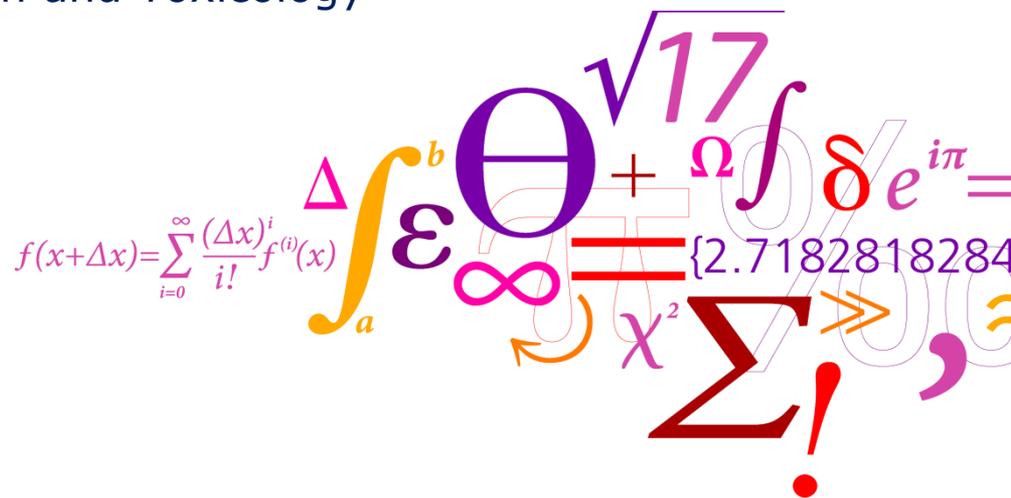


Development of computer models to predict chemicals interference with thyroid hormones

3R symposium 2017

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Division for Diet, Disease Prevention and Toxicology



