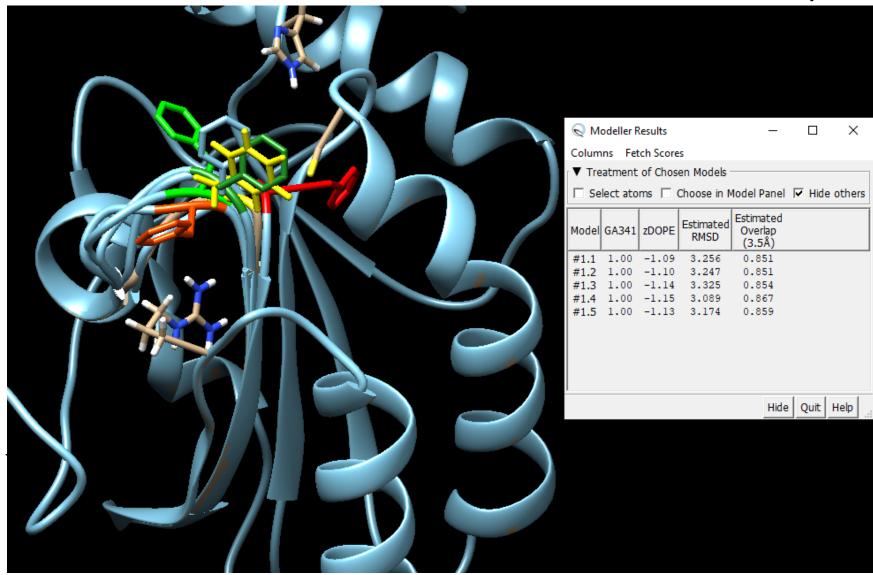
Human DIO3 cross-species-based site-directed mutagenesis modeling & docking

US EPA Great Lakes Toxicology and Ecology Division (GLTED) Bioinformatics Team

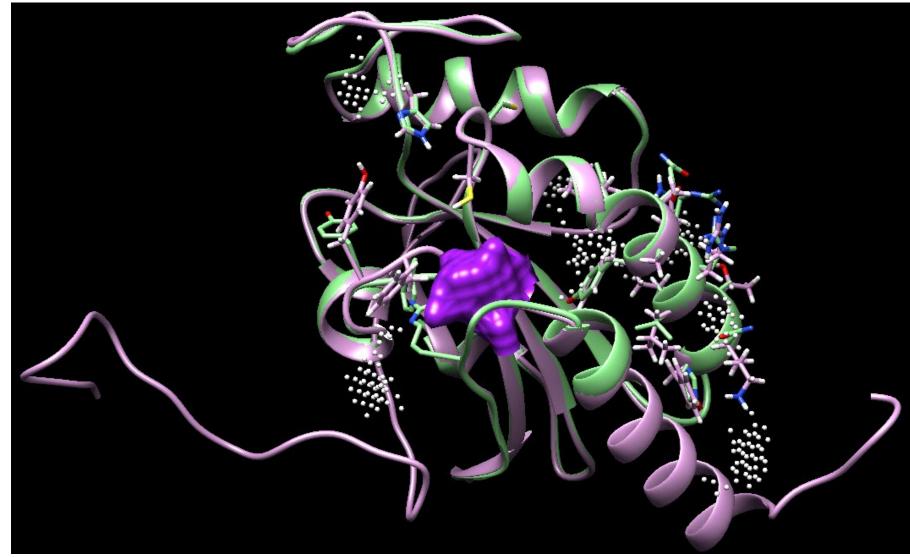
- **Purpose:** Empirical in vitro chemical screening across the human type 3 iodothyronine deiodinase (hDIO3) mutants will provide a hierarchy of chemical binding affinity based on IC50.
- This data will be compared with results of virtual docking of the same set of chemicals to molecular models of the hDIO3 wildtype and in silico mutated protein sequences to test the accuracy of virtual docking pipeline strategies.
- The comparison is also intended to provide a proof-of-concept demonstrating validity of modeling and virtual chemical screening of protein homologs across species.

