PASS

The acronym PASS stands for "Prediction of Activity Spectra for Substances". The system is based on concepts that were continuously developed over the past 40 years by Professor V. Poroikov and his team.

PASS uses 2D structural formulae of organic compounds to simultaneously predict many types of biological activities for them. The program can also estimate the influence of single atoms on the overall activity of the molecule. This allows the evaluation of the biological activity profiles for compounds even prior to their chemical synthesis and biological testing.

Activity prediction is based on a "structure-activity" relationship knowledgebase (SAR base), which is included in the program, but can also be created from scratch.

PharmaExpert

This is an optional extension of the PASS system, allowing for a systematic data mining and biological interpretation of PASS results.

PASS allows to:

- Predict reliable biological activity spectra for single structures and compound libraries;
- Create new SAR bases and adjust the included base for specialized activity prediction;
- Assess the influence of individual atoms on the activity spectrum of a substance.

Recent third-party publications with reference to PASS

Chand, B., Malik, M.A. *Biological-activity predictions, crystallographic comparison and role of packing interactions in androstane derivatives of steroids*. (2011) Journal of Chemical Crystallography, 41 (3), pp. 255-275.

Deshmukh, V.K., Raviprasad, P., Kulkarni, P.A., Kuberkar, S.V. *Design, synthesis and biological activities of novel 4H-pyrimido [2, 1-b] [1, 3] benzothiazole derivatives*. (2011) International Journal of ChemTech Research, 3 (1), pp. 136-142.

Sapa, J., Nowaczyk, A., Kulig, K. *Antiarrhythmic and antioxidant activity of novel pyrrolidin-2-one derivatives with adrenolytic properties*. (2011) Naunyn-Schmiedeberg's Archives of Pharmacology, 383 (1), pp. 13-25.

200 more publications can be found on our web page.

PASS

About geneXplain

The geneXplain GmbH is a young company with a growing portfolio of useful software for life scientists. Whether you are working on genome, network or compound analysis, we have what you need!

Our **geneXplain platform** is the online toolbox and workflow management system for scientists in the fields of transcriptomics and proteomics. Here, you can store and analyze your experimental data (including raw microarray results), search for master regulator molecules, map to GO terms, and even add your own workflows and scripts.

We distribute software developed by in silico molecular biology, Inc., Japan, for geneticists. **In-Silico Molecular Cloning (IMC)** lets you handle annotated DNA, conduct cloning experiments in silico, map features and sequences, and compare and align genomes. **GenomeTraveler (GT)** takes this to the next level by adding the possibility to visualize and interpret your Next Generation Sequencing (NGS) data.

For scientists working on drug discovery and drug optimization, we distribute a range of tools from the Institute of Biomedical Chemistry (IBMC), Russia. **PASS (Prediction of Activity Spectra for Substances)** predicts whole bioactivity spectra for your compounds qualitatively, based only on 2D structural formulae. **PharmaExpert** is the additional software to help you choose the most suitable substance from a set of PASS predictions. **GUSAR (General Unrestricted Structure-Activity Relationships)** predicts biological activities quantitatively, based on (Q)SAR models, which can also be created with the software.

It is geneXplain's mission to provide the computational methodology required to achieve the goal of "personalized pharmacogenomics". We wish to help academic researchers in their daily work with easy-to-use tools that are compatible with the low-budget requirements of most academic groups. At the same time, we shall provide high-end technology platforms to fulfill bioinformatics requirements to industrial standards. Finally, we intend to offer partnerships for research and training in the area of our expertise.

geneXplain GmbH
Am Exer 10b
D-38302 Wolfenbüttel, Germany

info@genexplain.com
www.genexplain.com
www.facebook.com/genexplain
www.linkedin.com/company/genexplain

Directors: E. Wingender, A. Kel • Commercial register:
HRB 202564, Amtsger. Braunschweig • VAT No.: DE271983408

