

University of Parma



3D molecular modelling meets toxicology A useful tool to investigate the TD and TK of food related toxicants

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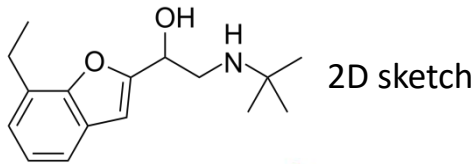
Terms of Reference

3D molecular modeling techniques refers to computational methods allowing to study the interaction between small molecules and biological (macro)molecules from a molecular standpoint

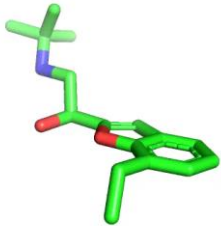
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PubChem

<https://pubchem.ncbi.nlm.nih.gov>



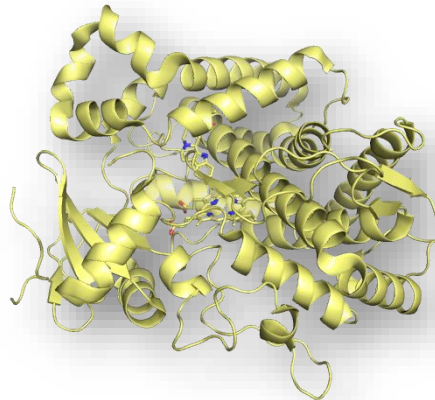
3D structure



②

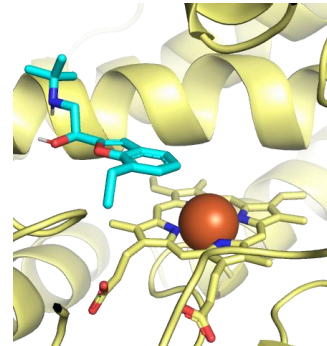
RCSB PDB
PROTEIN DATA BANK

<https://www.rcsb.org>



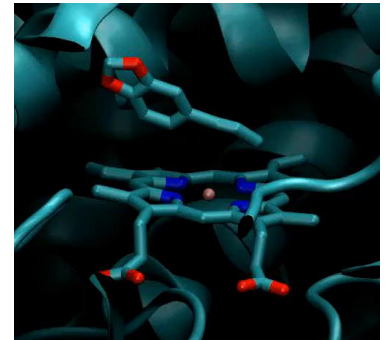
③

Simulate the binding event



④

Check the stability over time

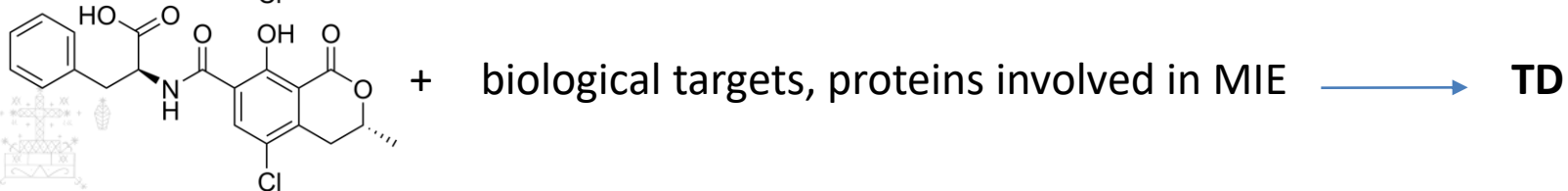
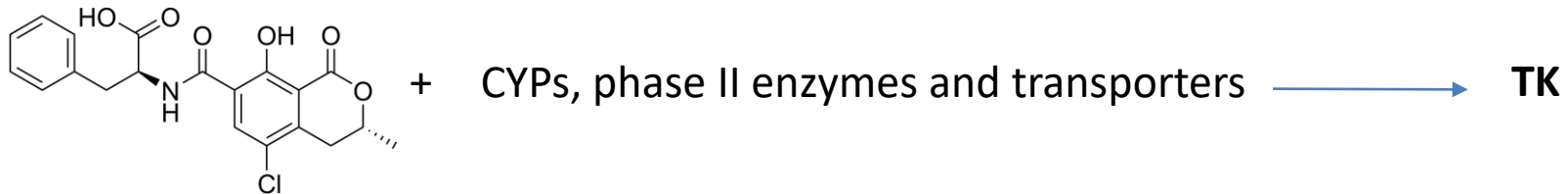