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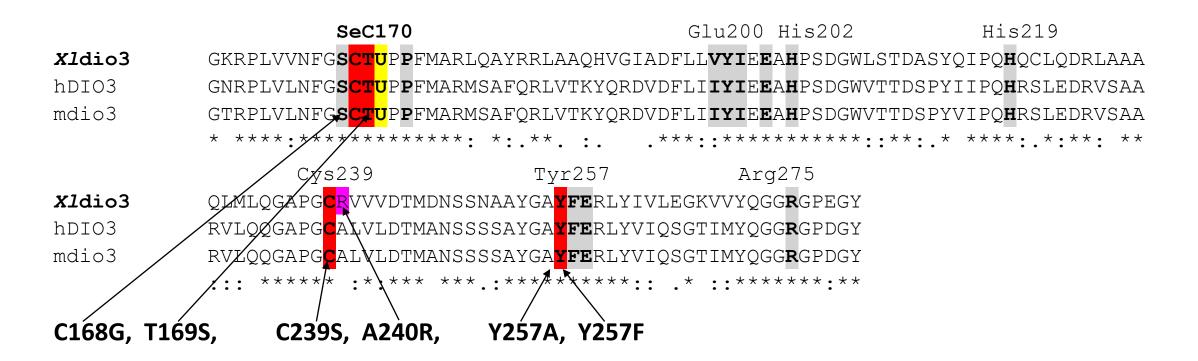
• I-TASSER→Chimera with MODELLER to remodel loops



- POCASA and FTMap to identify pockets and cavities
- Chimera/Autodock Vina

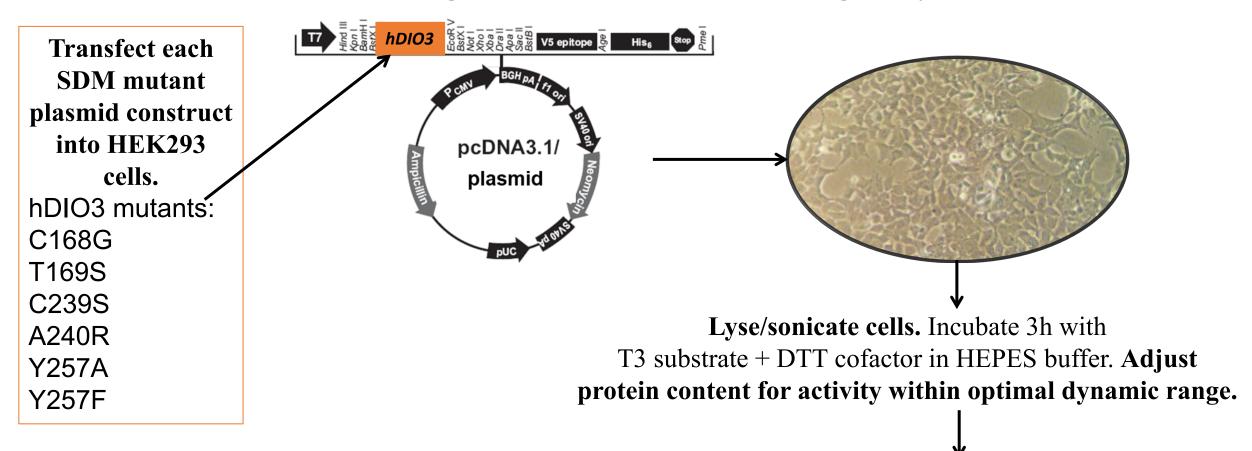


Selected mutations and cross-species dio3 sequence comparison



Plasmids with hDIO3 gene inserts synthesized by GenScript each have a single mutation.

