SwissADME

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SwissADME

- SwissADME: a free web tool to evaluate pharmacokinetics, druglikeness and medicinal chemistry friendliness of small molecules.
- The ADME studies results for new synthesized analogues reported by Swiss ADME server to demonstrate which is the safer and potent drug candidate(s), for excluding the tested compounds that may fail in the next stages of the drug development because of the uncomplimentary ADME results.



SwissADME submission page

 The actual input is a list of SMILES, which contains one molecule per line with an optional name separated by a space. Molecules can be directly pasted or typed in SMILES format, or inserted through the molecular sketcher. The latter enables importing from databases, opening a local file or drawing a 2D chemical structure to be transferred to the list by clicking on the double-arrow button. When the list of molecules is ready to be submitted, the user can start the calculations by clicking on the "Run" button.





Ideal parameters

- Lipinski rule related to the oral administration of the drugs that should have ≤ 5 hydrogen bonds donor, ≤ 10 hydrogen bond acceptor, LogP ≤ 5 and molecular weight (M.Wt.) ≤ 500 to be given orally.
- The topological polar surface area (TPSA) was calculated, because it consider as a very important characteristic that was associated with the bioavailability of the drugs. As a result, the passively absorbing molecules within a TPSA >140 A° are considered to have lower oral bioavailability
- Fingerprints of molecular drug-likeness structure keys such as LogP and Log S.

Ideal parameters

- Statistical performance of SVM classification models for substrate or inhibitor of pharmacokinetics-relevant protein, P-gp and CYP.
- The BOILED-Egg: allows for intuitive evaluation of passive gastrointestinal absorption (HIA) and brain penetration (BBB) in function of the position of the molecules.





BOILED EGG – for ketoprofen and final compounds.
Yellow ovule (yolk): are molecule predicted to passively permeate through blood-brain barriers.
White ovule (white): are molecule predicted to passively absorbed by the GIT.
PGP+: Blue dots are for molecules predicted to be effluxed from the CNS by the P-glycoprotein.
PGP-: Red dots are for molecules predicted not to be effluxed from the CNS by the P-glycoprotein.

References

- Christopher A. Lipinski. Rule of five in 2015 and beyond: Target and ligand structural limitations, ligand chemistry structure and drug discovery project decisions. Advanced Drug Delivery Reviews. Accepted 27 April 2016.
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