



Expert system to identify promising drug candidates

==> Lead selection

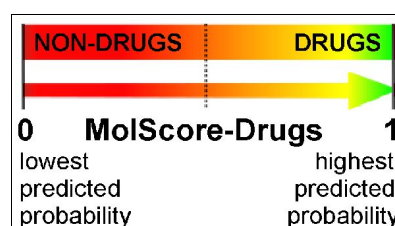
==> Prioritisation of drug candidates

MolScore-Drugs helps to identify and prioritise promising drug candidates with the maximum possibility of success in human trials.

The expert system is based on a variety of reliable models. Extremely large structure-activity relationships (SAR) with up to hundreds of thousands compounds allow the estimation of useful drug-like chemical space. Structure-property relationships (SPR) which are derived from PharmaInformatic's large in-house ADME/Tox-database can be applied to predict ADMET properties and to identify potential risks in order to reduce clinical failures.

MolScore-Drugs calculates a value between 0 and 1 for each substance. This value correlates with the predicted probability of a substance becoming a successful drug.

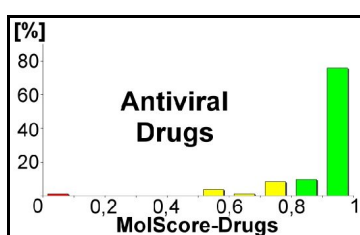
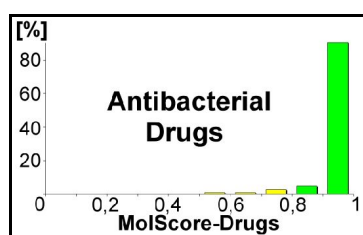
The expert system evaluates drug-candidates at an early state in order to reduce the costs and time for the development of novel drugs.



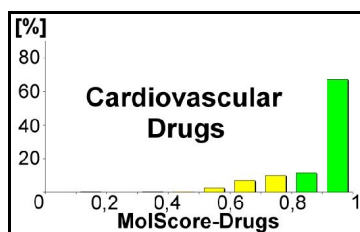
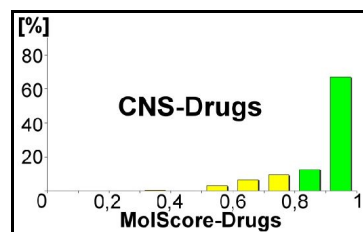
Application & Advantages

- Selects and prioritises promising drug candidates for further development
- Prioritises derivatives even of different lead structures
- Simple usage and integration of results
- Reduces clinical failures

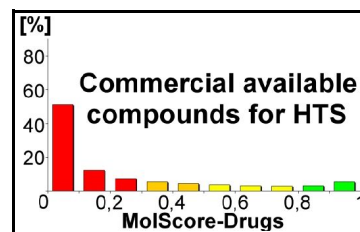
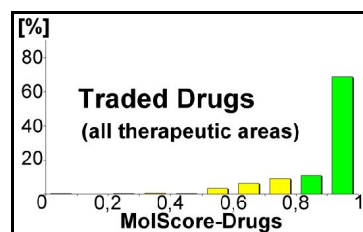
MolScore-Drugs prioritises drugs in multiple therapeutic areas correctly. Below are some prediction results of MolScore-Drugs on drugs, which are or have been on the market.



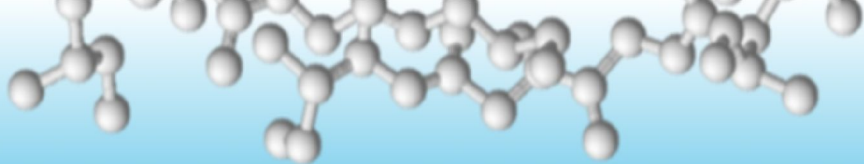
Despite the high variability of structures from marketed drugs, they have certain features in common. The expert system identifies general molecular patterns and properties of save and successful drugs.



MolScore-Drugs detects promising drug candidates in multiple therapeutic areas, including central nervous system diseases, infectious diseases, cardiovascular diseases, but is not limited to these.



The examination of more than 500.000 commercial available compounds used for HTS showed that only a low amount of these compounds will satisfy the requirements of becoming a promising drug.



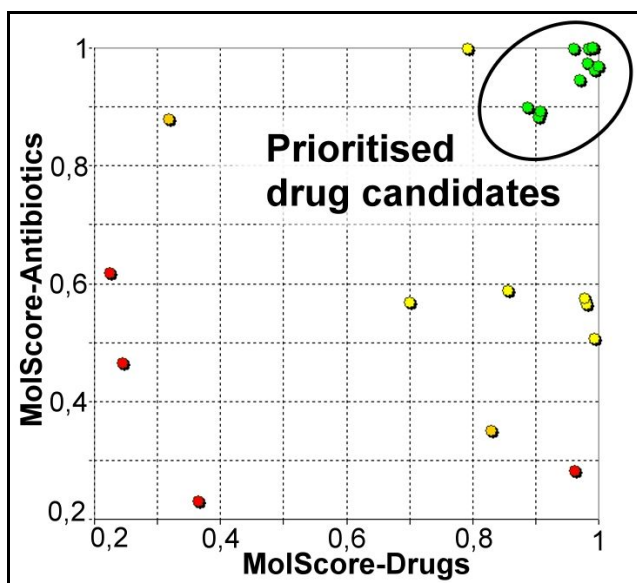
PharmaInformatic's ADME/Tox-Database

Structure-ADMET relationships based on a small number of compounds cannot describe the chemical space of drugs properly and possess only low predictive power on novel compounds. A few years ago we started to build up our comprehensive and highly annotated ADME/Tox database. This unique pharmacokinetic data collection currently contains more than 16.000 data entries. Reliable tools to predict ADME/Tox-properties can be derived from this database in order to identify and prioritise promising drug candidates:

- Bioavailability, clearance, elimination half life, type of elimination, metabolic stability
- Absorption, solubility, log P, log D, P-gp transport
- Volume of distribution, plasma protein binding
- Blood brain barrier permeability, CNS activity
- Toxicity, hepatotoxicity, cardiotoxicity, carcinogenicity, mutagenicity
- Drug-drug interactions, CYP450 inhibition/induction

Lead selection & prioritisation

MolScore-Drugs can be combined with other predictive tools to identify the most suitable drug candidates for further development. To provide an example we have used MolScore-Drugs and MolScore-Antibiotics to prioritise novel antibacterial lead structures.



Both expert systems are based on a variety of independent models which assess different molecular patterns and properties. Therefore a combination of both tools improves the drug candidate selection process.

MolScore-products are able to prioritise derivatives of lead structures. In practice the substitution of one functional group can have an important influence on biological activity & ADME-properties and this is reflected in the prediction result.

Application of customised tools derived from our ADME/Tox database will further improve the identification of potential risks in order to reduce clinical failures.

About PharmaInformatic

PharmaInformatic provides cheminformatic services and predictive tools to improve drug discovery and preclinical compound selection. Specialised expert systems in different therapeutic areas help to discover and validate hits, followed by selection and prioritisation of suitable compounds.

PharmaInformatic was founded in 2004 by Dr. Wolfgang Boomgaarden. He has developed virtual screening and drug design products, which have been successfully used for a number of years in the pharmaceutical world. Before he founded the company, he worked as a professor in bioinformatics at the University of Applied Science in Emden, Germany. PharmaInformatic's technology is continually being developed by an interdisciplinary network of biologists, medicinal chemists and bio-IT professionals.

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