are expected to protect fish, invertebrates, and other aquatic life from unacceptable adverse effects associated with short-term (acute) or long-term (chronic) exposure.”
- The process traditionally used by the USEPA’s Office of Water (OW; 1985) to derive ALC, while thorough, is:
  - time- and resource-intensive
  - requires extensive literature review
  - often limited by data availability
  - *in vivo*-focused
  - based on apical outcomes
- Required set of toxicity tests is exhaustive enough that for most chemicals the requisite information is not available
- ALC have been established by USEPA for <50 chemicals



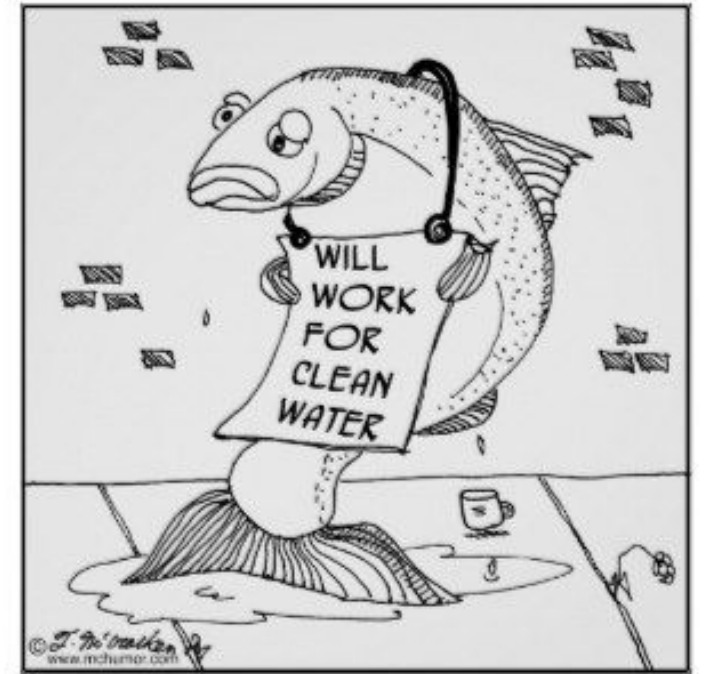


# Background on NAMs

- New approach methodologies (NAMs) can provide data to fill gaps in hazard assessment and exposure characterization
- Thousands of datapoints from a single toxicity experiment and/or rapid and cost-effective screening using batteries of high throughput *in vitro* assays
- EPA's Toxicity Forecaster (ToxCast)
  - 10,000 chemicals across more than 1,000 *in silico* and *in vitro* assays have been screened
- NAM-based data can be used to calculate point-of-departure (POD) estimates that may serve as lower bound, protective, estimates of *in vivo* effect

## ***GOAL: Leverage NAMs data to derive in vitro-based benchmarks as supplement to traditional ALC process***

- develop provisional prioritization and screening levels
  - guide resource prioritization (e.g., data generation and collection) for stakeholders (tribes, states, etc.)
- infer molecular mechanisms of action
- develop a process which is scalable and accessible



Theresa McCracken



# Objectives

## **1. *Derive chemical potency estimates (PODs) from ToxCast data***

- 4-nonylphenol
- Pentachlorophenol
- PFOA
- PFOS
- Compare to available aquatic benchmarks

## **2. *Use NAM data to investigate potential mechanisms of toxicity***

- Three model chemicals with well-defined MoA as proof of concept
  - Celecoxib
  - Pioglitazone
  - TCDD
- Four aforementioned industrial chemicals with published aquatic benchmarks