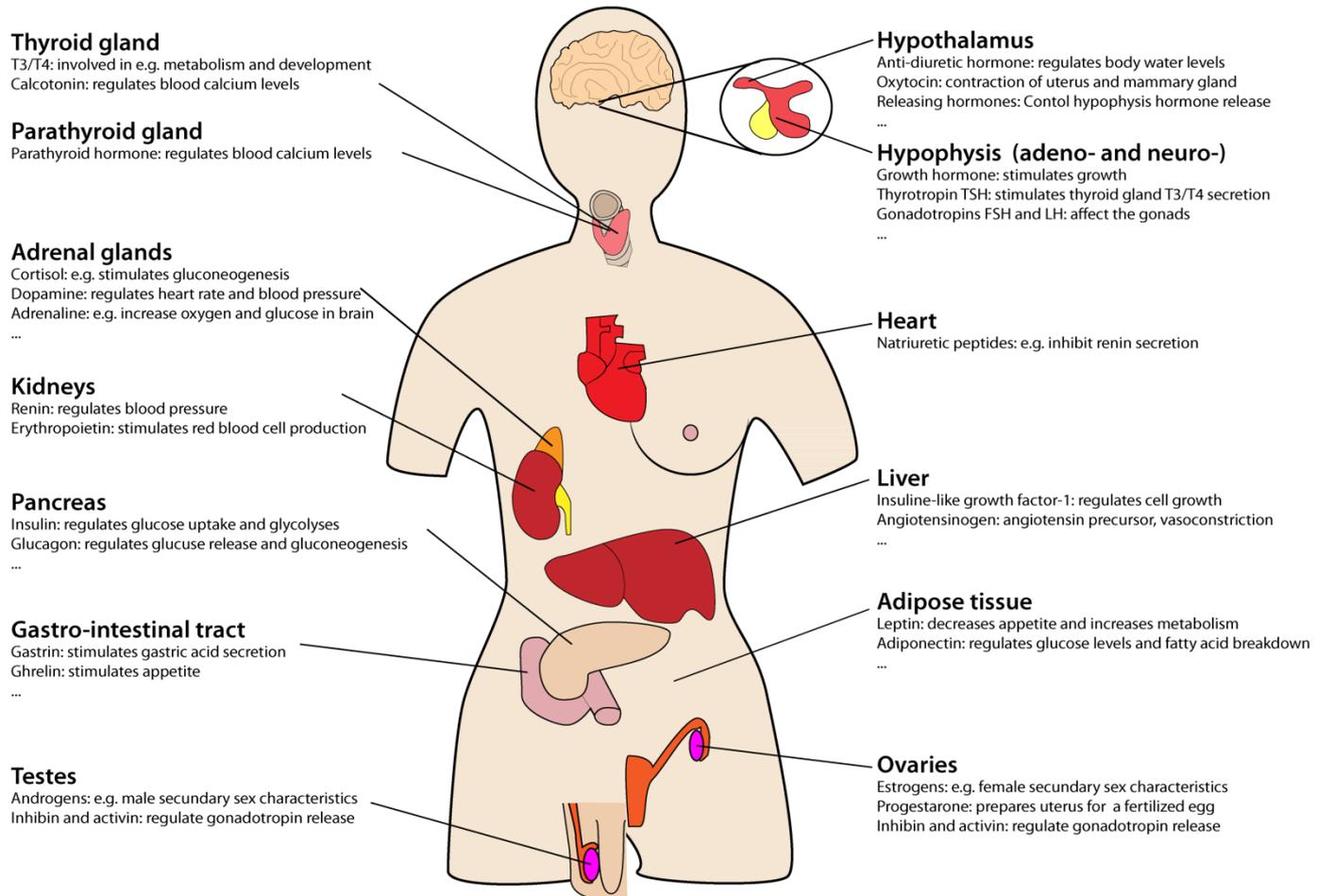
The aim of the project

- The aim of the present project was to develop **computer models** for some of the most important mechanisms known to disturb the **thyroid hormone** balance.
- The models are so-called **QSARs** (quantitative structure-activity relationships), that can predict effects of chemicals based on their **molecular structure**.

