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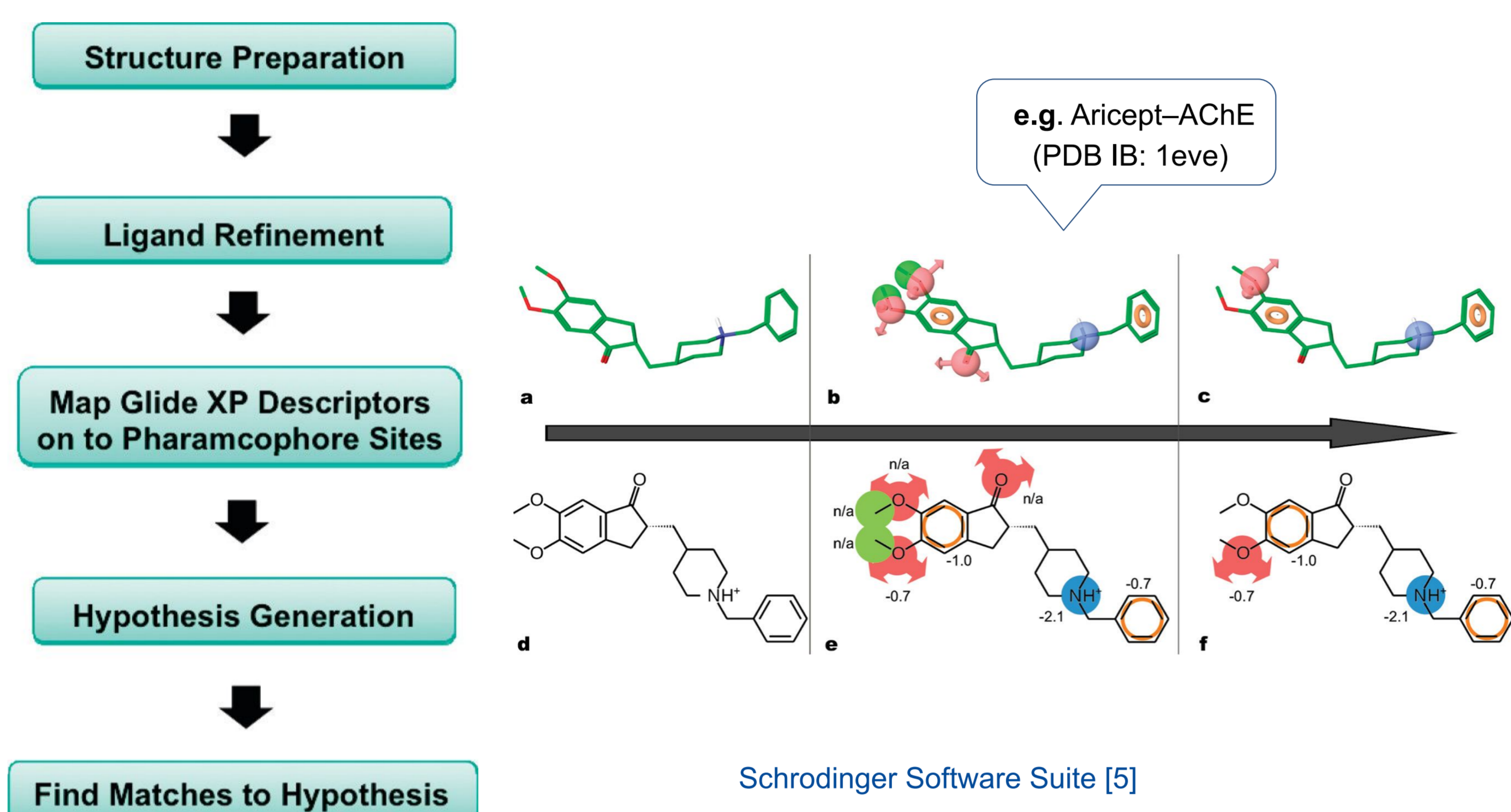
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## Introduction

