GUSAR

The acronym GUSAR stands for "General Unrestricted Structure-Activity Relationships". The system has been developed by the team of Professor Vladimir Poroikov in Moscow, Russia.

The GUSAR software is designed to create reliable quantitative QSAR/QSPR models. GUSAR uses unique algorithms like self-consistent regression, and supports the use of nearest neighbors, consensus models and applicability domains.

GUSAR allows to:

•Create QSAR/QSPR models;

•Quantitatively predict biological activities based on these models;

•Calculate consensus models for prediction;

•Validate internal and external models;

•Apply ready-trained QSAR models to predict toxicity in mice and rat as well as to predict possible effects on antitargets.

Recent GUSAR publications

Dmitriev A, Rudik A, Filimonov D, Lagunin A, Pogodin P, Dubovskaja V, Bezhentsev V, Ivanov S, Druzhilovskiy DS, Tarasova O, Poroikov V. (2017) Integral estimation of xenobiotics' toxicity with regard to their metabolism in human organism. Pure and Applied Chemistry, doi: https://doi.org/10.1515/pac-2016-1205

Rudik AV, Bezhentsev VM, Dmitriev AV, Druzhilovskiy DS, Lagunin AA, Filimonov DA, Poroikov VV. MetaTox: Web Application for Predicting Structure and Toxicity of Xenobiotics' Metabolites. (2017) J Chem Inf Model. **57**, 638-642.

Zakharov AV, Varlamova EV, Lagunin AA, Dmitriev AV, Muratov EN, Fourches D, Kuz'min VE, Poroikov VV, Tropsha A, Nicklaus MC. QSAR Modeling and Prediction of Drug-Drug Interactions. Mol. Pharm. 2016, 13(2), 545-556.

GUSAR

About geneXplain

GeneXplain's mission is to provide a comprehensive platform for bioinformatic, systems biological and cheminformatic tools. The raison d'être of this platform is to assist translational research in the life sciences, mainly in the context of personalized medicine and pharmacogenomics. We intend to make our expertise available to academic and commercial partners in collaborative research projects.

To achieve this, geneXplain offers:

•The geneXplain platform providing a large number of bioinformatic and systems biological data analysis workflows. Unique is geneXplain's Upstream Analysis for causal interpretation of expression data.

•TRANSFAC®, the most comprehensive database on eukaryotic transcription regulation. TRANSFAC® is now also available under the geneXplain platform, providing the most comprehensive collection of TF DNA-binding profiles.

•TRANSPATH®, one of the largest pathway/network databases presently available, particularly well suited for geneXplain's proprietary *Upstream Analysis*.

•HumanPSD, a rich information resource connecting pathways with targets, drugs and clinical trials.

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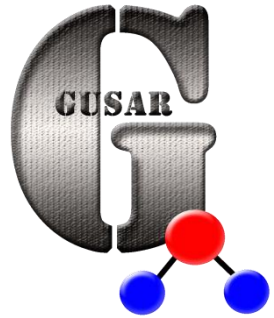
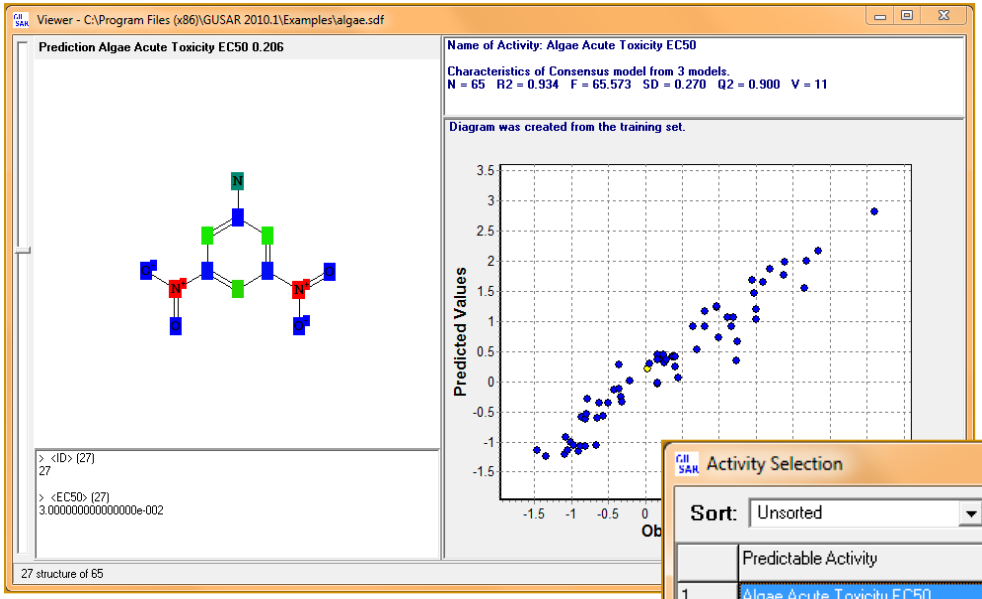
GUSAR