Background

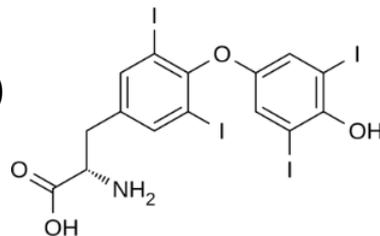


The hormone (or endocrine) system

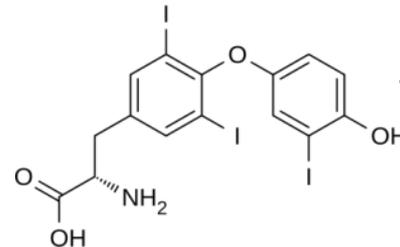


Thyroid hormones

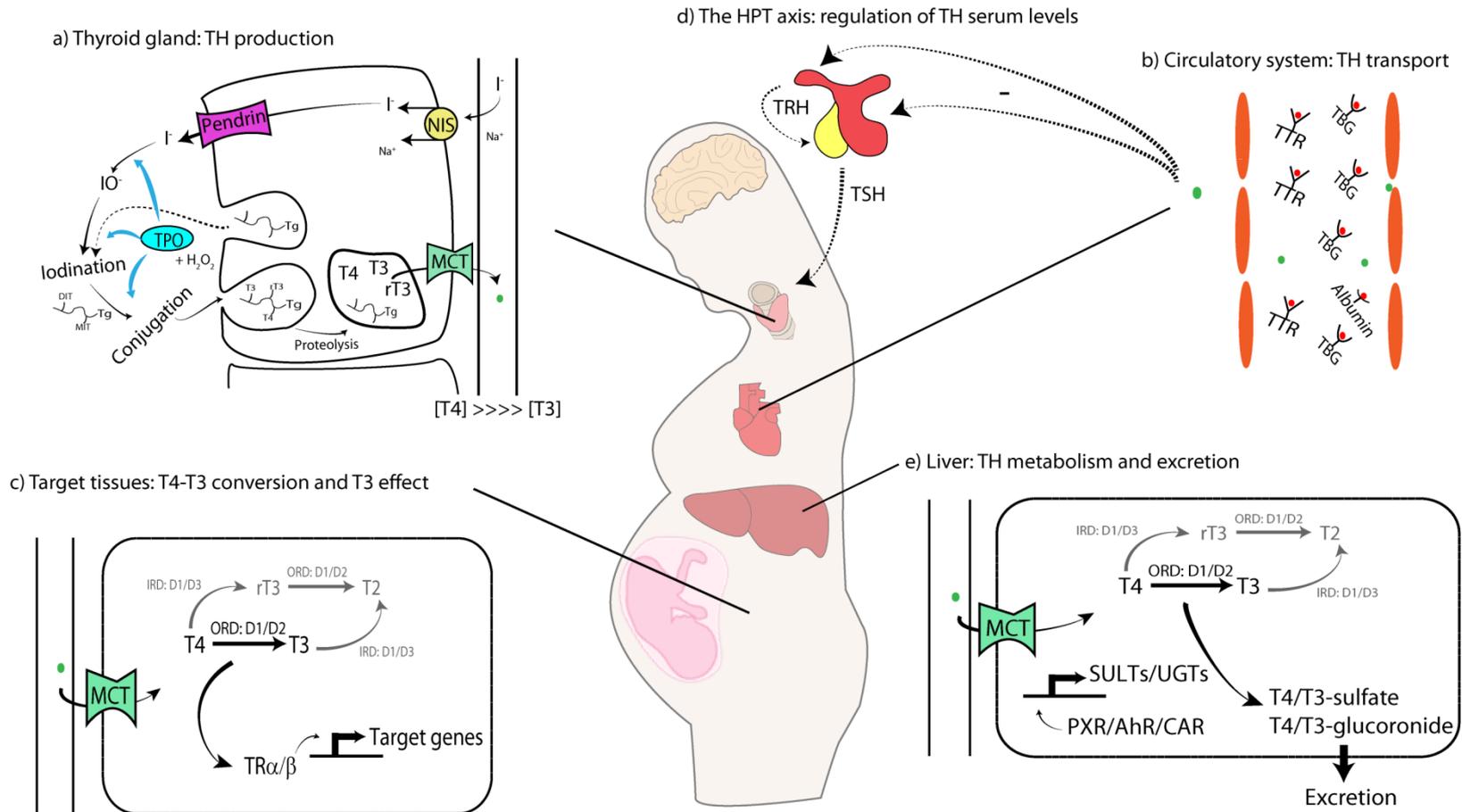
T4 (thyroxine)



T3 (triiodothyronine)