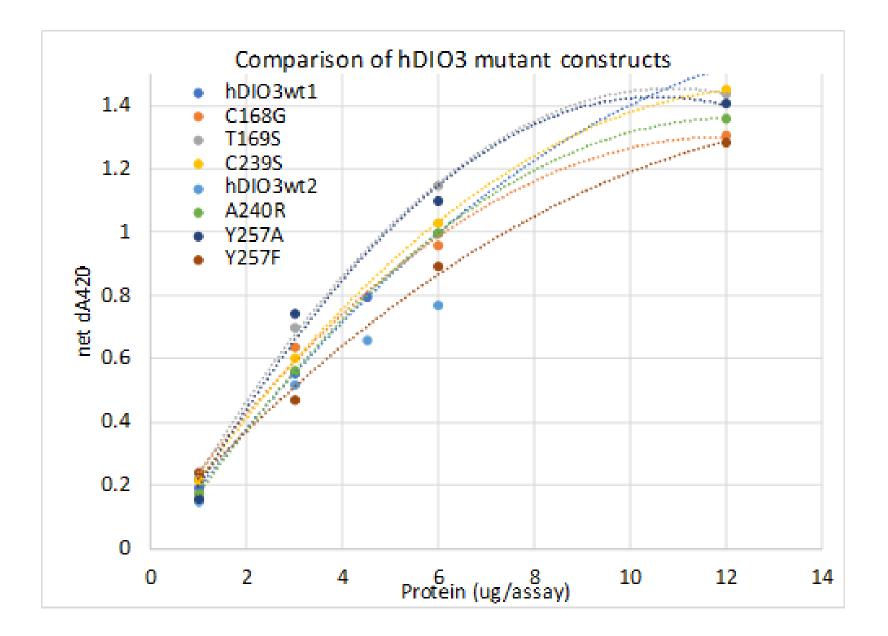
Test mutants using deiodinase in vitro screening assay



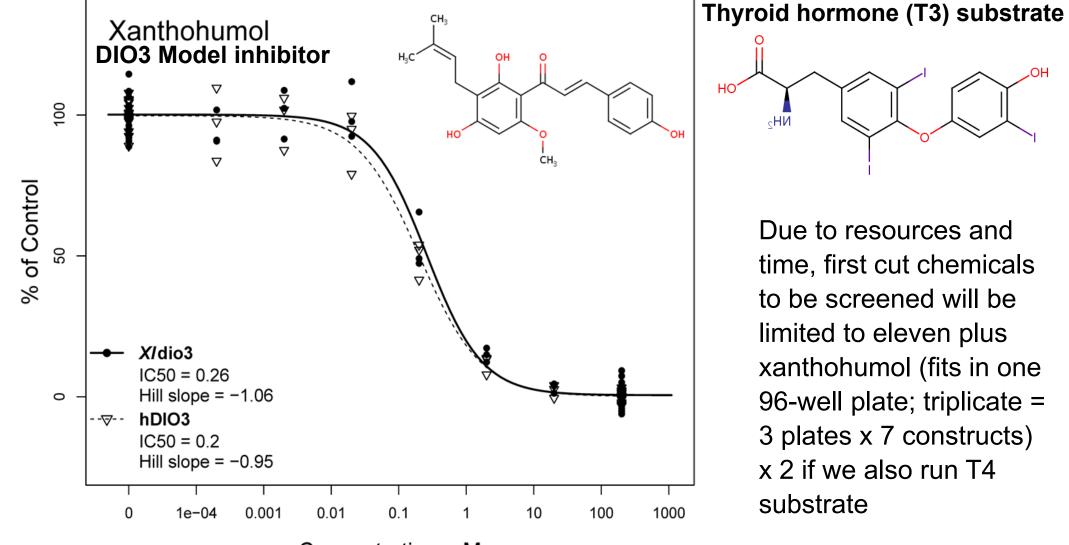
Sandell-Kolthoff assay

detect free iodide at absorbance of 420 nm in a 96-well plate reader.