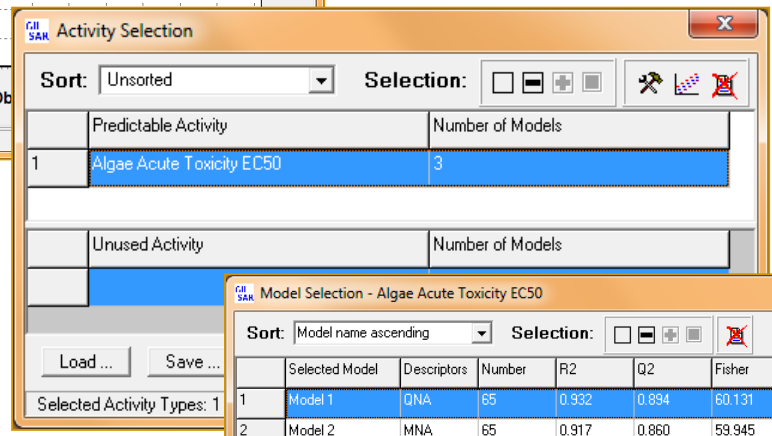
The tool to create models on quantitative structure- activity relationships

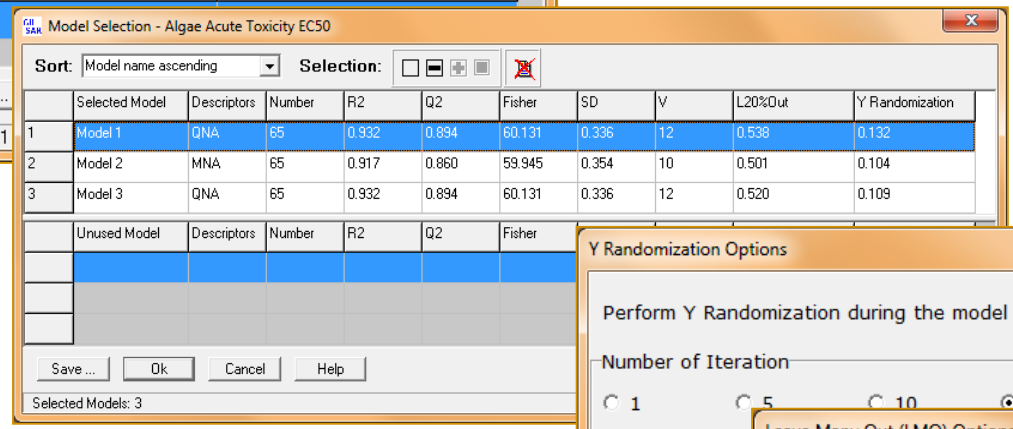


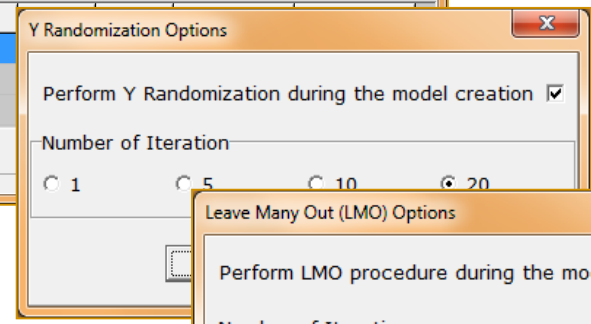
geneXplain

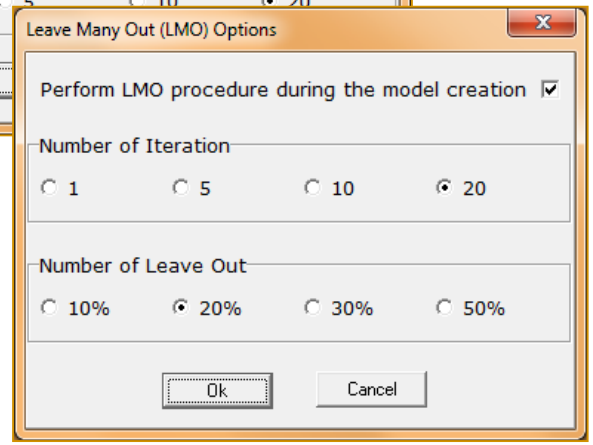
GUSAR – a software for the creation of quantitative SAR/SPR models











Chemical structure description in GUSAR

2D structures are represented by MNA (Multilevel Neighborhoods of Atoms) and/or QNA (Quantitative Neighborhoods of Atoms) descriptors and biological activity descriptors that are based on the **PASS** prediction results. QNA descriptors easily reflect the nature of intermolecular interactions. Models developed using biological activity descriptors enable to reveal key mechanisms of action of complex biological effects.

Key benefits

- Fast creation of high quality QSAR models
- Optimized lead identification through *in silico* screening with GUSAR models
- Creation of QSAR models for different biological activities, suitable for their simultaneous prediction
- Revealing key mechanisms of action when modeling complex biological effects like acute toxicity, carcinogenicity, hepatotoxicity etc.

Key features

- Unique descriptors and mathematical algorithms,
- Creation of QSAR models for large data sets, up to 30,000 chemical compounds,
- High speed of predictions,
- Easy-to-use interface,
- Selection of the most predictive models,
- Uploading of SD files for batch predictions,
- Saving GUSAR output predictions in SDF and CSV formats for subsequent analyses.

