

## **(Quantitative) structure-activity relationship models for genotoxicity**

**Commonly used acronym:** (Q)SAR models for genotoxicity

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## **SCOPE OF THE METHOD**

<b>The Method relates to</b>	Human health
<b>The Method is situated in</b>	Basic Research, Regulatory use - Routine production, Translational - Applied Research
<b>Type of method</b>	In silico

## **DESCRIPTION**

### **Method keywords**

VEGA Hub  
Derek Nexus  
Sarah Nexus  
bacterial mutagenicity  
chromosome damage  
prediction models  
in vitro micronucleus  
ames test

### **Scientific area keywords**

in silico models  
DNA damage  
genotoxicity  
Toxicology

### **Method description**

*In silico* tools are computer-assisted methodologies with a high-throughput that allow to predict the toxic potential of compounds without experimental testing. Consequently, *in silico* tools are time-, cost- and animal-saving in nature. The most commonly used

methods are (quantitative) structure-activity relationship ((Q)SAR) models. These methodologies are based on the hypothesis that similar structures are expected to display similar biological (or toxicological) properties and mechanisms of action. Especially for (bacterial) mutagenicity, a wide variety of (Q)SAR models with good reliability exist. The bacterial reverse gene mutation test (often referred to as 'Ames test') has been the golden standard for testing mutagenicity for decades and consequently, a large collection of data is available to build robust prediction models. For the other toxicological endpoints including chromosome damage, (Q)SAR models are often still in a less advanced state although important progress has been made over the last years. (Q)SAR models are particularly of interest for priority setting or when no or limited amounts of the compound are available. Within our lab, we have the most experience with the genotoxicity models present in the open source VEGA Hub and with the commercial software Derek and Sarah Nexus.

### **Lab equipment**

Computer software:

- Commercial software: Derek Nexus, Sarah Nexus
- Open source software: VEGA Hub (<https://www.vegahub.eu/>)

### **Method status**

Published in peer reviewed journal

## **PROS, CONS & FUTURE POTENTIAL**

### **Advantages**

(Q)SAR models are time-, cost- and animal-saving in nature. Moreover, the (Q)SAR models in the VEGA Hub are freely available.

### **Challenges**

The reliability of the (Q)SAR models will depend on the quality of the data that have been used to build the model. For bacterial mutagenicity, large datasets are available, and consequently, a large number of relatively robust (Q)SAR models have been developed. Less data are available for other genotoxic endpoints such as *in vitro* and *in vivo* chromosome damage resulting in general in models with lower reliability.

### **Modifications**

By extending/improving the underlying datasets and/or the underlying mathematical tools, new and/or updated (Q)SAR models for genotoxicity are constantly being developed.

### **Future & Other applications**

Currently, we have the most experience with the application of (Q)SAR models for genotoxicity. However, we are also exploring their use for other toxicological endpoints such as carcinogenicity and endocrine activity.

## **REFERENCES, ASSOCIATED DOCUMENTS AND OTHER INFORMATION**

### **References**

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