

In silico and cheminformatics enrichment analysis to increase confidence in *in vitro* high-throughput screening (HTS) results: Application to Tox21 thyrotropin-releasing hormone receptor (TRHR) assay

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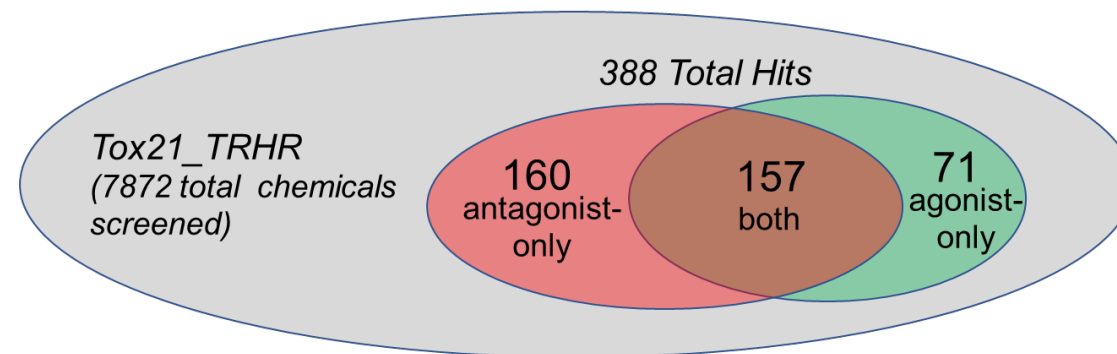
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Background

- Relating biochemical outputs to molecular initiating events (MIEs) and adverse outcome pathways (AOPs) is challenging, particularly when the relationship between the biochemical output and MIE is indirect, as is the case here
- Tox21 thyrotropin-releasing hormone receptor (TRHR) is a potential target in the thyroid hormone AOP, but is lacking confirmatory or orthogonal assays (*K. Paul Friedman, 2019*)



- TRHR is a GPCR (G protein-coupled receptor) with few known agonists or antagonists.
- Assay measures agonism or antagonism for TRHR through the Gq-Ca²⁺ pathway.



Objectives

- **Challenge:** prioritize Tox21_TRHR assay actives for hazard evaluation based on likelihood of binding to the receptor

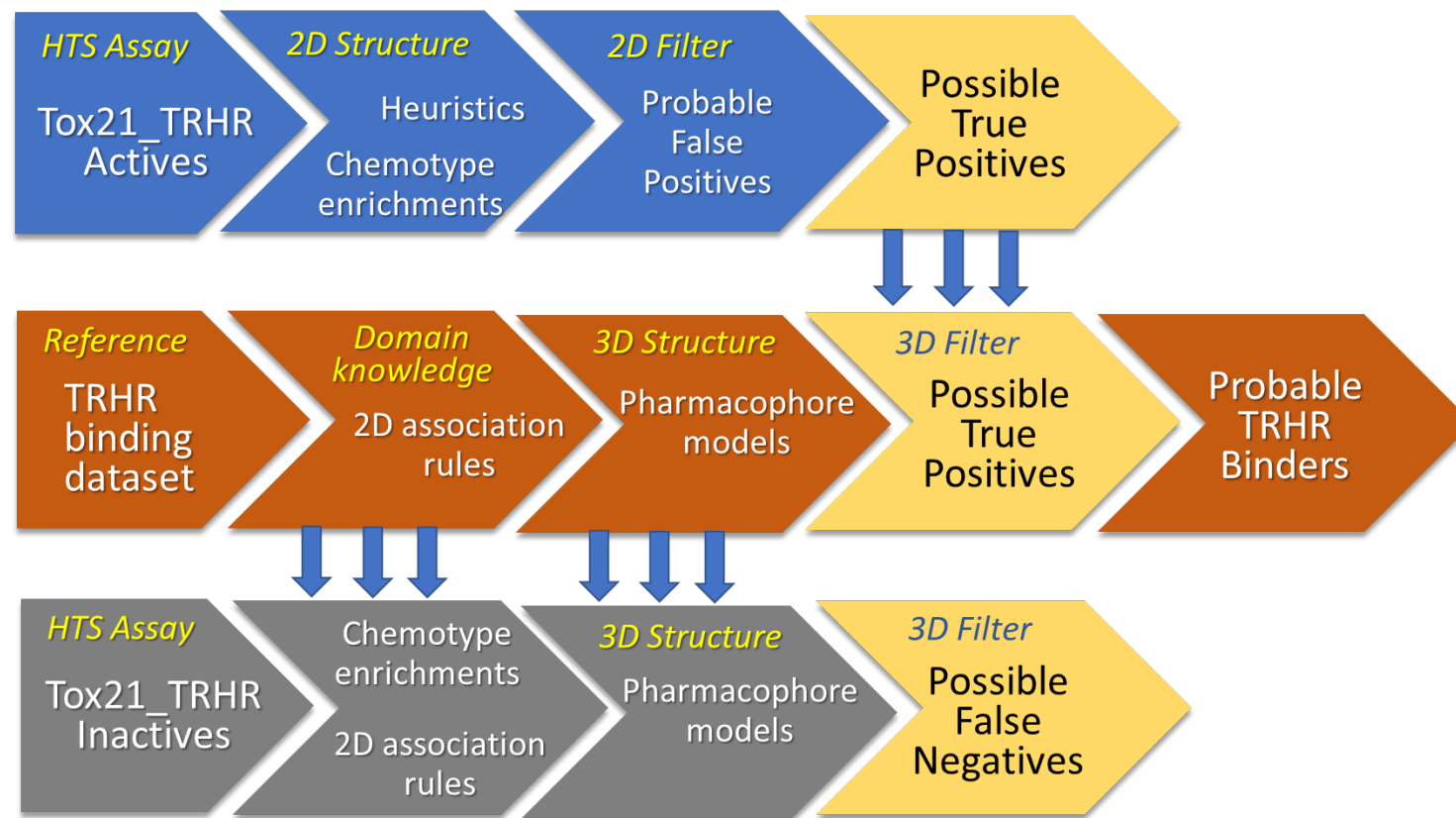
Develop and apply a structure-based data enrichment and knowledge contextualization workflow to identify likely TRHR false positives and discriminate true receptor binders