Mathematical algorithm

The unique algorithm of a self-consistent regression allows to select the best set of descriptors for a robust and reliable QSAR model. It is based on the statistical regularization of ill-posed problems, and uses the same data samples to estimate both the regression coefficients and the regularization parameters.

Ready-Trained Models

Ready-trained QSAR models for GUSAR are available on request.

The models on acute rat toxicity and acute mice toxicity contain four activities (LD_{50} for different administration options).
Lagunin A., Zakharov A., Filimonov D., Poroikov V. (2011) QSAR modelling of rat acute toxicity on the basis of PASS prediction. Mol Inform 30:241–250.

The model on the affinity of substances to antitargets contains 32 activities (IC_{50}, K_i and K_{act}).
Zakharov, A.V., Lagunin, A.A., Filimonov, D.A., Poroikov, V.V. (2012) Quantitative prediction of antitarget interaction profiles for chemical compounds. Chem. Res. Toxicol. 25:2378–2385.

Validation

In comparison with a number of 3D and 2D QSAR methods, the predictivity of GUSAR was superior to that of most other QSAR methods both on heterogeneous and on homogeneous data sets, as published in

Filimonov D.A., Zakharov A.V., Lagunin A.A., Poroikov V.V. (2009). QNA based 'Star Track' QSAR approach. SAR QSAR Environ. Res. 20: 679-709.

A slide show with screenshots can be found on our homepage (www.genexplain.com) and our Facebook account (www.facebook.com/genexplain).