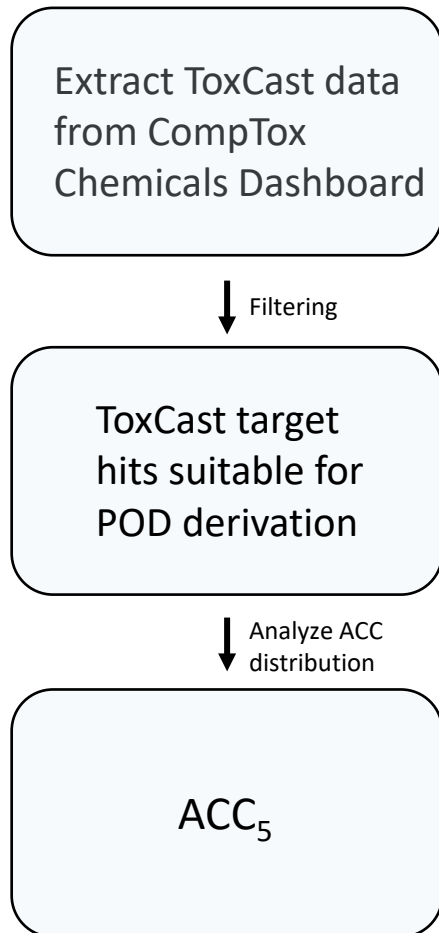
## **3. *Define the taxonomic domain of applicability for putative mechanisms of toxicity***

- Evaluate across species meeting OW minimum data requirements (MDR)



# Objective 1: Approach

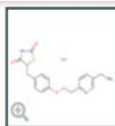
## ***Derive chemical potency estimates (PODs) from ToxCast data***



- I. Filtered by hit call status: “ACTIVE”
- II. Only used hits active at concentrations below lower bound “cytotoxic burst”
- III. Hits flagged with “only highest conc above baseline, active” and “only one conc above baseline, active” were removed for the POD calculation to minimize false positive hits
- IV. Used activity concentrations at cut-off (ACC) as basis for benchmarks
- V. From consequent ACC distribution, took 5<sup>th</sup> percentile as protective estimate of *in vivo* effect concentration; resulting “ACC<sub>5</sub>” used as POD



# Example ToxCast Summary



Pioglitazone hydrochloride

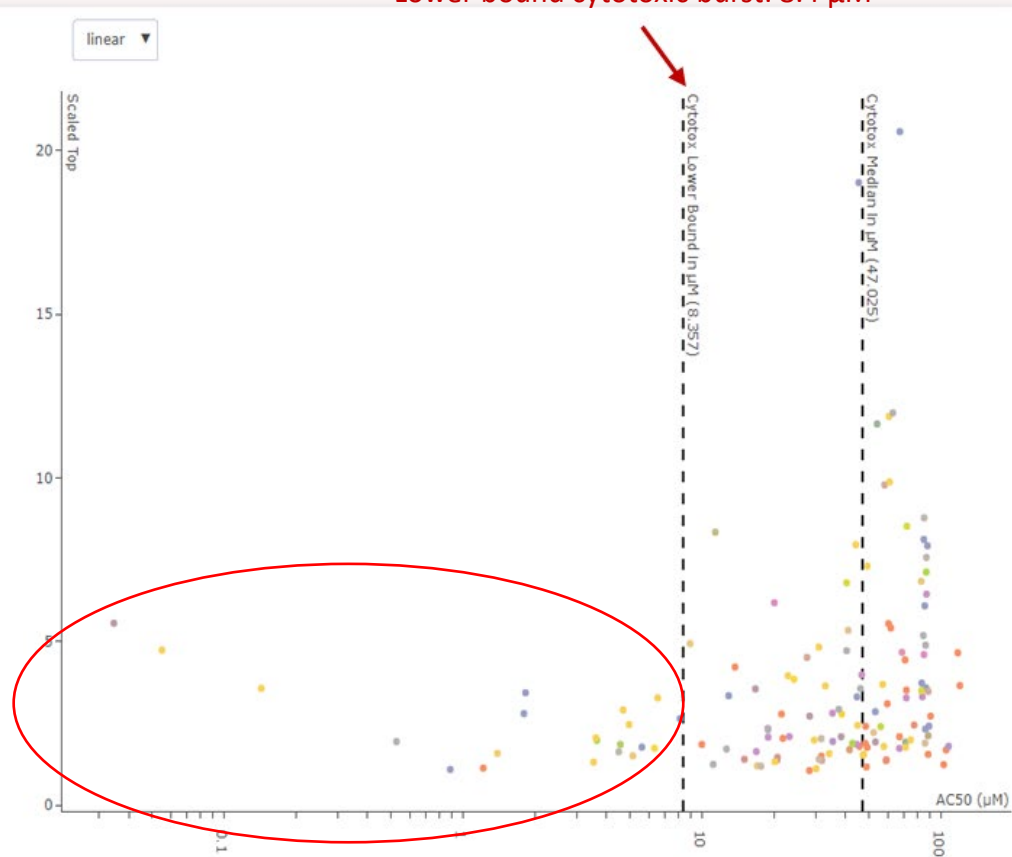
112529-15-4 | DTXSID3044203

Searched by DTXSID3044203.

