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.

PharmaExpert

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

Recent PASS publications

Popugaeva E. et al. (2019) Derivatives of Piperazines as Potential Therapeutic Agents for Alzheimer's Disease.
Mol. Pharmacol. **95**, 337-348.

Merlani M. et al. (2019) New Caffeic Acid Derivatives as Antimicrobial Agents: Design, Synthesis, Evaluation and Docking.
Curr. Top. Med. Chem. **19**, 292-304.

Gaur AS et al. (2018) Molecular property diagnostic suite for diabetes mellitus (MPDS(DM)): An integrated web portal for drug discovery and drug repurposing. J Biomed Inform. **85**, 114-125.

Vil VA et al. (2018) Peroxy steroids derived from plant and fungi and their biological activities. Appl Microbiol Biotechnol. **102**, 7657-7667.

More publications can be found on our web page http://geneXplain.com/pass/

PASS

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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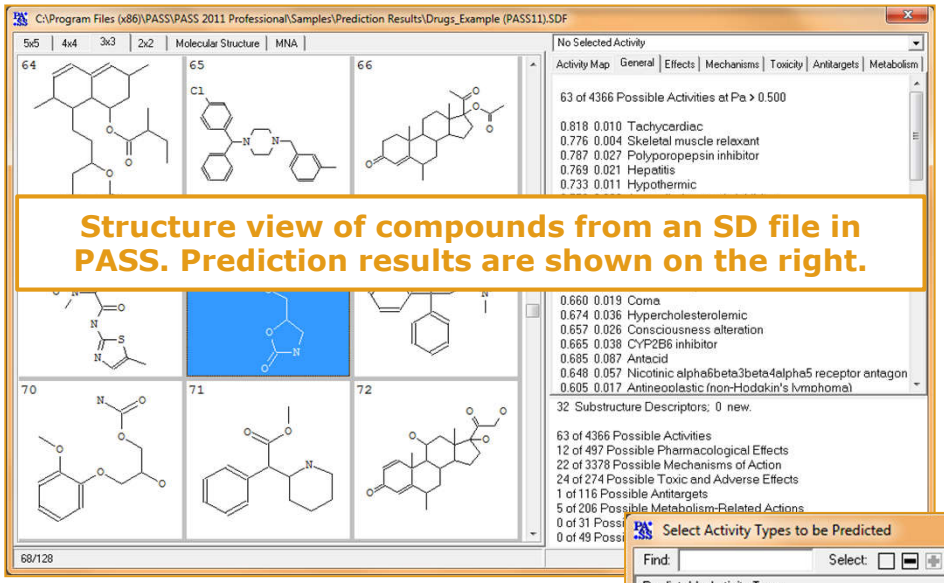
PASS

The tool to link chemical structures with biological activities

PASS

geneXplain

PASS - 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.

Bio-activities predicted by PASS

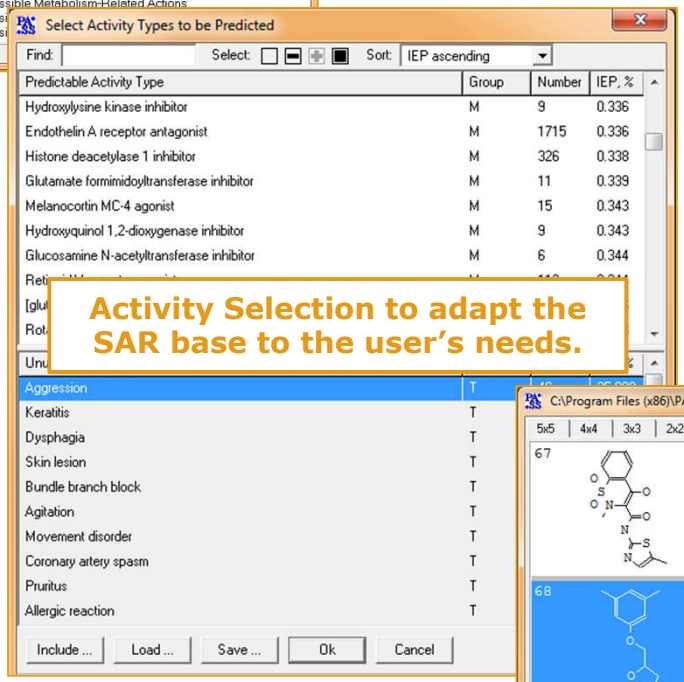
The current version, **PASS2017**, predicts 5,050 biological activities with an average prediction accuracy of 96,5%. Additional 2,500 of biocativities can be added for predictions. Predictable biological activities include:

- over **500 pharmacotherapeutic effects** (*antihypertensive, hepatoprotective, sedative, etc.*);
- more than **4,100 biochemical mechanisms of action** (*5-hydroxytryptamine agonist, acetylcholinesterase inhibitor, adenosine uptake inhibitor, etc.*);
- over **450 adverse & toxic effects** (*carcinogenic, hallucinogenic, hepatotoxic, etc.*);
- more than **2,100** terms for **gene expression**;
- **250** terms for **drug metabolism** and **transport** (*CYP1A substrate, P-glycoprotein inhibitor, APOA1 expression enhancer, etc.).*

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.

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.*

Mathematical algorithm

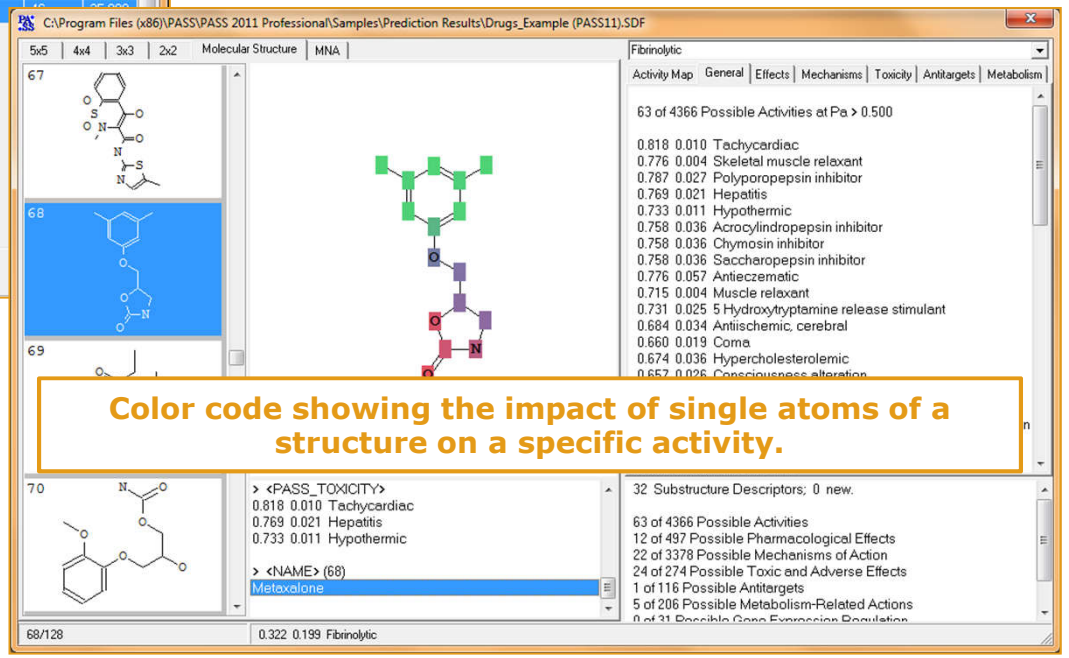
The prediction algorithm is based on Bayesian estimates of probabilities for a compound to belong to the classes of active or inactive compounds, respectively. The mathematical method is described in several publications, one of the most recent:

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.

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).