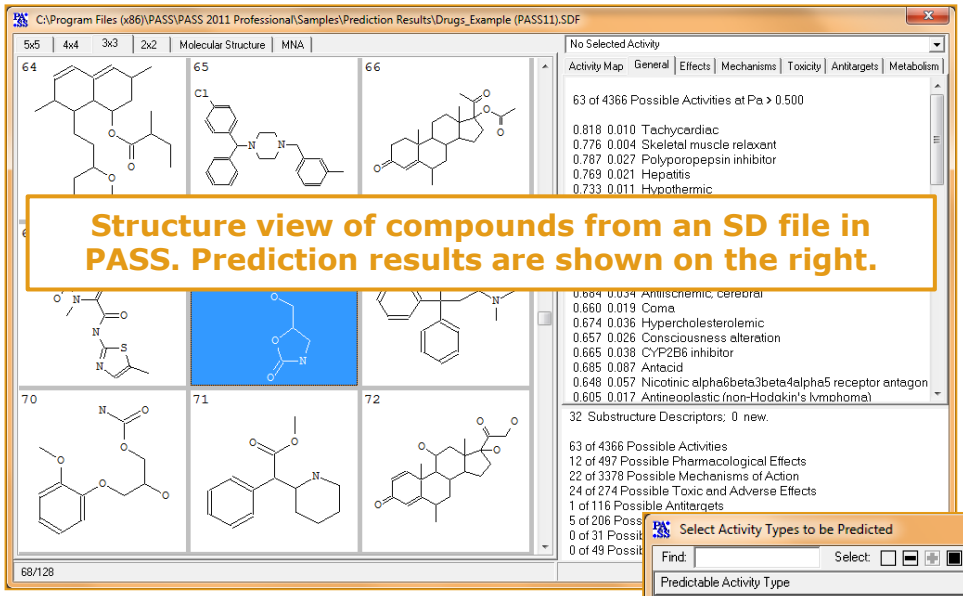
PASS

The tool to link chemical structures with biological activities

PASS

geneXplain

PASS - the software to link chemical structures with biological activities



Structure view of compounds from an SD file in PASS. Prediction results are shown on the right.

List of activities predicted by PASS

The current version of PASS (11.4.12) predicts 4,444 kinds of biological activity with an average prediction accuracy of 95%.

Predictable biological activities include:

- about 500 **pharmacotherapeutic effects** (*antihypertensive, hepatoprotective, sedative, etc.*);
- more than 3,300 **biochemical mechanisms of action** (*5-hydroxytryptamine agonist, acetylcholinesterase inhibitor, adenosine uptake inhibitor, etc.*);
- about 280 **adverse & toxic effects** (*carcinogenic, hallucinogenic, hepatotoxic, etc.*);
- about 100 **antitargets** (*ATPase inhibitor, CYP3A4 inhibitor, HERG channel blocker, etc.*);
- about 250 terms related to **gene expression**, and **drug metabolism** and **transport** (*CYP1A substrate, P-glycoprotein inhibitor, APOA1 expression enhancer, etc.).*

Chemical structure description in PASS

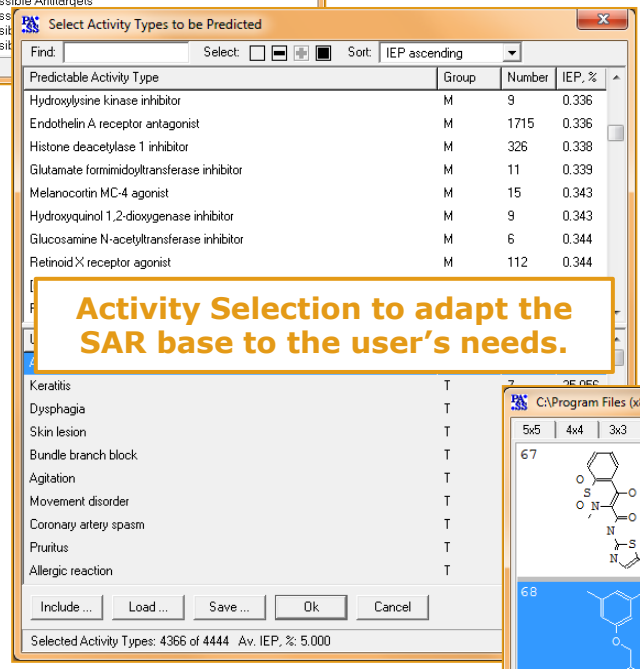
Multilevel Neighborhoods of Atoms (MNA) descriptors are applied to describe the 2D structural formulae of organic compounds. The molecular structure is represented in PASS by the set of unique MNA descriptors of the 1st and 2nd levels, as published in

Filimonov D., Poroikov V., Borodina Yu., Gloriozova T. (1999). Chemical Similarity Assessment through multilevel neighborhoods of atoms: definition and comparison with the other descriptors. J. Chem. Inf. Comput. Sci. ***39****: 666-670.*

Creation of a proprietary SAR base

Additionally to the SAR base that comes with PASS, there is the possibility to train a new SAR base on any SD file containing structures of compounds and names of their biological activities.