## Bioactivity - TOXCAST Summary

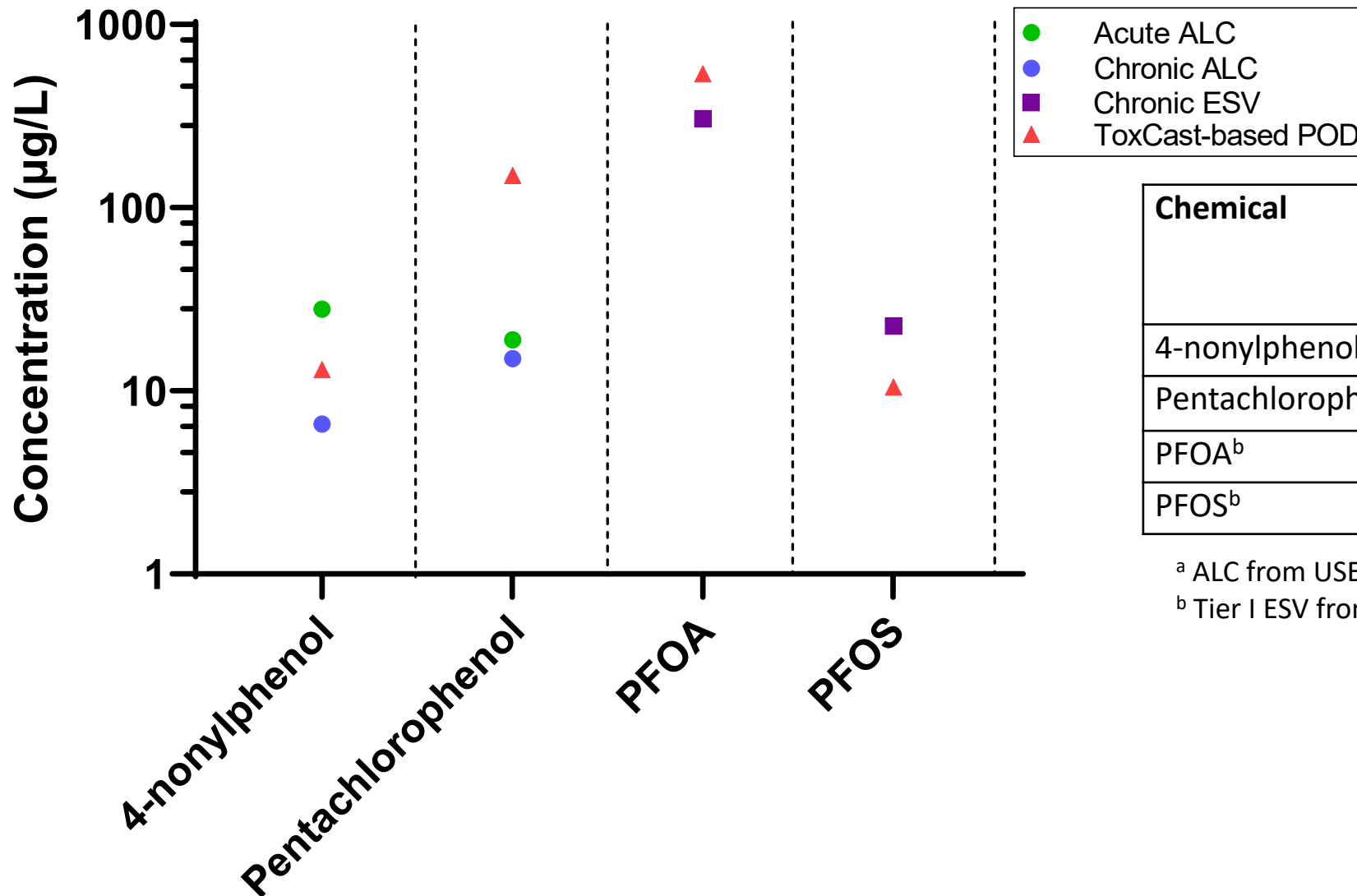
- Details
- Executive Summary
- Properties
- Env. Fate/Transport
- Hazard
- Safety > GHS Data
- ADME > IVIVE
- Exposure
- Bioactivity
- ToxCast: Summary**
- Conc. Response Data
- PubChem
- ToxCast Models
- Synonyms
- Literature
- Links
- Comments