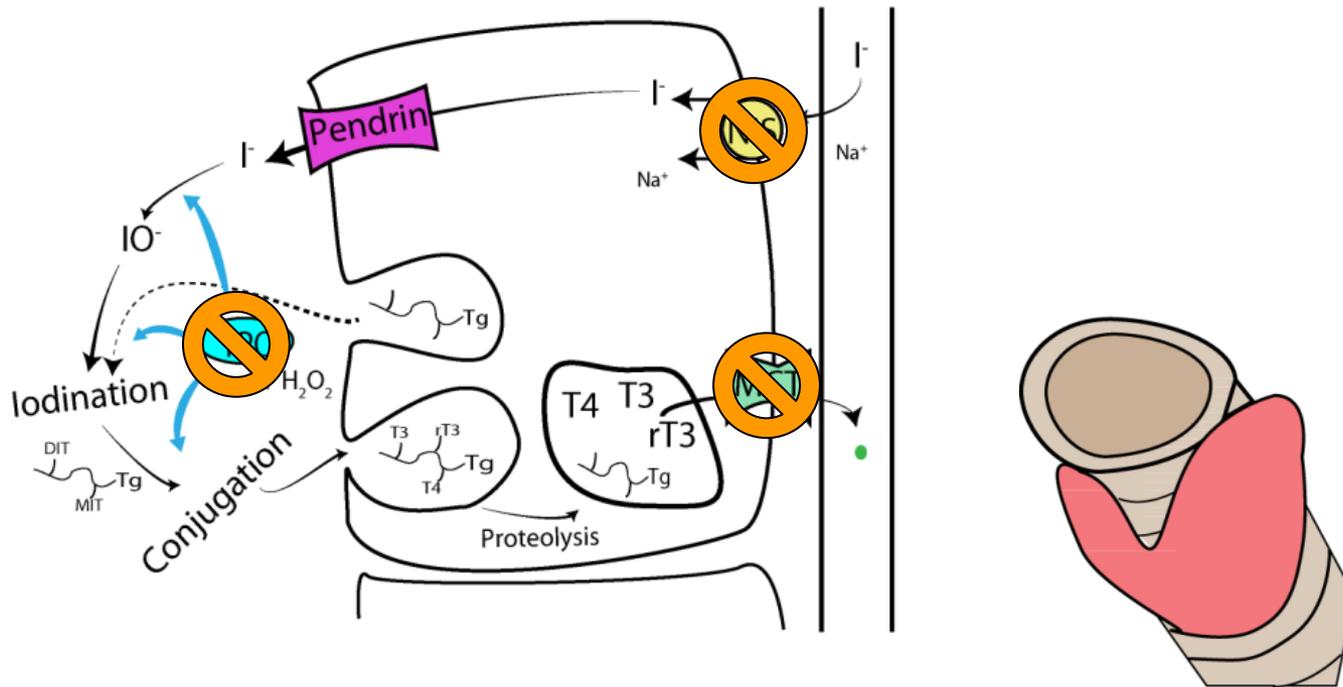


The thyroid hormone system

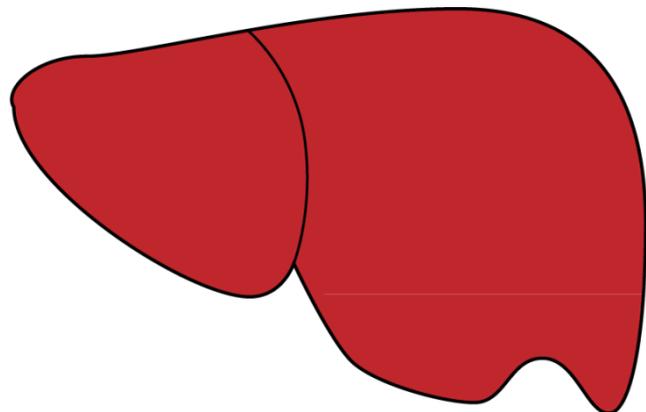


Thyroid disrupting chemicals

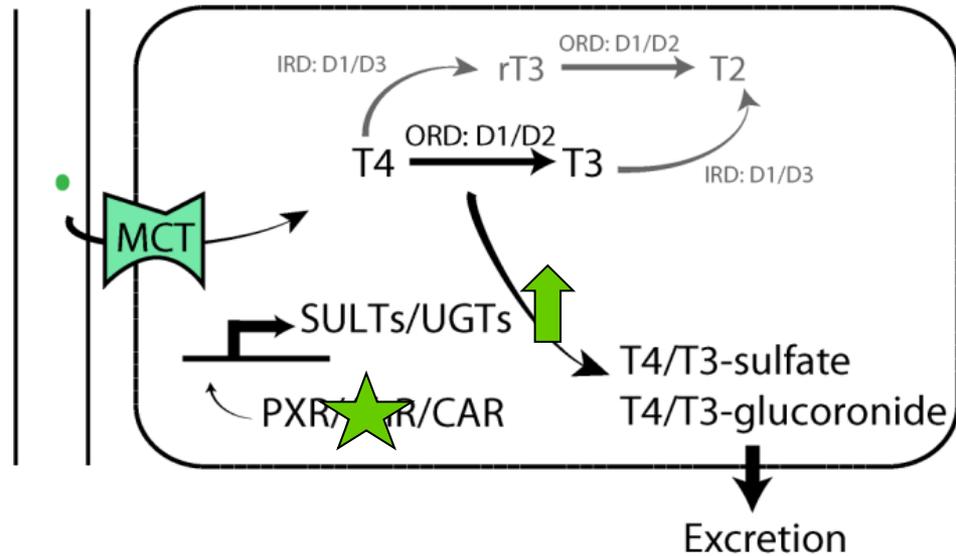
a) Thyroid gland: TH production



Thyroid disrupting chemicals



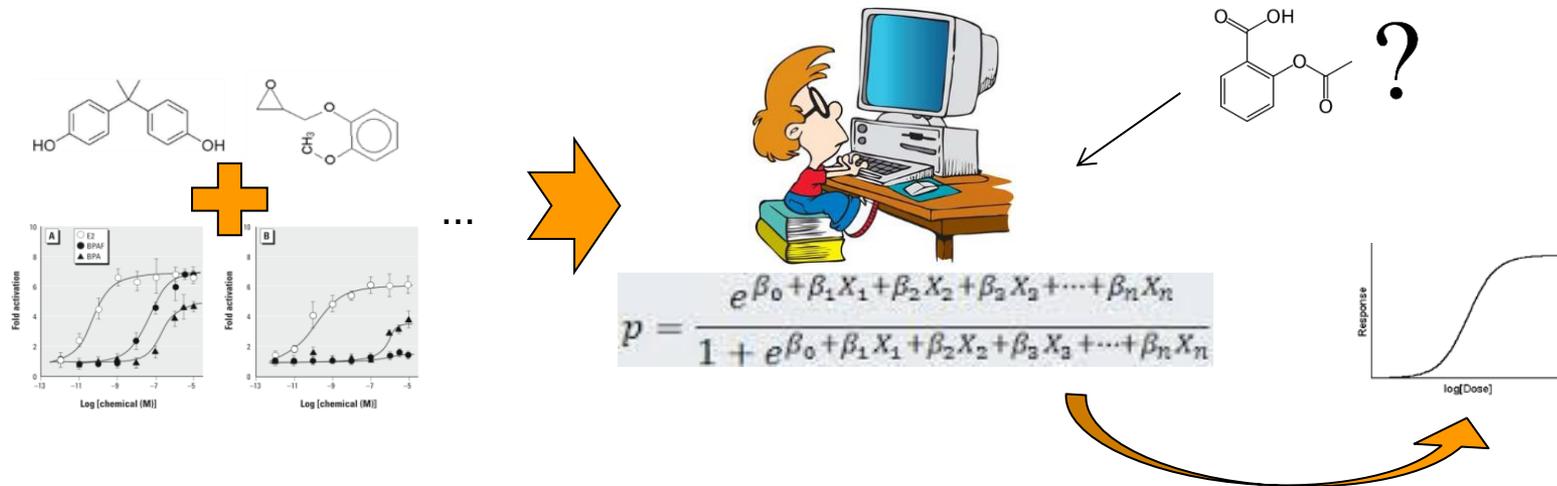
e) Liver: TH metabolism and excretion



A role for computer models

- Chemicals may interfere with the thyroid hormones in **many different ways** (hormone production, metabolism etc).
- A **battery** of test methods is therefore needed to cover all mechanisms, and this is a very resource-consuming task for the **many 1000s of untested chemicals**.
- To facilitate this task, computer models have become an important tool to **screen and prioritize chemicals** for further experimental testing, thereby reducing costs and number of test animals.

