

OASIS TIMES Skin sensitization model

Predicting pre- and pro- electrophilic activation of chemicals in skin sensitization assessment

Laboratory of Mathematical Chemistry University Prof. Assen Zlatarov, Bourgas, 2015

- TIMES Skin sensitization model
- Predicting skin sensitization in TIMES:
 - ✓ Mechanism of Skin sensitization
 - ✓ Main concept of the model
 - ✓ Simulators for (a)biotic transformations
 - \checkmark Model reliability and mechanistic justification
- Summary

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TIMES Skin Sensitization model

Short description

TIMES Skin Sensitization (SS) model is an expert system describing **structure-toxicity** and **structure-metabolism** relationships through a number of transformations simulating skin metabolism and interaction of generated reactive metabolites with skin proteins.

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Mechanism of skin sensitization

Assumptions:

- 1. Chemicals always penetrate stratum corneum
- 2. Formation of protein conjugates is a premise for ultimate effect
- 3. Metabolism may play significant role in skin sensitization



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Predicting skin sensitization in TIMES Main concept

In order to predict skin sensitisation effect taking into account metabolic activation of chemicals in same platform are combined:

- *Toxicokinetics* specific metabolism
 - ✓ Pre-electrophilic activation Autoxidation reactions
 - ✓ Pro-electrophilic activation Phase I and Phase II reactions
- *Toxicodynamic* interaction with macromolecules



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Simulators for (a)biotic transformations

LMC has published several papers where we shared our experience in the computerized management of metabolic data and the development of simulators of metabolism for predicting toxicity of chemicals.



SAR and QSAR in Environmental Research Vol. 23, Nos. 5-6, July-September 2012, 553-606



Simulation of chemical metabolism for fate and hazard assessment. V. Mammalian hazard assessment

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Laboratory of Mathematical Chemistry, University "Prof. As. Zlatarov", Bourgas, Bulgaria

Simulators for (a)biotic transformations

The toxicokinetic part of the TIMES-SS model is represented by two simulators:

- Abiotic Autoxidation (AU) simulator
- Skin metabolic (SM) simulator

Simulators for (a)biotic transformations

•Abiotic Autoxidation (AU) simulator

It represents a set of more than 260 generalized autoxidation molecular transformations developed on the basis of chemicals with documented AU pathways including *terpenes*, *simple aliphatic* and *polyethylene glycol ethers*, *aldehydes*, *aminophenols*, etc.



Simulators for (a)biotic transformations

- <u>Skin metabolic (SM) simulator</u> consisting of 420 hierarchically ordered transformations based on empiric and theoretical knowledge and peer-reviewed by experts:
 - ✓ Non-enzymatic transformations such as Hydrolysis of salts, Formaldehyde releasing, etc.
 - ✓ Enzyme-mediated reactions (*Phase I and Phase II*) such as Chydroxylation, Glucoronidation, etc.
 - ✓ Protein binding reactions (PBR) illustrating the covalent interactions of chemicals/metabolites with skin proteins
- Currently, the skin metabolic simulator has been upgraded and adjusted to simulate the documented *in vitro* metabolism of 151 chemicals

Simulators for (a)biotic transformations

Different types of principle transformations

Proteins binding reactions

Nucleophilic substitution on halogenated C sp3 atom



Schiff base formation with aldehydes



15

Simulator of metabolism

Principle transformations

Metabolites



Simulator of metabolism

Principle transformations























Documented and OASIS simulated metabolism

Autoxidation simulator

Autoxidation pathway of Limonene



Simulators for (a)biotic transformations

TIMES-SS Predicted metabolism of Isoeugenol accounting AU and SM activation



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Model reliability and mechanistic justification

TIMES-SS model reliability relies on:

- 1. Model applicability domain
- 2. Transformation/ Alert Performance the ratio between the number of correct (Positive and Negative) predictions and the total number of chemicals within the local training set
- 3. Number of chemicals in the local training sets
- 4. Mechanistic justification

Applicability domain of TIMES-SS model is built following the step wise approach as described by *Dimitrov et.al*. and consists of:

- general parametric requirements include ranges of molecular weight MW and log Kow defined on the basis of correctly predicted training set chemicals
- structural domain based on atom-centered fragments extracted from correctly and incorrectly predicted training chemicals accounting for the atom type, hybridization and attached H-atoms
- mechanistic domain characterizes specific functional group associated to skin sensitization effect

S. Dimitrov, G. Dimitrova, T. Pavlov, D. Dimitrova, G. Patlevisz, J. Niemela, and O. Mekemyan, A stepwise approach for defining the applicability domain of SAR and QSAR models, *J. Chem. Inf. Model.* 45 (2005), pp. 839–849. 32

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View of TIMES-SS model

Generation of metabolic map with highlighted the activated metabolites

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View of TIMES-SS model

Generation of metabolic map with highlighted the activated metabolites

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View of TIMES-SS model

Generation of metabolic map with highlighted the activated metabolites





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Patlewicz G, Kuseva C, Mehmed A, Popova Y, Dimitrova G, Ellis G, Hunziker R, Kern P, Low L, Ringeissen S, Roberts DW, Mekenyan O, **TIMES-SS--recent refinements resulting from an industrial skin** sensitisation consortium, SAR QSAR Environ Res. 2014;25(5):367-91

SAR and QSAR in Environmental Research, 2014 Vol. 25, No. 5, 367–391, http://dx.doi.org/10.1080/1062936X.2014.900520



TIMES-SS – Recent refinements resulting from an industrial skin sensitisation consortium^{\$}

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TIMES Skin sensitization model

Summary

TIMES-SS model is an unique non-testing system:

- Simulating:
 - \checkmark Pre- and Pro-electrophilic activation in skin
 - \checkmark covalent interactions of activated metabolites with proteins
- Generating activation pathways with quantitative distribution of the metabolites
- Providing reliability of the prediction in terms of:
 - ✓ alert performance
 - \checkmark mechanistic justification of protein binding
- Estimating belonging of chemicals in the parametric, structural and mechanistic boundaries of the model applicability domain