How to tackle TK and TD

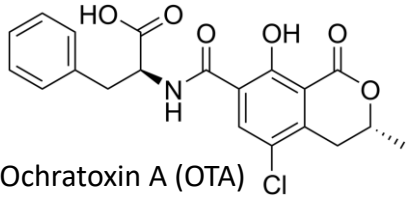


3D modeling studies the interaction between small molecules and proteins

The type of protein under investigation switches the focus on TK or TD



Addressing Ochratoxin A TK

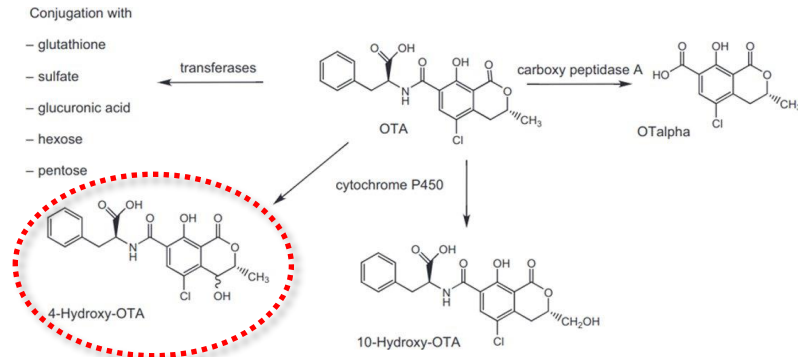


Rapidly absorbed after oral ingestion with a bioavailability ranging from 40% to 66% depending on the species and the dose

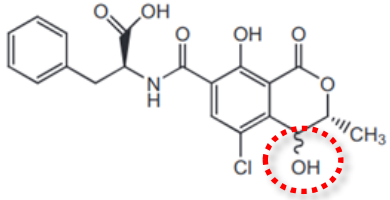
Extensively bound to albumin and other serum proteins (up to 99.98% in humans)

In humans and monkeys prevails renal excretion involving Organic Anion Transporters (OATs)

Biotransformation of OTA appears to be low and mostly limited to hydrolysis of the amide bond to form OTalpha *in vivo*



Addressing Ochratoxin A TK

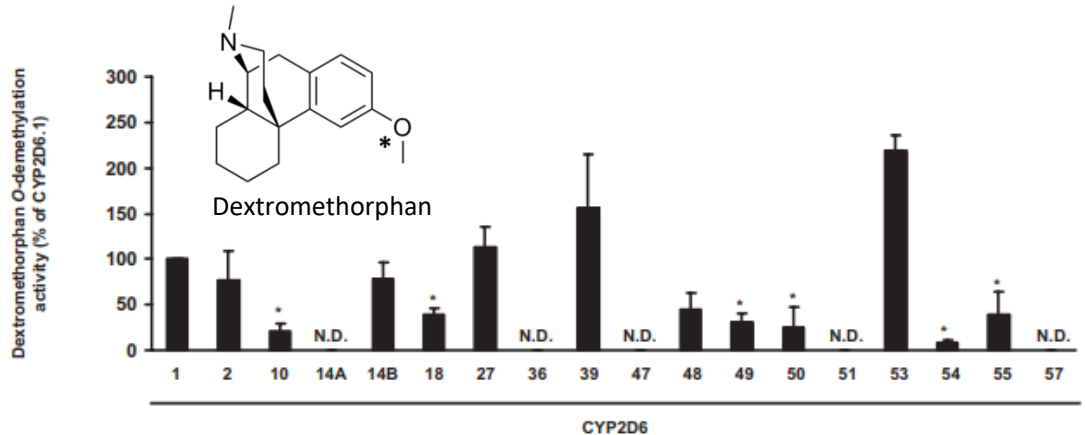


Described *in vitro* and *in vivo* as a minor metabolic route

Less toxic than OTA, unclear the effects of 4-OH on OTA's TK and TD

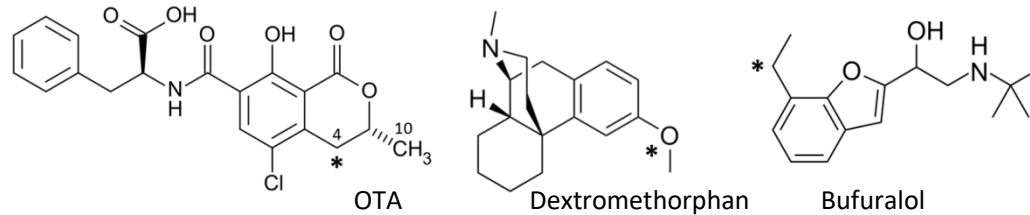
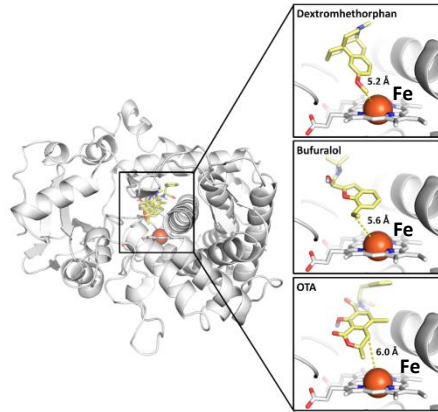
CYP2D6 together with CYP2B6 have been shown to be involved in the formation of 4-OH-OTA

CYP2D6 is highly polymorphic, and polymorphism may change drastically change the transformation of given substrates



Is there any CYP2D6 polymorphism with an altered capability to form 4-OH-OTA?