- apolipoprotein
- background measurement
- catalase
- cell adhesion molecules
- cell cycle
- cell morphology
- channel 1
- channel 2
- cyp
- cytokine
- cytokine receptor
- dna binding
- esterase
- filaments
- growth factor
- kinase
- ligase
- lyase
- membrane protein
- metabolite
- microrna
- mutagenicity response
- nuclear receptor
- oxidase
- oxidoreductase
- phosphatase
- protease
- steroid hormone
- transferase
- transporter
- NA





# Objective 1: Results (Benchmark Comparisons)



Chemical	Freshwater Benchmark		ToxCast
	Acute (µg/L)	Chronic (µg/L)	ACC <sub>5</sub> (µg/L)
4-nonylphenol <sup>a</sup>	28	6.6	13.0
Pentachlorophenol <sup>a</sup>	19	15	162
PFOA <sup>b</sup>	-	307	538
PFOS <sup>b</sup>	-	22.6	10.5

<sup>a</sup> ALC from USEPA

<sup>b</sup> Tier I ESV from DOE/Argonne National Laboratory, 2021





## Objective 2: Approach

### ***Probe potential mechanisms of toxicity using NAM data***

- The further below the cytotoxic concentration a response is observed, the more likely the response is reflective of a chemical-specific mode-of-action
  - Thus, target hits with  $ACC \leq 0.333$  of lower-bound cytotoxic burst were used for mechanistic inference
- First, evaluated three chemicals with clear mechanisms of action/toxicity to confirm viability of approach
- Next, used approach to parse molecular targets of interest for nonylphenol, pentachlorophenol, PFOA, and PFOS



# Suitable Target Hits

Target hits with  $ACC \leq 0.333$  of cytotoxic burst were evaluated to probe potential molecular pathways of toxicity

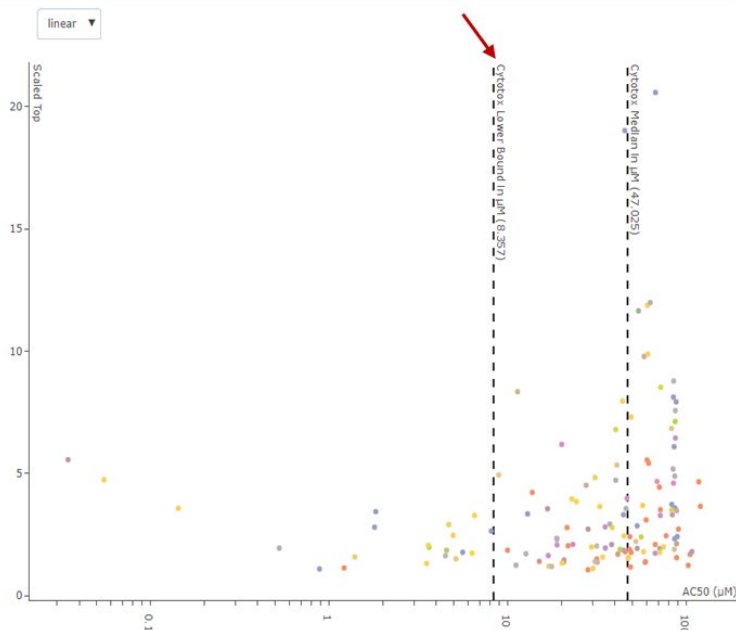


**Pioglitazone hydrochloride**  
112529-15-4 | DTXSID3044203  
Searched by DTXSID3044203.

## Bioactivity - TOXCAST Summary

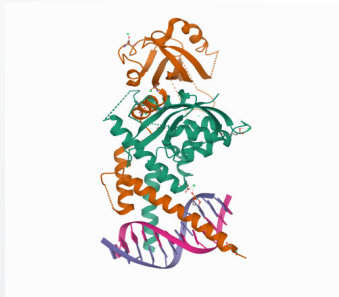
Lower bound cytotoxic burst: 8.4  $\mu\text{M}$