QSAR: Quantitative Structure-Activity Relationship



Assumption: the **structural similarity principle**, i.e. structurally similar chemicals exert similar properties

A **mathematical model** based on existing experimental data (training set), which relates **chemical structures** and a property →

It can **predict** the property of an **untested chemical** based on its structure information

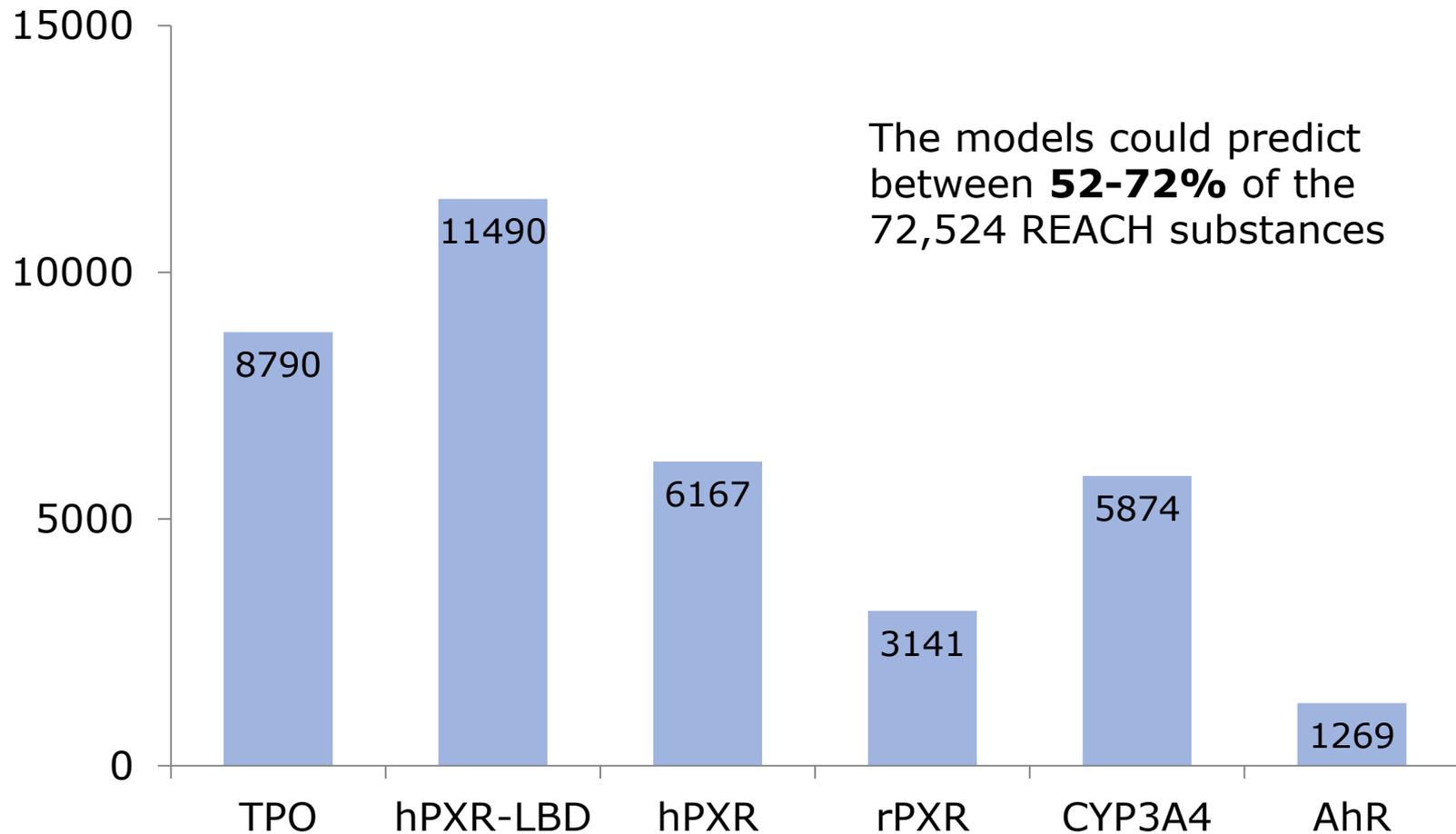
This project

Experimental data used to make the models (training sets)

Model	Total	Active	Inactive	Source
TPO inhibition	1519	230	1289	US-EPA
hPXR binding	1537	143	1394	NIH
hPXR activation	1644	207	1437	NIH
rPXR activation	1671	97	1574	NIH
CYP3A4 induction	1676	179	1497	NIH
AhR activation	4160	832	3328	PubChem