A computational workflow was setup to estimate the capability of CYP2D6 polymorphisms to transform probe substrates



* Atom undergoing the reaction

The atom undergoing the reaction must be closely and stably oriented toward the Fe-Heme ¹

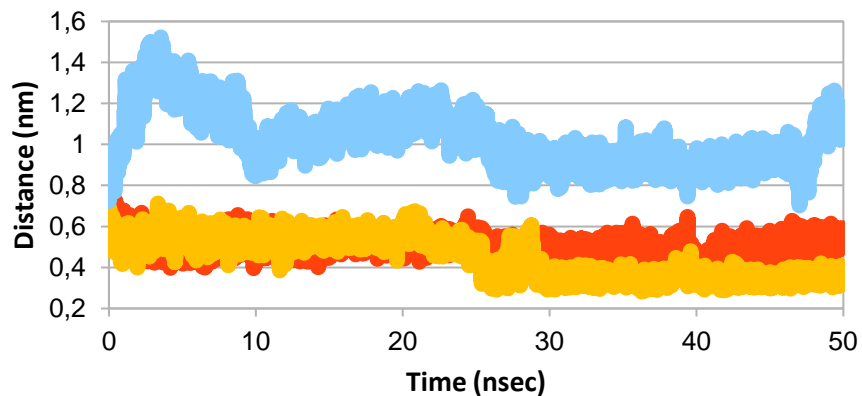
Molecular modeling could estimate the likeliness of molecules to be transformed monitoring their geometry of binding to Fe-Heme

Molecular modeling may estimate whether the residue substitution of CYP polymorphisms may influence the proper orientation of molecules to undergo the reaction

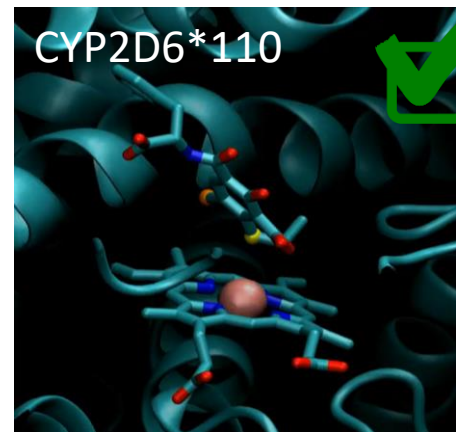
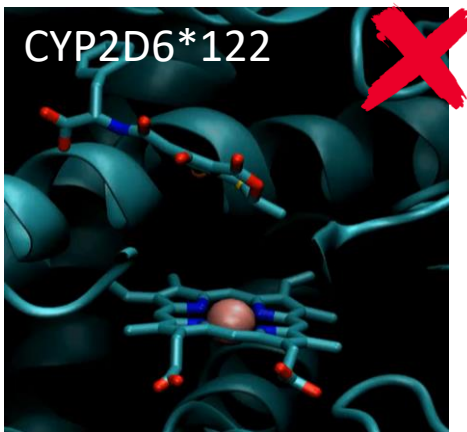
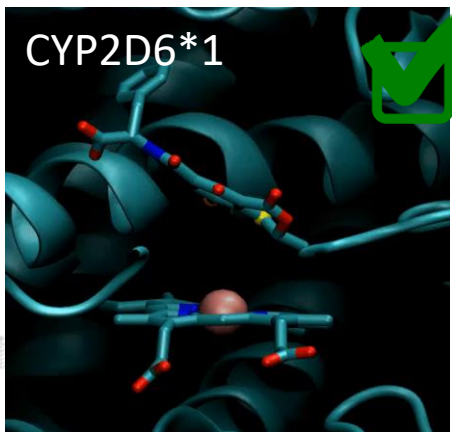
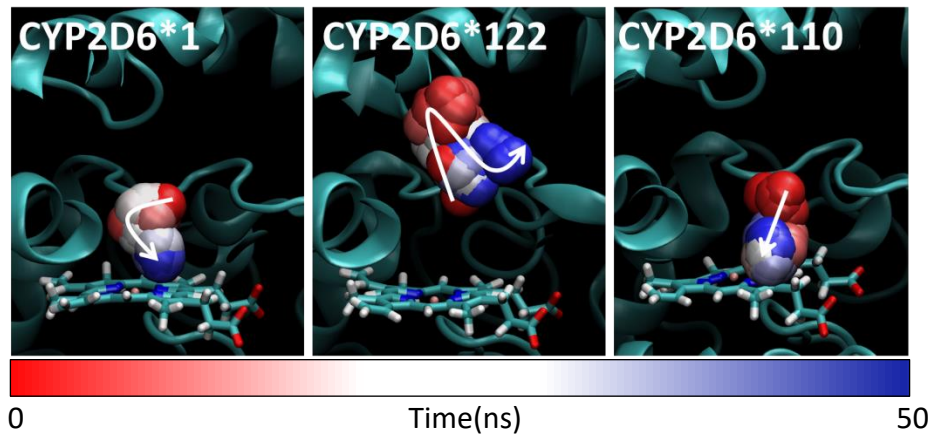
¹ Xu and Chen, 2020. Sci. Rep. 10, 1–14