- ✓ identify structure-activity patterns using chemotype-enrichment analysis (*Wang et al., 2019*)
- ✓ filter noise from cytotoxicity or assay interference (*Borrel et al., 2020*)
- ✓ use 3D pharmacophore modeling to prioritize chemicals capable of binding to TRHR as well as modulators likely to interfere with binding (*Kaur et al., 2005*)

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Approach



Prioritize subset of actives (true hits) and inactives (potential false negatives) for follow-up testing using:

- *domain knowledge*
- *2D association rules*
- *chemotype enrichments*
- *QSAR models*
- *3D pharmacophore models*

Methods

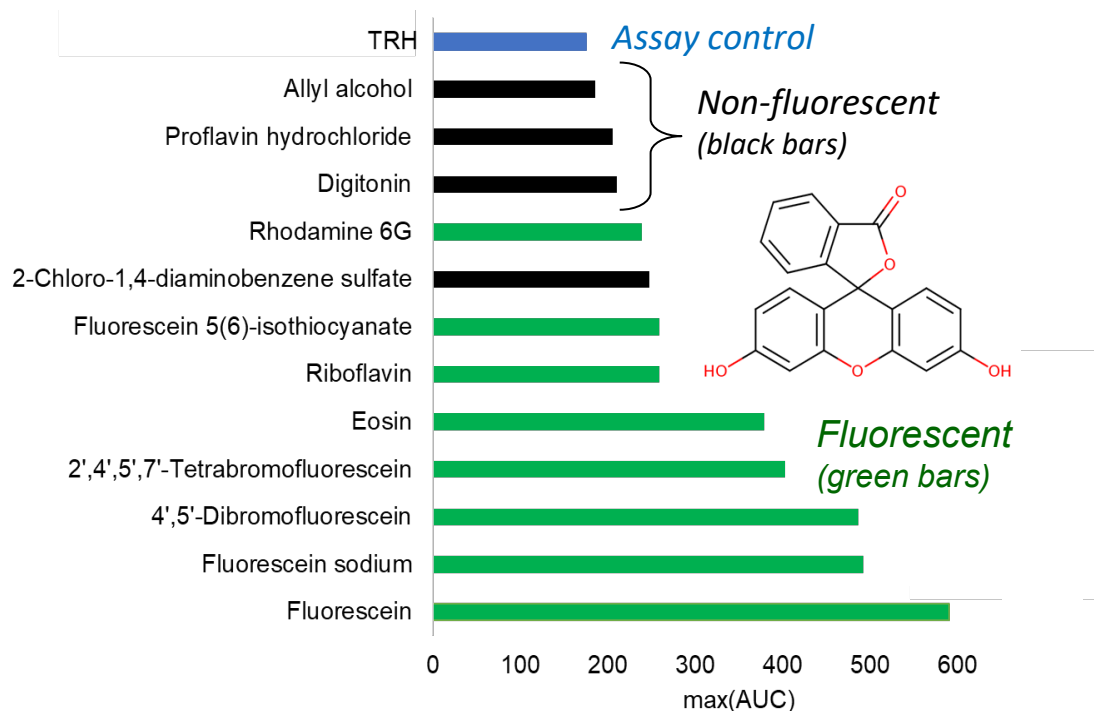
- ❑ Structures and Tox21_TRHR assay data downloaded from EPA dashboard <https://comptox.epa.gov/dashboard>
- ❑ Statistical analysis code at <https://github.com/mshobair/cheminf>; structures visualized <https://chemotyper.org/>
- ❑ Chemotype enrichment workflow (CTEW) and statistics described in Wang et al., 2019; ToxPrints at <https://toxprint.org/>
- ❑ Fluorescence prediction using InterPred web service for Machine Learning <https://sandbox.ntp.niehs.nih.gov/interferences>
- ❑ Pharmacophore modeling using Molecular Operating Environment (MOE) <https://www.chemcomp.com/Products.htm>