The accuracy of the QSAR models were between 75-93%, which means that the models are highly predictive

Number of REACH compounds predicted active



Danish (Q)SAR Database

The Danish (Q)SAR Database includes estimates from more than 200 (Q)SARs from free and commercial platforms and related to physicochemical properties, ecotoxicity, environmental fate, ADME and toxicity. (Q)SAR predictions for more than 600,000 chemical substances can be searched, sorting can be made on chemical similarity, and profiles for individual substances can be downloaded.

The database is developed by the National Food Institute, Technical University of Denmark, with support from the Danish Environmental Protection Agency, the Nordic Council of Ministers and the European Chemicals Agency.

[Search](#)

[User manual](#)

[Contact](#)



<http://qsar.food.dtu.dk>

Free online database

Predictions for > 600,000 compounds

>200 QSAR predictions (e.g. phys.-chem. properties, health effects)

Danish (Q)SAR Models – coming soon

- On-the-fly predictions for user-defined chemical substances in >20 models from the Danish (Q)SAR database

Danish (Q)SAR Models

powered by Leadscope Predictive Data Miner

Ministry of Environment and Food of Denmark

Leadscope®

DTU Food National Food Institute

New query User manual Model documentation About Contact
Danish (Q)SAR Database

Select models

7 models selected

- Amies test
 - Bacterial reverse mutation test (Amies test in *S. typhimurium* (in vitro))
- Other in vitro endpoints
 - Chromosome Aberrations in Chinese Hamster Lung Cells
 - Mutations in Thymidine Kinase Locus in Mouse Lymphoma Cells
 - Mutations in hprt Locus in Chinese Hamster Ovary Cells
 - Unscheduled DNA Synthesis in Rat Hepatocytes
 - Syrian Hamster Embryo Cell Transformation
- In vivo endpoints
 - Sex-Linked Recessive Lethal Test in *Drosophila m.*
 - Micronucleus Test in Mouse Erythrocytes
 - Dominant Lethal Mutations in Rodents
 - Sister Chromatid Exchange in Mouse Bone Marrow Cells
 - Comet Assay in Mouse

Input structure



Predict and download report

QSAR Results				
Model	Probability	Prediction	Report	
ER alpha binding (human in vitro), all	0.155	NEG_IN	↓	
ER alpha activation (human in vitro)	0.0186	NEG_IN	↓	
Androgen receptor antagonism (human in vitro)	0.138	NEG_IN	↓	
Unscheduled DNA Synthesis in Rat Hepatocytes	0.308	NEG_OUT	↓	
Micronucleus Test in Mouse Erythrocytes	0.96	POS_IN	↓	
Dominant Lethal Mutations in Rodents	0.979	POS_IN	↓	
Maximum recommended daily dose (MRDD) in Humans	0.51	POS_OUT	↓	

Publication will be announced

on the Danish (Q)SAR Database homepage: <http://qsar.food.dtu.dk>



Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

Computational Toxicology

journal homepage: www.elsevier.com/locate/comtox



QSAR development and profiling of 72,524 REACH substances for PXR activation and CYP3A4 induction



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QSAR models for thyroperoxidase inhibition and screening of U.S. and EU chemical inventories[☆]