Polymorphisms from Pharmacogene Variation Consortium (PharmVar; www.pharmvar.org)



— OTA in CYP2D6*1 — OTA in CYP2D6*110 — OTA in CYP2D6*122

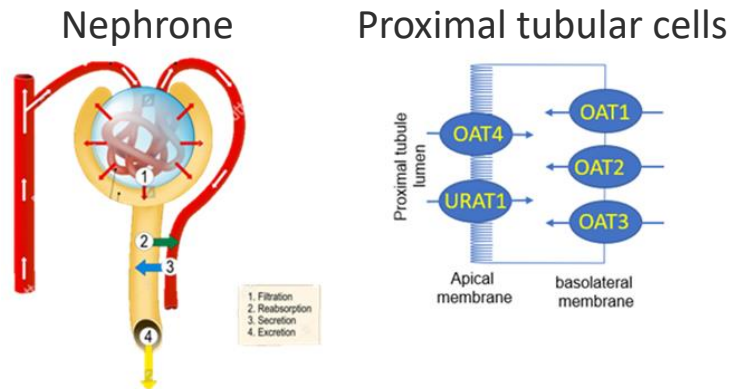


Is there any mutated transporters with an altered capability to transport OTA?



Investigating the interaction between organic anion transporter 1 and ochratoxin A: An *in silico* structural study to depict early molecular events of substrate recruitment and the impact of single point mutations