- apolipoprotein
- background measurement
- catalase
- cell adhesion molecules
- cell cycle
- cell morphology
- channel 1
- channel 2
- cyp
- cytokine
- cytokine receptor
- dna binding
- esterase
- filaments
- growth factor
- kinase
- ligase
- lyase
- membrane protein
- metabolite
- microna
- mutagenicity response
- nuclear receptor
- oxidase
- oxidoreductase
- phosphatase
- protease
- steroid hormone
- transferase
- transporter
- NA

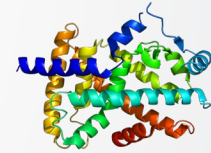
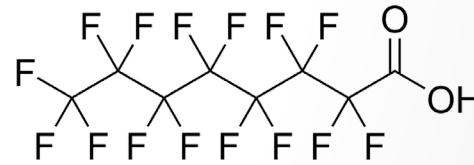
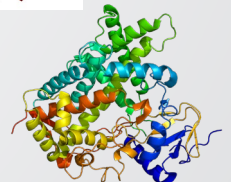
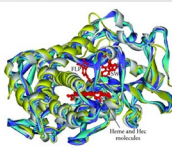


ToxCast target changes for pioglitazone at or below 2.8  $\mu\text{M}$ :

Chemical	Target	Full Name	Protein Accession	Assay ID	ACC ( $\mu\text{M}$ )
Pioglitazone	-	-	-	TOX21_PPARG_BLA_Agonist_ch2	0.00431
	PPARG	peroxisome proliferator-activated receptor gamma	NP_056953.2	TOX21_PPARG_BLA_Agonist_ratio	0.00951
	PPARG	peroxisome proliferator-activated receptor gamma	NP_056953.2	ATG_PPARG_TRANS_up	0.0444
	LPL	lipoprotein lipase	NP_000228.1	LTEA_HepaRG_LPL_up	0.315
	FABP1	fatty acid binding protein 1, liver	NP_001434.1	LTEA_HepaRG_FABP1_up	0.549
	PDK4	pyruvate dehydrogenase kinase, isozyme 4	NP_002603.1	LTEA_HepaRG_PDK4_up	0.552
	CYP4A11	cytochrome P450, family 4, subfamily A, polypeptide 11	NP_000769.2	LTEA_HepaRG_CYP4A11_up	0.656
	CYP4A22	cytochrome P450, family 4, subfamily A, polypeptide 22	NP_001010969.2	LTEA_HepaRG_CYP4A22_up	0.913
	CYP2C8	cytochrome P450, family 2, subfamily C, polypeptide 8	NP_000761.3	LTEA_HepaRG_CYP2C8_up	1.20
	PPARG	peroxisome proliferator-activated receptor gamma	NP_056953.2	NVS_NR_hPPARG	1.78
	Maob	monoamine oxidase B	NP_037330.1	NVS_ENZ_rMAOBC	2.11
	GADD45G	growth arrest and DNA-damage-inducible, gamma	NP_006696.1	LTEA_HepaRG_GADD45G_up	2.76

NS(=O)(=O)c1ccc(cc1)n2cc(C(F)(F)F)c(C3=CC=CC=C3C)nn2CC1=CC=CC=C1N(C1)CCOC2=CC=C(C=C2)CC3C(=O)NC(=O)S3Clc1cc(Cl)cc2c1Oc3cc(Cl)cc(Cl)c3O2CCCCCCCCCc1ccc(O)cc1Oc1cc(Cl)c(Cl)c(Cl)c1Cl