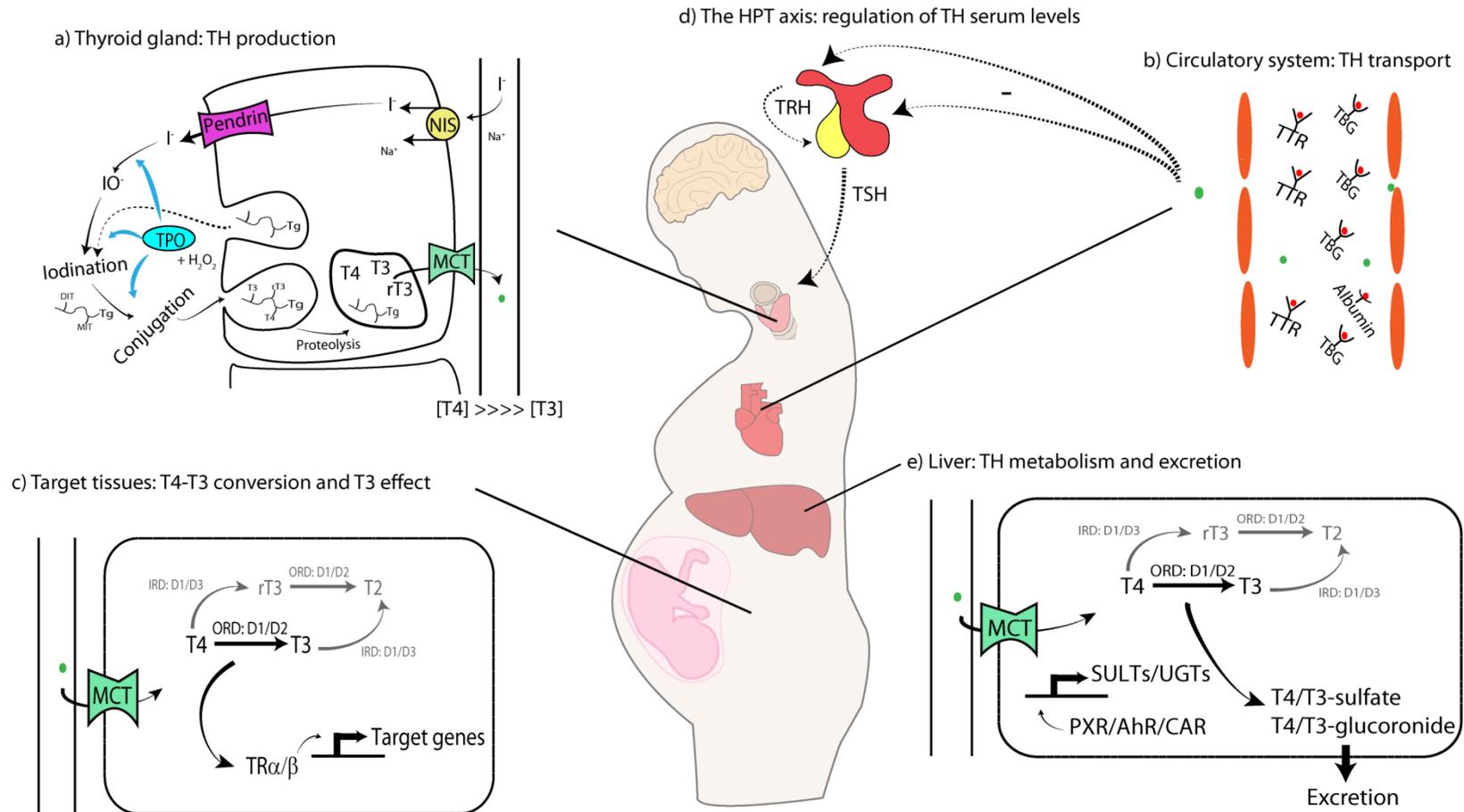


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Future research



In summary

- A number of **QSAR models** covering different mechanisms have been developed and validated. The models can predict if chemicals can interfere with the production and metabolism of thyroid hormones.
- The developed models have been used to screen around 70,000 REACH chemicals, i.e. chemicals potentially available at the European market.
- In this way, knowledge from experimental data on a limited number of chemicals was used to **generate information for 10,000s of untested chemicals.**

Conclusion

- The models can in a **fast and cost-efficient** way identify potential hormone disrupting chemicals in our food, environment and consumer products. The new models can also contribute to **future design of safer chemicals and drugs**.
- Results from the project was published recently in *Computational Toxicology* 2017; 1:39-48 and *Computational Toxicology* 2017; 4:11-21. The results are also included in a PhD report by Sine Rosenberg.

Thank you for listening