Jochem Louisse^a, Jean Lou C.M Dorne^b, Luca Dellafiora^{c,*}

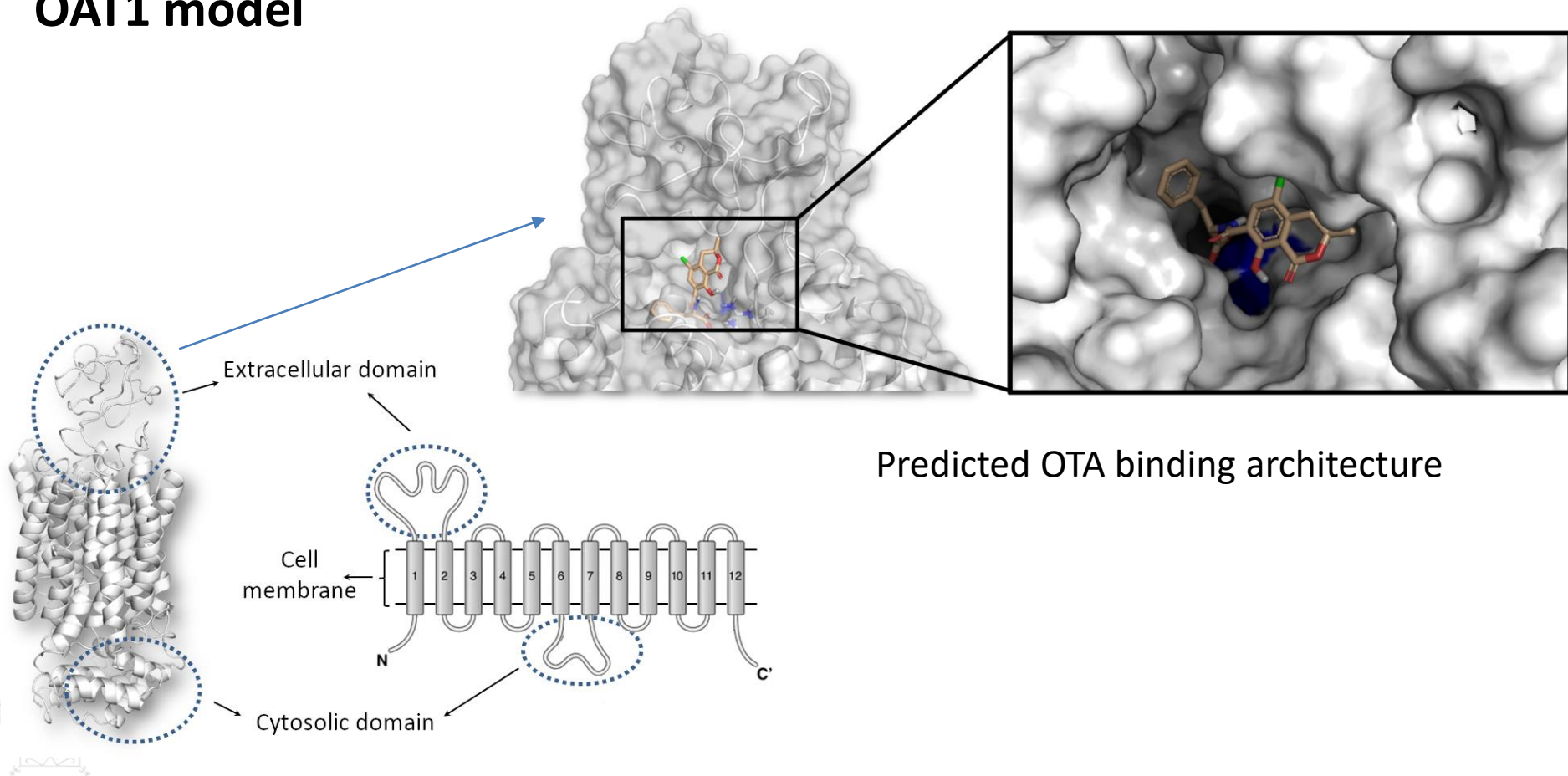


The excretion pathway of OTA via urine involves OAT1, OAT2 and OAT4

OAT1 has the highest affinity, and a prominent role has been inferred accordingly

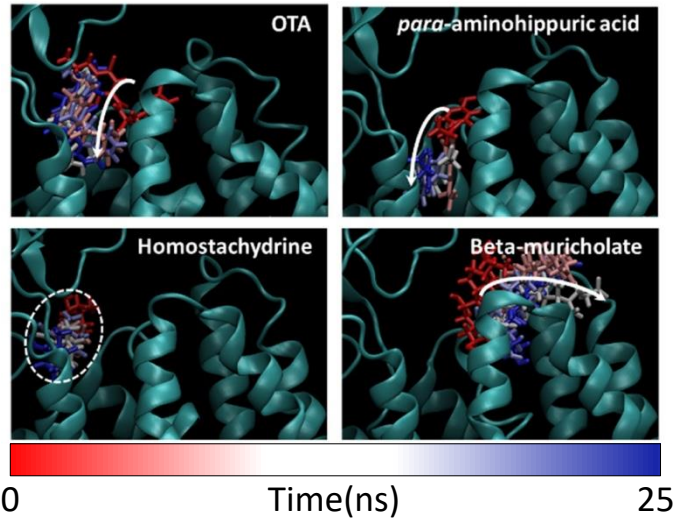


OAT1 model

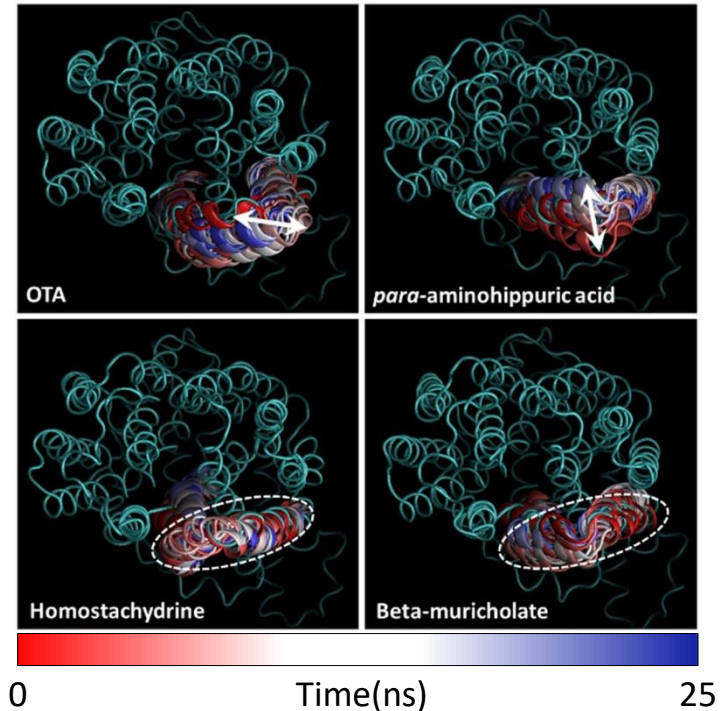


Assessment of OAT1 model reliability

OAT1 was found to open when bound to probe substrates like OTA and p-amminohippuric drawing an inward trajectory, while it laid closed bound to non-substrates (like homostachydrine and beta-muricholate)