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Results: Cheminformatics Analysis

Dose-response curve analysis

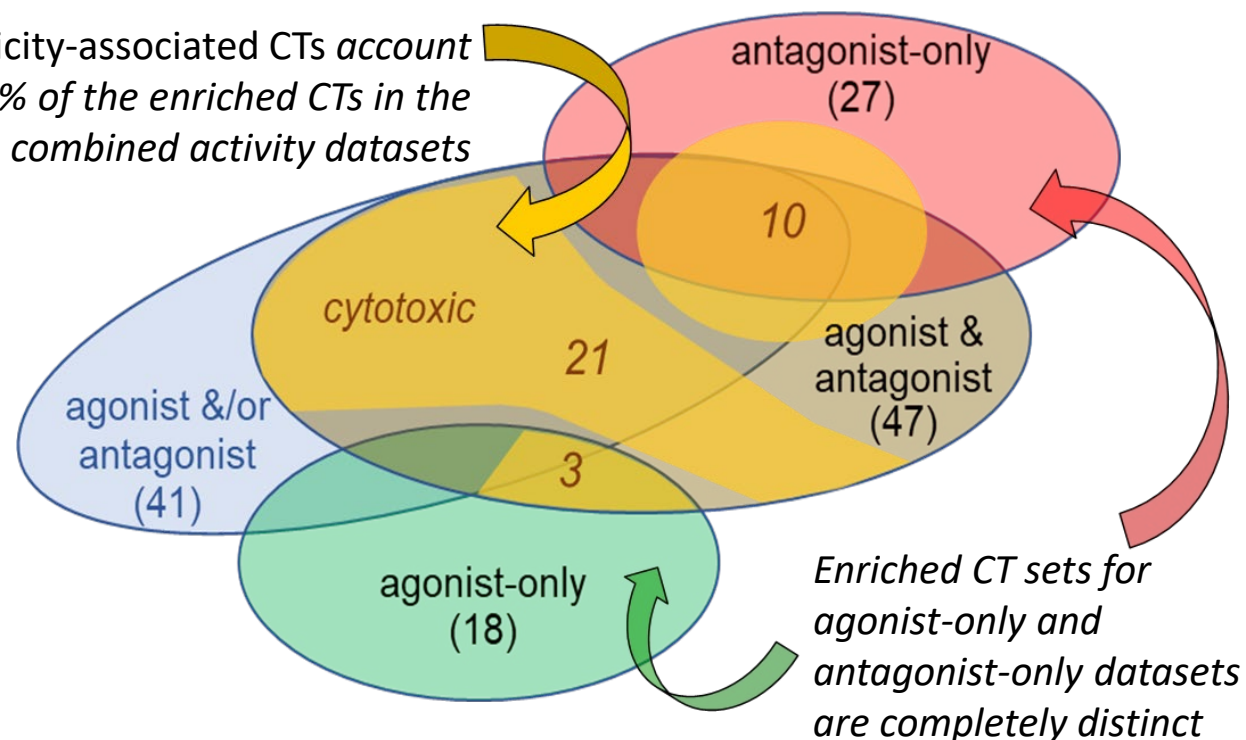


Maximum Area-Under-the-Curve (AUC) values per chemical computed for both agonist and antagonist endpoint data.