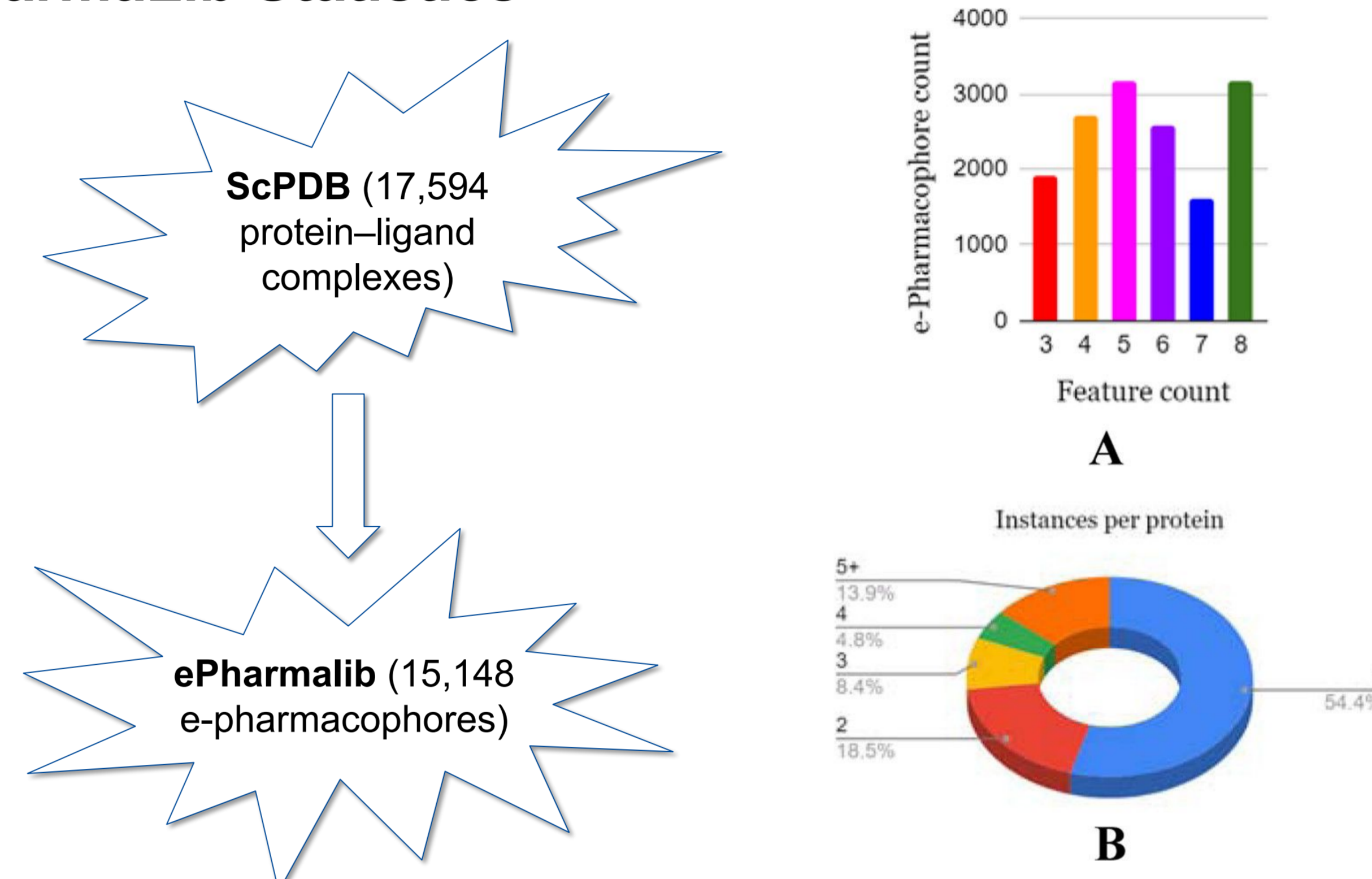
- Pharmacology operates on the axiom: “*corpora non agunt nisi fixata*”, famously stated by Paul Ehrlich in 1909 [1].
- Nowadays, it is widely acknowledged that bioactive compounds oftentimes bind to several target proteins thereby exhibiting polypharmacology [2].
- Experimentally determining drug–target interactions (DTIs) is however laborious and costly, whereas computational methods are faster and cheaper.
- To this end, we created ePharmaLib [3], an open-access library of e-pharmacophores modeled from the solved cocrystal structures of 17,594 therapeutically relevant protein–ligand complexes from the scPDB [4].