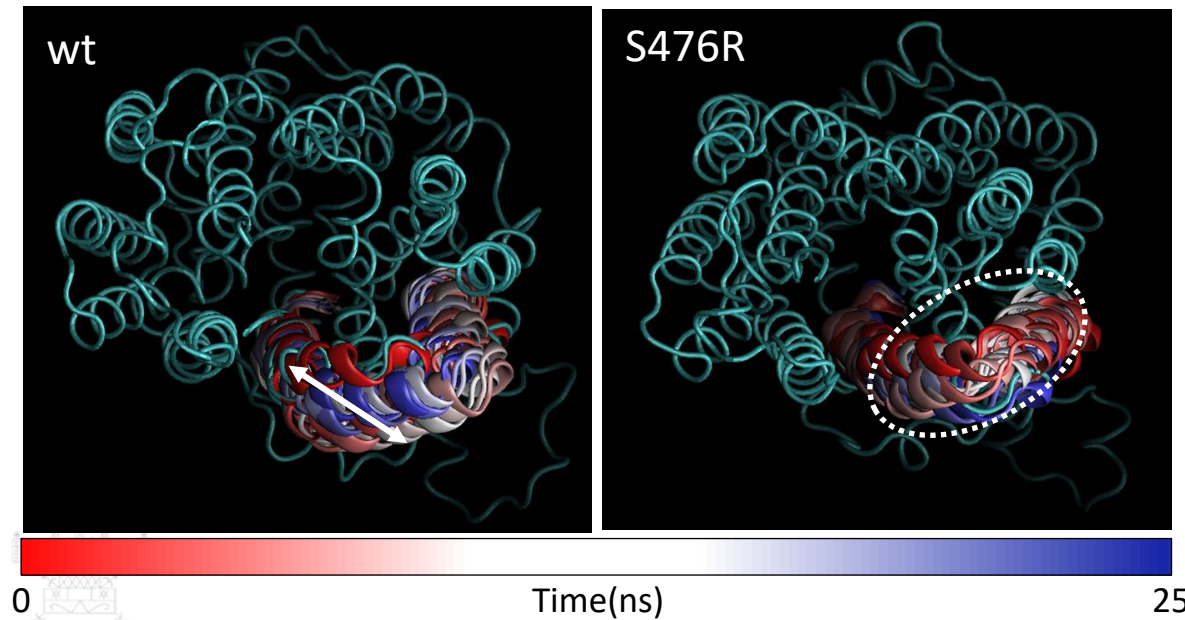
Geometrical features and ligand trajectories could be used to distinguish transported substrates from non-substrates



A set of OAT1 mutations found occurring in the human population have been investigated

Mutated variants were retrieved from BioMuta DB¹ that collects mutations occurring in cancer

The analysis focused on mutations surrounding the calculated OTA initial binding site: S476R, R423P, D359N, Q361K, and E480K



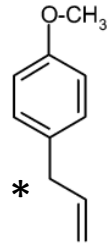
S476R may hinder OAT1 opening, reducing the transmembrane transport of OTA

S476R bearing subjects may show differences in OTA TK

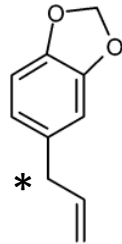


Addressing the bioactivation of alkenylbenzenes

Preliminary results



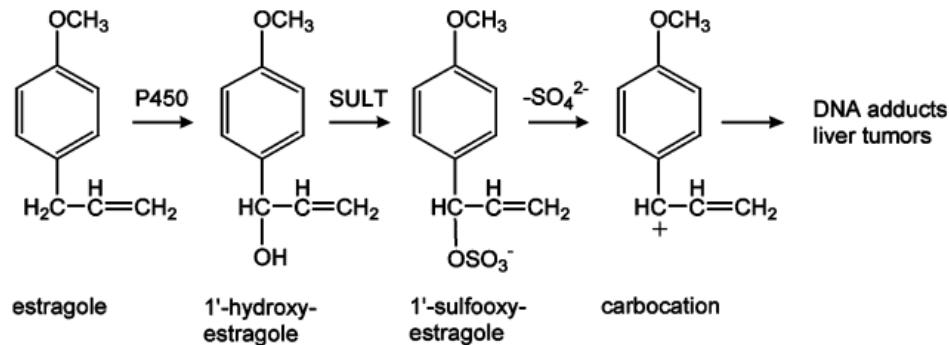
estragole



safrole

enzyme	enzyme efficiency k_{cat}/K_m ($\text{min}^{-1} \text{mM}^{-1}$)	
	estragole	safrole
P450 1A2	59	ND ^a
P450 2A6	341	160