➤ *Majority of top potent/efficacious hits enriched in autofluorescent molecules, indicating source of false positive (FPos) activity.*

Chemotype-enrichment (CTE) analysis

Cytotoxicity-associated CTs account for >50% of the enriched CTs in the combined activity datasets



Number of ToxPrint chemotypes (CTs) identified from CTE analysis for 4 separate assay activity-datasets are shown.

CTs included in the "cytotoxic" regions are significantly enriched in >10/42 Tox21 cytotoxicity-labeled assays

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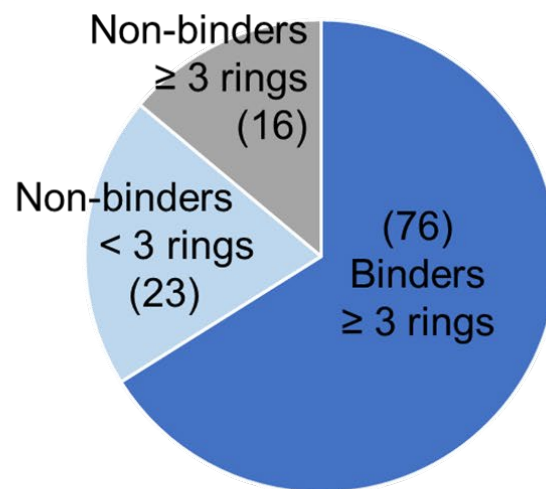
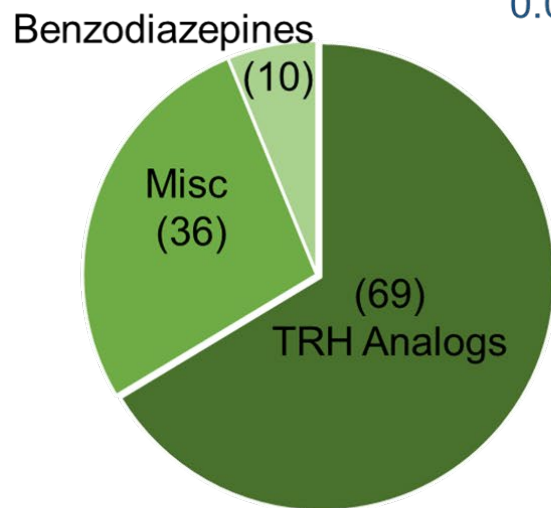


Results: TRHR Binding Studies

TRHR Binding Literature Survey

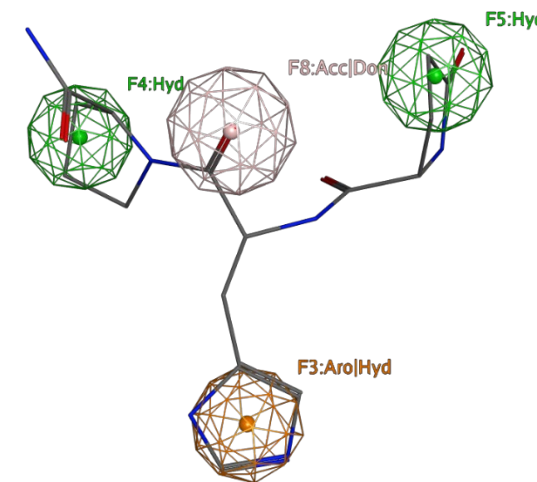


K_i or IC_{50}
0.01 – 300 μ M

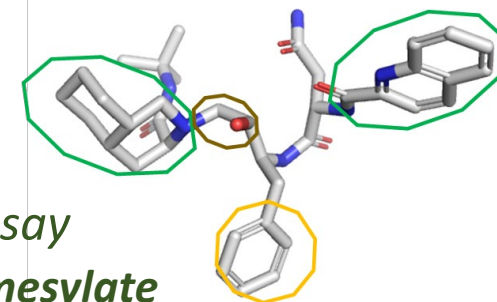


- Limited structural diversity of known TRHR binders
- Majority are TRH analogs containing 3 or more rings
- Benzodiazepines are known drug class of TRHR binders

TRHR Pharmacophore Modeling



High probability binders limited to TRH analogs (mostly drugs)