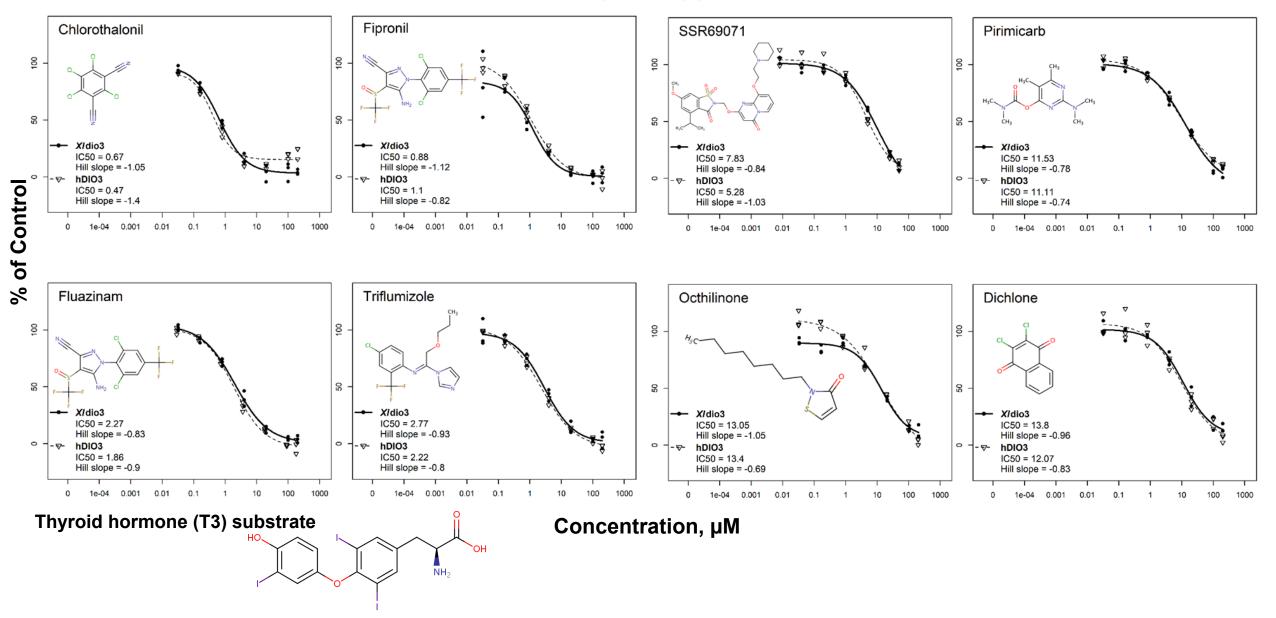


SDM chemicals to be selected from previous in-vitro hDIO3 and Xenopus dio3 screening of environmental chemicals



Concentration, µM

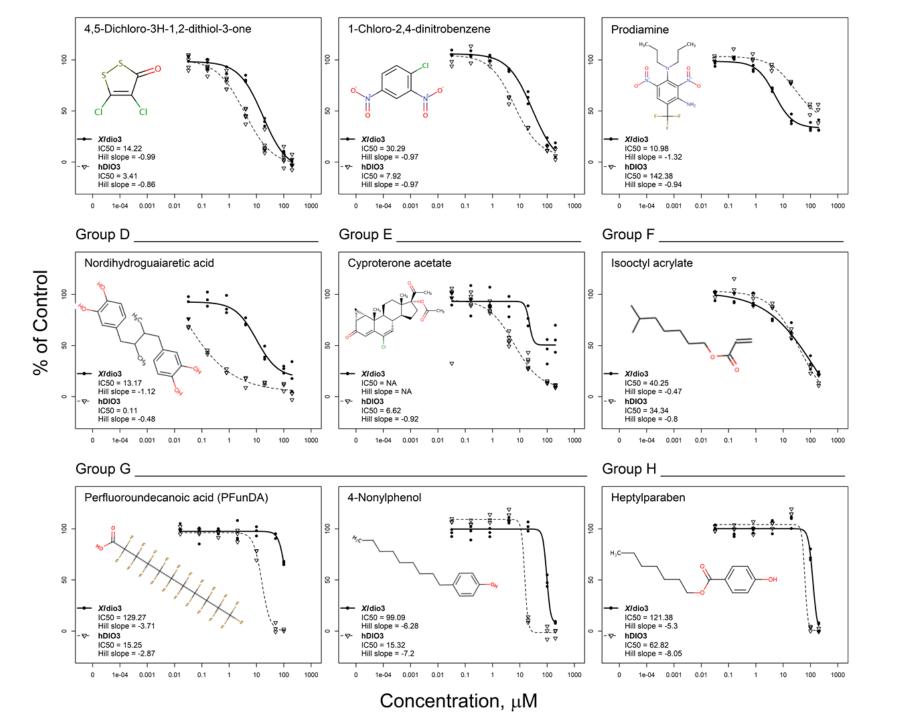
Potential specific, competitive inhibitors of human and Xenopus type 3 deiodinase



Example concentrationresponse curves with potential artifacts due to aggregates, micelles or precipitation in the assay, indicated by curve shape:

- steep slope
- incomplete inhibition

This gives us a basis for eliminating chemicals that are likely causing artifacts from consideration for the mutant *in vitro* screening.



Will virtual screening help distinguish between differences in IC50 due to structure vs assay artifact?