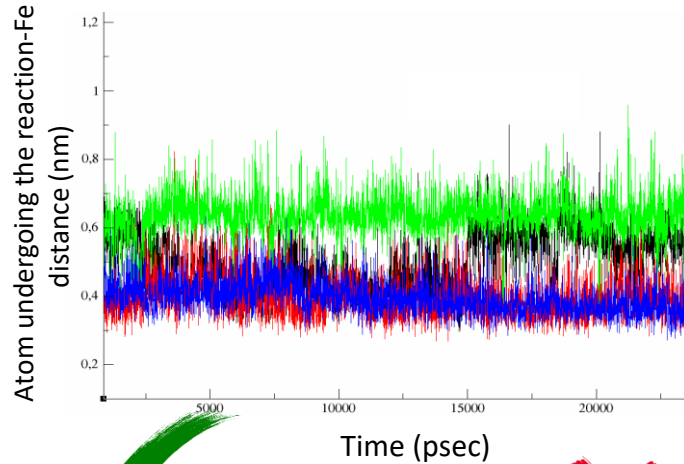
The CYP-dependent oxidation at the * position to form hydroxylated derivatives is important to activate compound toxicity



Addressing the bioactivation of alkenylbenzenes

Applying the rule described for OTA-CYP2D6 we can distinguish substrates from non substrates

enzyme	enzyme efficiency k_{cat}/K_m ($\text{min}^{-1} \text{mM}^{-1}$)	
	estragole	safrole
P450 1A2	59	ND ^a
P450 2A6	341	160



Alkenylbenzenes may be present in feed

Animal CYPs homologues to human CYP1A2 and CYP2D6 were screened for their theoretical efficiency to transform safrole

The study focused on: rat, mouse, dog, rabbit, pig, chicken, goat and sheep

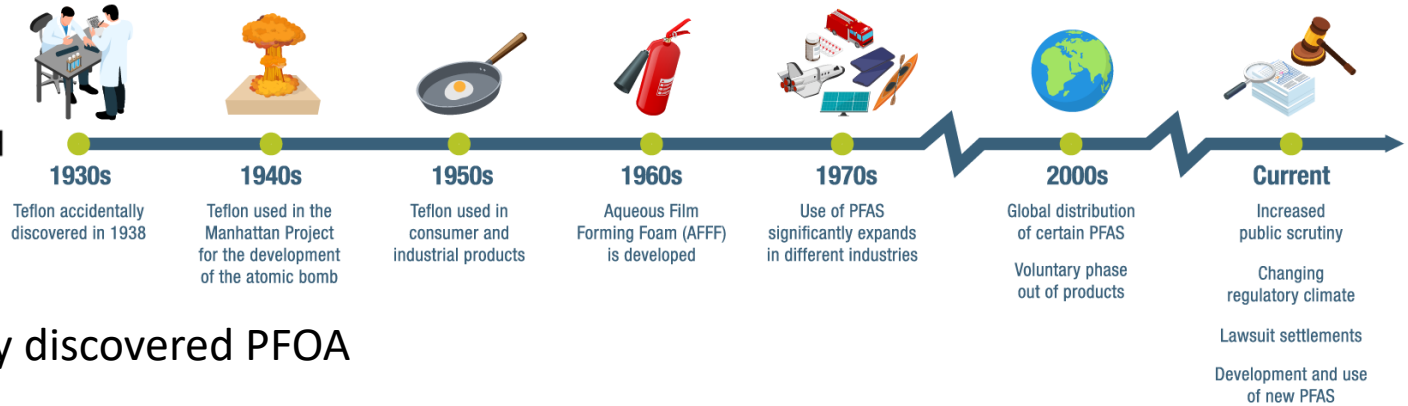
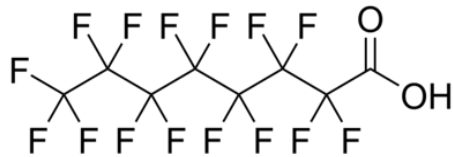
enzyme	enzyme efficiency k_{cat}/K_m ($\text{min}^{-1} \text{mM}^{-1}$)	
	estragole	safrole
P450 1A2	59	ND ^a
P450 2A6	341	160

Safrole in animal homologues to human CYP2A6 showed a worse interaction compared to human suggesting a lower yield of transformation (lower toxicity?), with the exception of sheep and goat where the interaction was similar to that within human CYP2A6

Safrole in animal homologues to human 1A2 showed a better interaction compared to human suggesting a higher yield of transformation (higher toxicity?), with the exception of pig where the interaction was similar to that within human CYP2A6

Addressing the transport of PFAS

Polyfluoroalkyl substances (PFAS)



1947: USA, 3M firstly discovered PFOA

1949: USA, 3M started producing PFOA and PFOS

1950: First use in Teflon

1950-2000: PFOA and PFOS have been used in many applications

2000: USA, 3M ended producing long chain PFAS (like PFOA and PFOS)