It is also possible to combine newly created SAR bases with the existing SAR base.



Activity Selection to adapt the SAR base to the user's needs.

Mathematical algorithm

The prediction algorithm is based on Bayesian estimates of probabilities for a compound to belong to the classes of active or inactive compounds, respectively. The mathematical method is described in several publications, one of the most recent:

Filimonov D.A., Poroikov V.V. (2008). Probabilistic approach in activity prediction. Eds. Alexandre Varnek and Alexander Tropsha. Cambridge (UK): RSC Publishing, p.182-216.

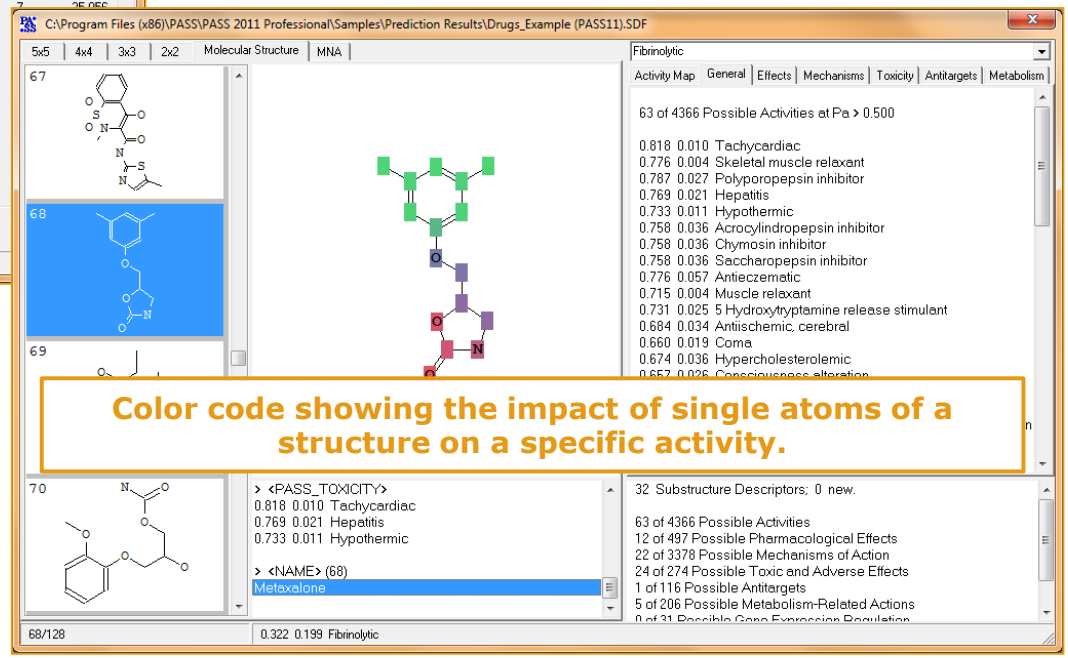
The predicted activity spectrum is presented in PASS by the list of activities, with probabilities "to be active" ***Pa*** and "to be inactive" ***Pi*** calculated for each activity.

Application areas

- Medicinal chemistry
- Computational chemistry
- Drug discovery / drug development
- Drug repositioning
- Chemical toxicity
- Safety assessment
- Pharmacogenomics, chemogenomics
- SAR (qualitative structure-activity relationship)
- Natural compound effects
- Translational research / translational medicine

The color schema shows the contribution of each atom in a molecule to the selected biological activity.

Green: positive impact;
Red: negative impact;
Blue, Grey: neutral.



Color code showing the impact of single atoms of a structure on a specific activity.

A slide show with screenshots can be found on our homepage (www.genexplain.com) and our Facebook account (www.facebook.com/genexplain), and recommendations from experts can be found on LinkedIn (http://www.linkedin.com/company/genexplain/products).