PPAR $\alpha$   
PPAR $\gamma$

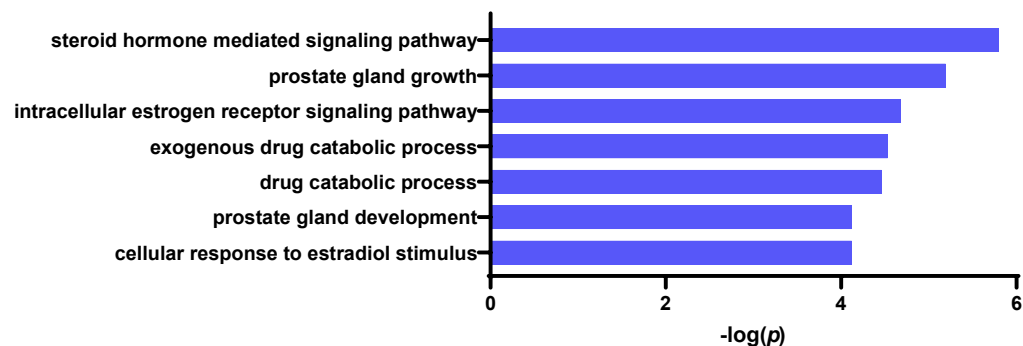
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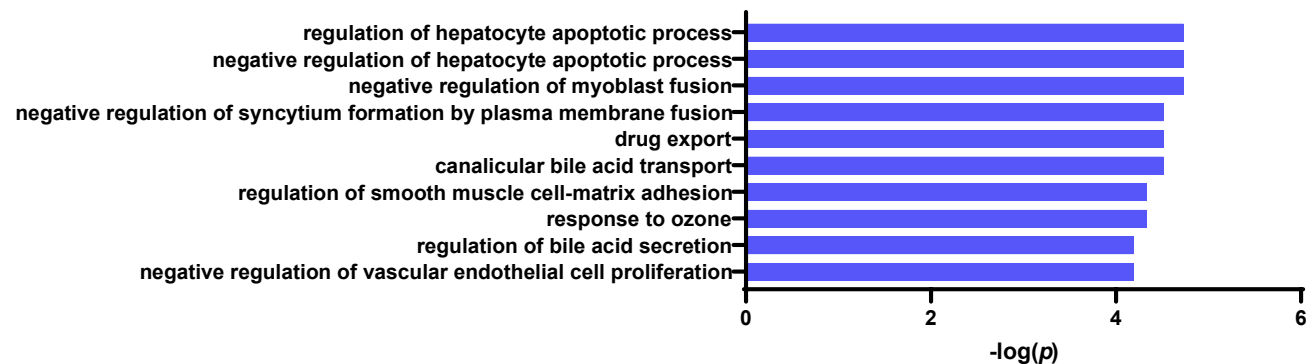