Today: PFAS are super resistant food and environmental contaminants

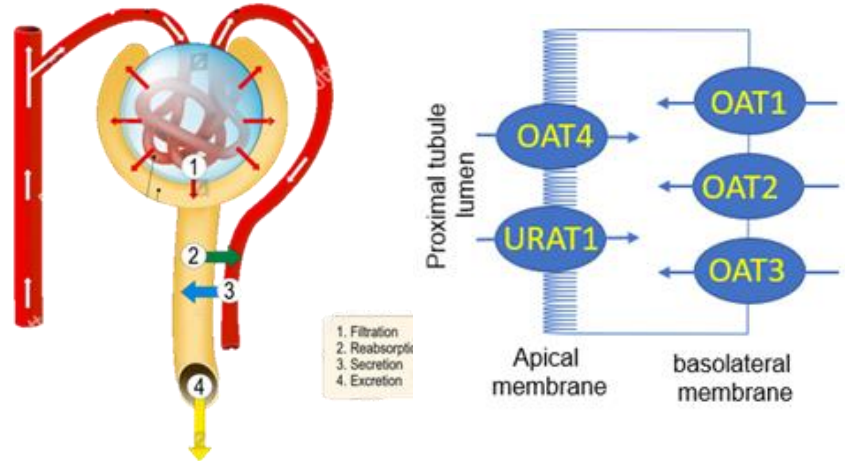
Effects of PFAS on living organisms

They disrupt peroxisome activity, lipids metabolism, reproductive and nervous system, liver functionality

PFAS	Chain carbon number	Half-life based on literature
PFHpA	7	1.2 years
PFOA	8	2.7 years
PFNA	9	4.3 years
PFDA	10	9.2 years

Some information on PFOA:

- Active reabsorption possible via OAT4 and URAT1
- Active excretion may play a role as well via OAT1/OAT2/OAT3



3D modelling may help shading light on TK/TD of PFAS

Most of PFAS need to be characterized in this sense!



Addressing the transport of PFAS

3D molecular modeling integrated to experimental trials to provide more insights into the transport of PFASs by OAT4 and URAT1

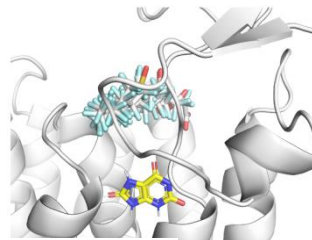
Preliminary results

Docking scores of PFAS and probe substrates of URAT1 and OAT4

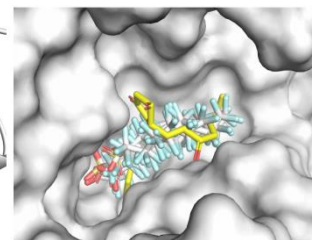
Compound	OAT4		URAT1	
	Score (kcal/mol)	Substrate	Score (kcal/mol)	Substrate
PFHpA	-6.1	Yes	-5.5	No
PFOA	-6.2	Yes	-6.0	No
PFNA	-6.8	Yes	-6.6	No
PFDA	-7.1	Yes	-6.7	No
PFHxS	-6	Yes	-7.3	No
PFOS	-7.3	Yes	-6.8	No
PFBS	-5.5	No	-4.9	No
Uric acid	---	---	-6.6	Yes
Prostaglandin E2	-6.2	Yes	---	---

Docking poses and MD results

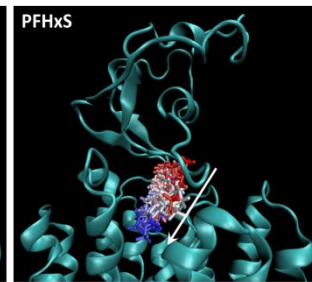
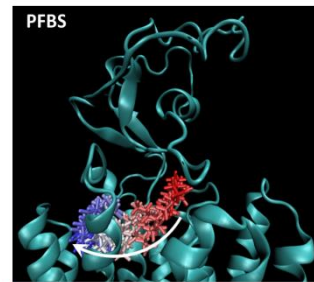
URAT1



OAT4



OAT4



0

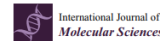
Time (nsec)

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Take home message

3D molecular modeling may investigate the interaction between toxicants and TK actors

Analysis has been already successfully applied to SULTs and serum transporters



Article

Interaction of Mycotoxin Alternariol with Serum Albumin

Eszter Fliszár-Nyuj^{1,2}, Beáta Lemli^{2,3}, Sándor Kunsági-Máté^{2,4}, Luca Dellaflora⁵, Chiara Dall'Asta⁵, Gabriele Cruciani⁶, Gábor Pethő^{1,7} and Miklós Póór^{1,2,*}

The approach may provide useful means to broadly study TK-related aspects of small molecules toxicology to:

- Achieve a more informed understanding of molecular basis underpinning toxicants action
- Predict toxicokinetics of poorly studied compounds and/or in scarcely characterized species

May provide useful mechanistic insights either to refine other modeling techniques or to informedly plan further experiments

Thanks for your attention!



More details of related works @:



Further info: luca.dellafiora@unipr.it



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