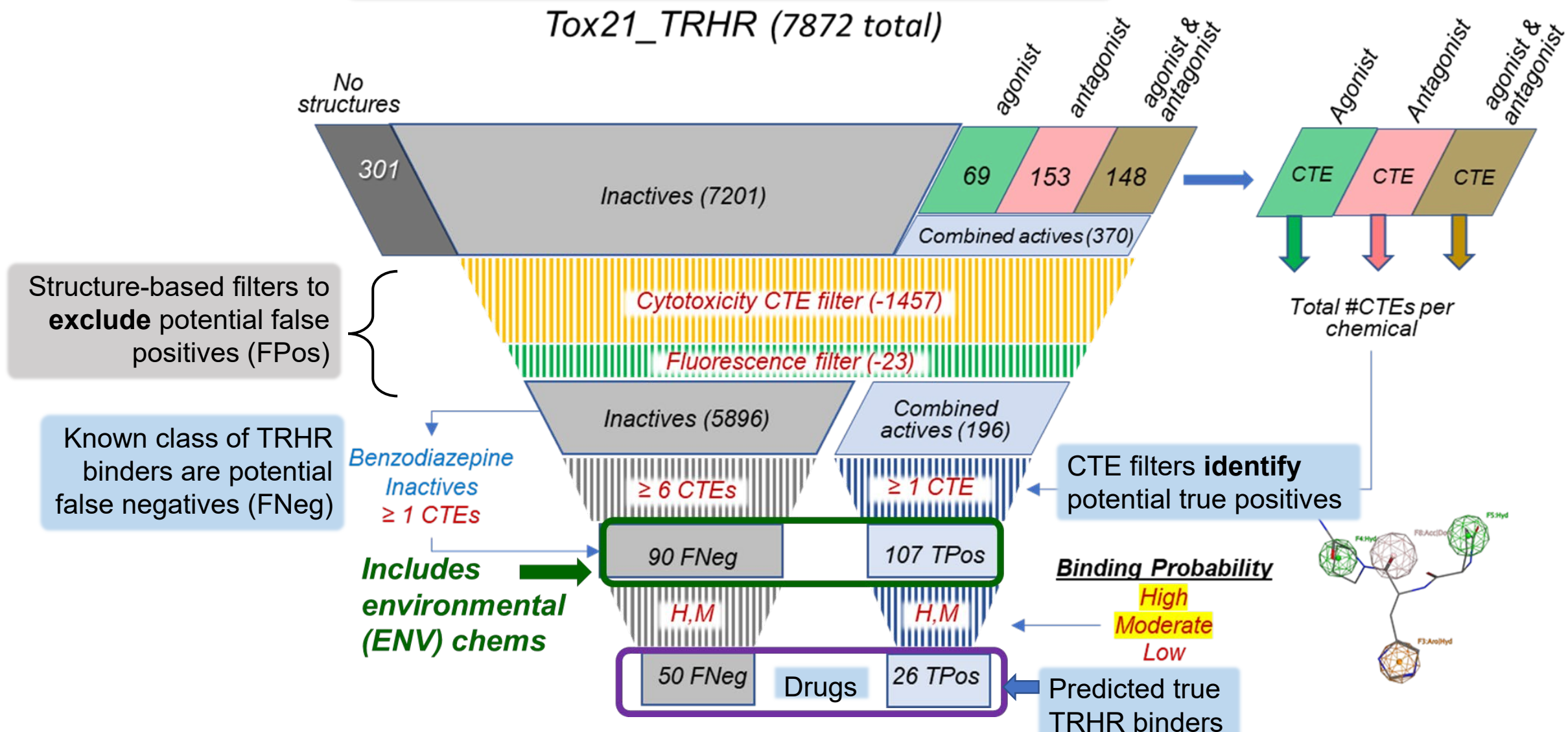


Sample TRH-like assay
active: **Saquinavir mesylate**

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Results: Structure-based prioritization workflow

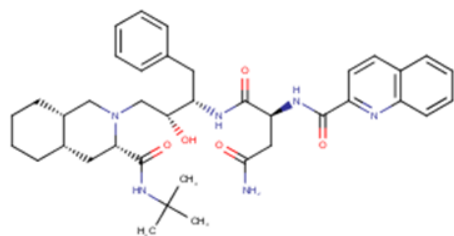


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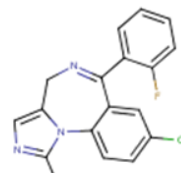
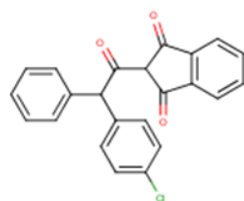