# Gene Ontology Pathway Enrichment

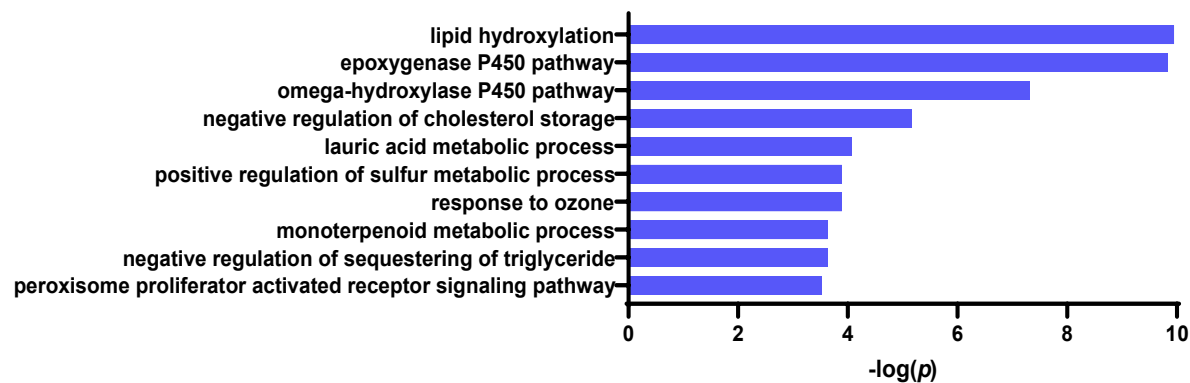
**4-nonylphenol**



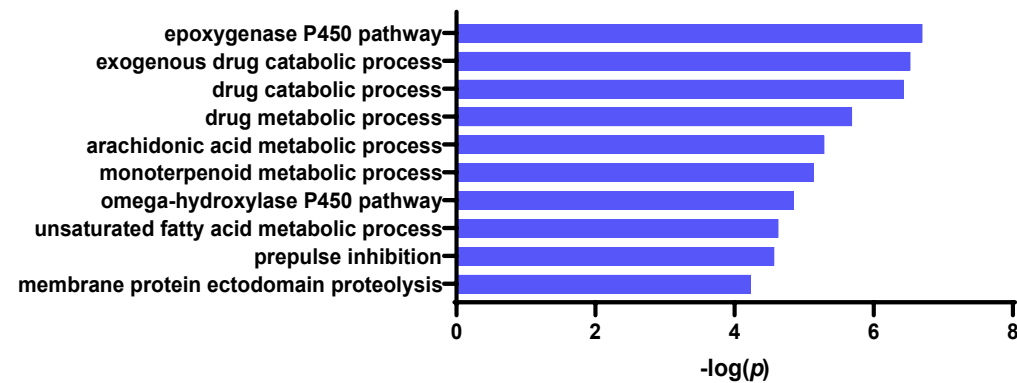
**Pentachlorophenol**



**PFOA**

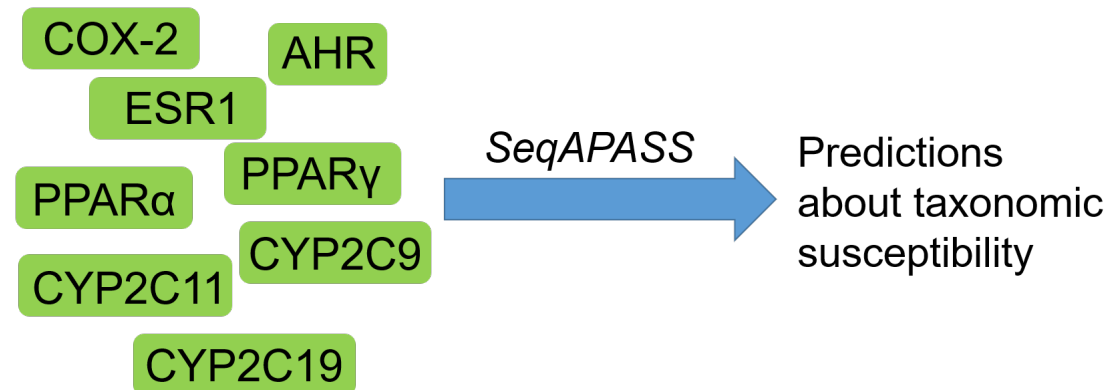


**PFOS**



### ***Define the taxonomic domain of applicability for putative mechanisms of toxicity***

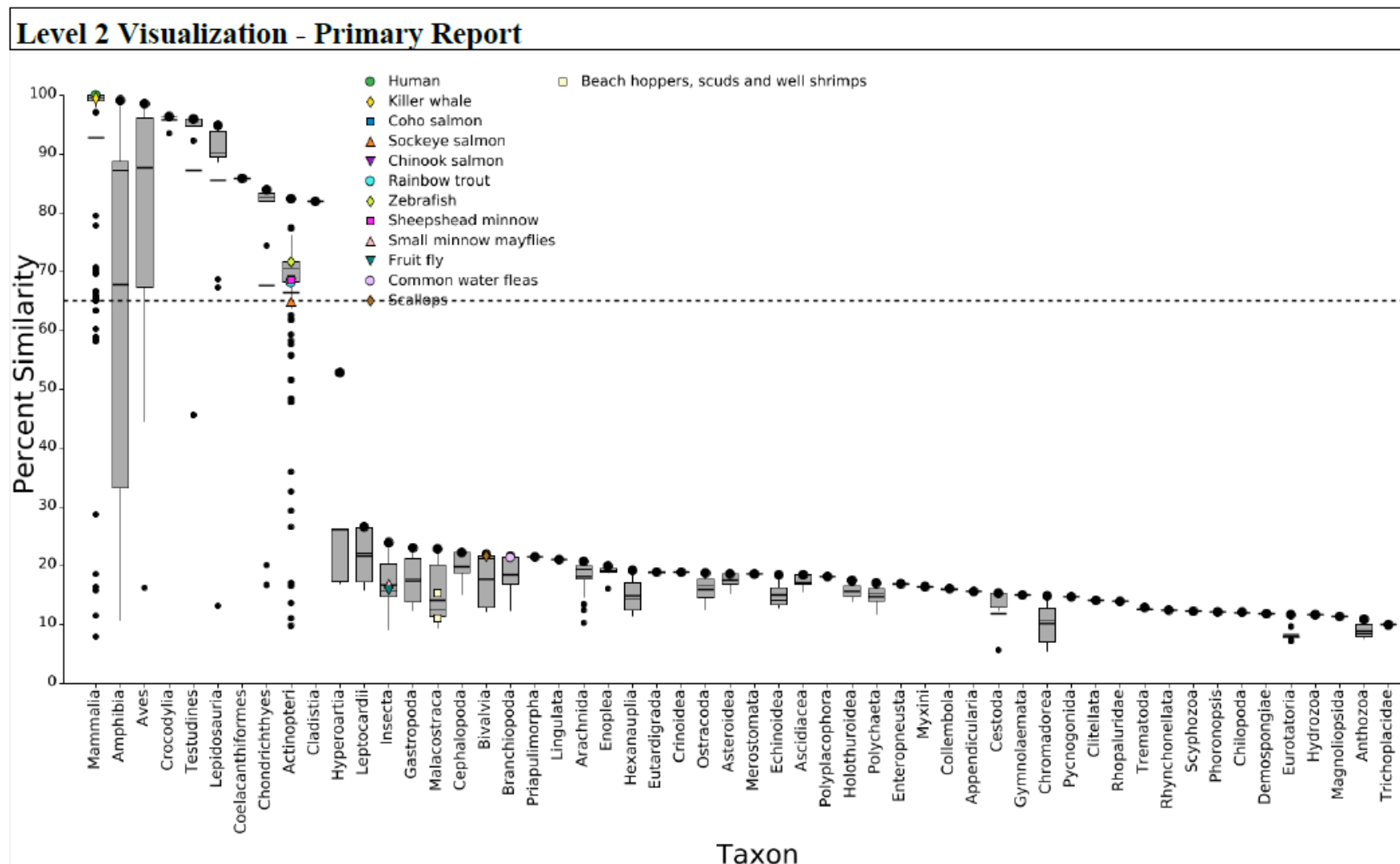
- Use EPA's Sequence Alignment to Predict Across Species Susceptibility (SeqAPASS) to determine whether chemical-specific mechanisms of toxicity identified through our approach are applicable across taxa
- Analysis incorporated at least one representative species within each MDR grouping (phylogenetically different taxa) required by OW for ALC derivation
  - Can inform which species might drive assessment and help focus data generation/collection





# Example SeqAPASS Evaluation: PPAR $\gamma$

*Sequence similarity in ligand binding domain (LBD)*







## Objective 3: Results

### *Taxonomic susceptibility predictions from SeqAPASS*

Chemical	Target	Taxon					
		Mammalia	Actinopteri	Insecta	Bivalvia	Branchipodia	Malacostraca
Celecoxib	COX-2	●	●	○	●	●	●
Pioglitazone	PPAR $\gamma$	●	◐	○	○	○	○
TCDD	AHR	●	●	○	○	○	○
4-nonylphenol	ESR1	●	●	○	○	○	○
Pentachlorophenol	-	-	-	-	-	-	-
PFOA	PPAR $\alpha$	●	●	○	○	○	○
	PPAR $\gamma$	●	◐	○	○	○	○
PFOS	CYP2C9	●	◐	○	○	○	○
	CYP2C11	●	●	○	○	○	○
	CYP2C19	●	◐	○	○	○	○



# Conclusions

- Overall, this work supports the use of NAM-based data to support/supplement formal ALC derivation, especially for data-poor chemicals
  - Accessible, scalable
- ToxCast-derived PODs generally aligned well with ALC/ESVs for chemicals examined without application of uncertainty or modifying factors
- NAM data can be used to infer prospective mechanisms of toxicity
  - Proof of principle with more targeted chemicals
  - Inferences about MOAs for industrial chemicals may be difficult given these compounds are generally not designed to exert effects on specific molecular pathways (e.g., pentachlorophenol)
- Use of bioinformatic tools such as SeqAPASS can be used as a line of evidence for predicting taxonomic susceptibility to environmentally-relevant chemicals
- Future directions include expanding analysis to larger set of compounds and incorporating data from other NAM approaches (e.g., high-throughput transcriptomics)



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OAK RIDGE  
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