Recommendations for future testing

Drug TPos

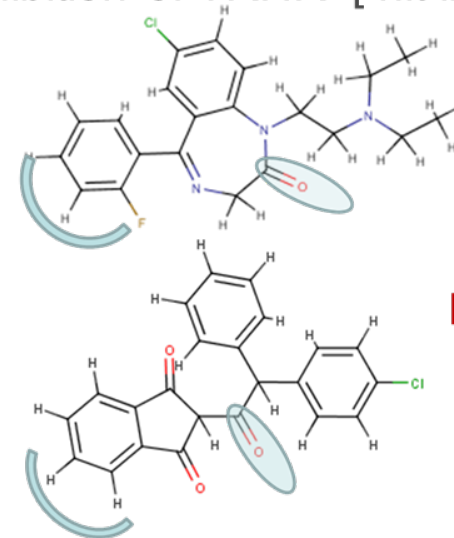


ENV TPos



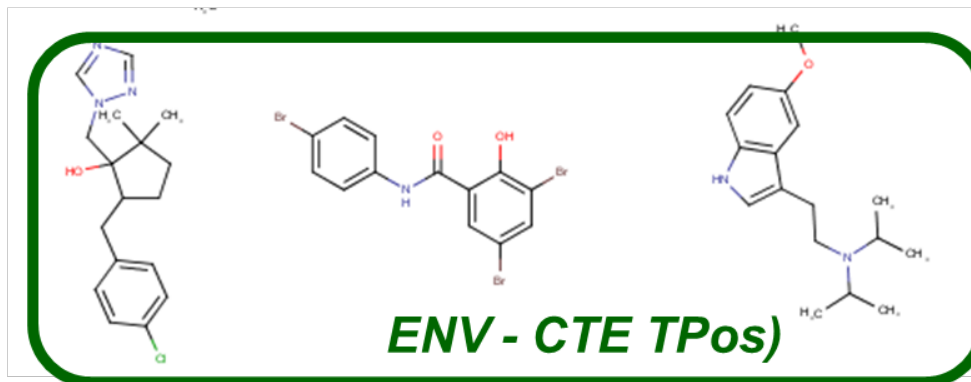
H,M Binders (left to right): saquinavir, chlorophacinone and midazolam

Chlorophacinone (no CTE) has structural features associated with Benzodiazepine inhibition of TRHR [hit in 5 models]



TRHR antagonist
DTXSID1023071

DTXSID2032348



ENV - CTE TPos

- **Chlorophacinone** predicted to be High binder but did not contain enriched CT for agonist or antagonist model;
- After filters and CTE analysis 3 environmental chemicals (left to right) – **Metconazole, Tribromsalan, 5-Methoxy-N,N-diisopropyltryptamine** – are predicted to be TPos;
- Recommend follow-up testing of the limited set of ENV TPos to substantiate TRHR or TR-related activity predictions.

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Results Summary

- 3D pharmacophore modeling and domain knowledge predict small set of mostly drugs to be high probability binders to TRHR (not all are active in Tox21_TRHR assay)
- Structure-based tiered workflow led to a 4-fold reduction in the number of predicted true positives for Tox21_TRHR assay, which included some environmental chemicals of potential concern for follow-up testing
- Environmental chemicals in this set are predicted to be low probability or weak receptor binders but with potential to impact TRHR activity

Conclusions

- In the absence of orthogonal or confirmatory assays, structure-based filtering and domain knowledge can help to filter out artifacts and identify potential true positives and false negatives in Tox21/ToxCast HTS assay results
- CTE approaches can leverage information from other Tox21 assays (e.g., cytotoxicity) and can help to isolate and amplify structure-activity signals
- A structure-based tiered workflow, such as presented here, can inform interpretation of HTS target-based assay results and can be used to prioritize chemicals for further testing

References

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3. Borre, A., Huang, R. et al. (2020) High-Throughput Screening to Predict Chemical-Assay Interference. *Sci Rep* 10, 3986 (2020). <https://doi.org/10.1038/s41598-020-60747-3>
4. Kaur, N., Lu, X. et al. (2005). Thyrotropin-releasing hormone (TRH) analogues that exhibit selectivity to TRH receptor subtype 2. *J. Med. Chem.*, 48(19), 6162–6165. <https://doi.org/10.1021/jm0505462>