## ePharmaLib Development



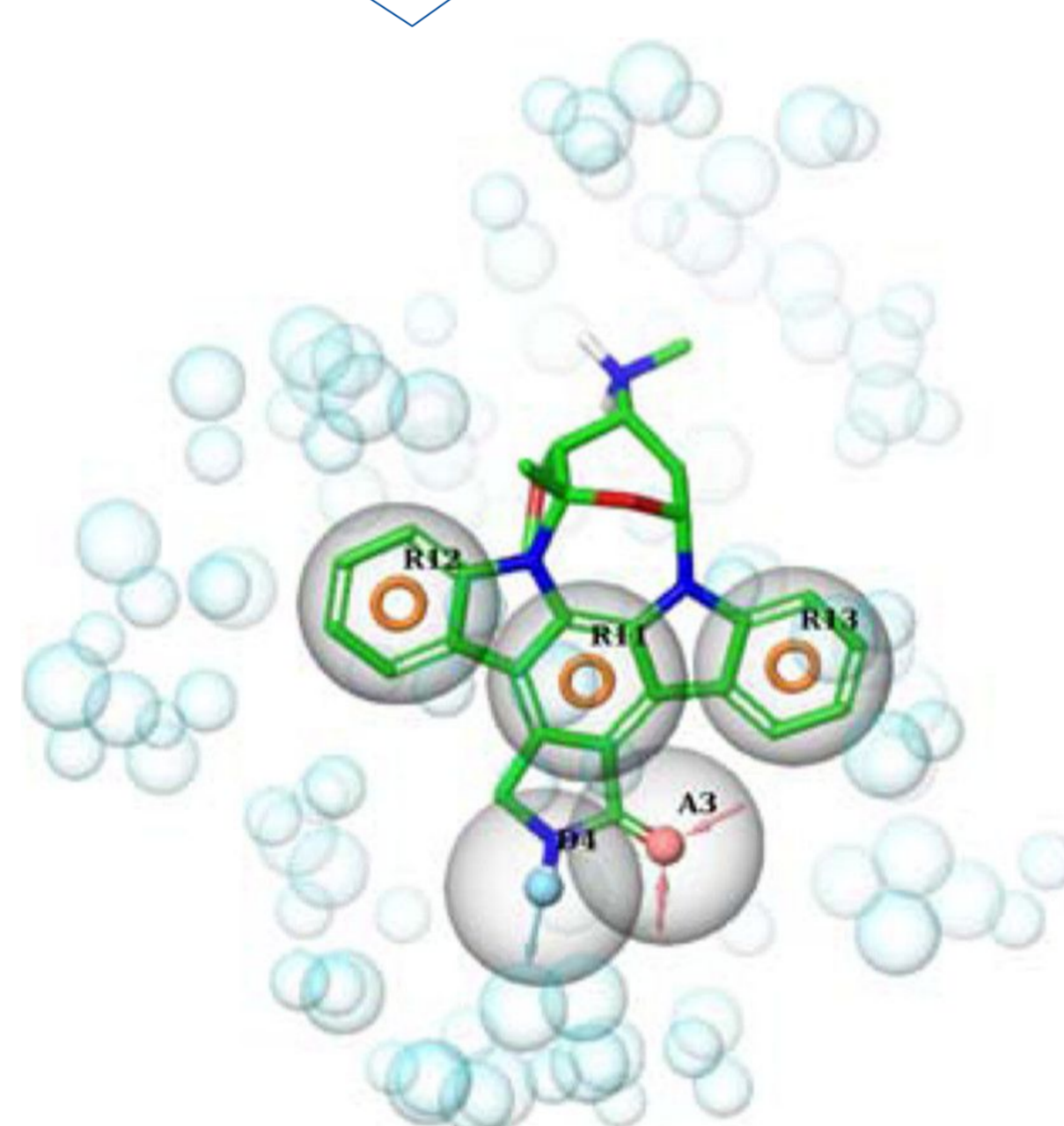
## ePharmaLib Statistics



## Retrospective Validation

- A target fishing study was carried out with ligands from the StreptomeDB [6], notably staurosporine (STU), an indolocarbazole displaying highly potent pan-kinase inhibition.
- Predicted targets are ranked in terms of an RMSD-based metric known as *Fitness*. It ranges between 3 (perfect alignment) and -1 (non-alignment).
- In total, 490 PDB protein hits (253 unique proteins) were retrieved. Strikingly, out of the top-50 protein hits, 41 (first 13 in a row) are STU-bound proteins, i.e., “known–known” DTI pairs.
- The general observation that can be made from this ranking of protein hits is the high self-retrieval rate of known targets.

Overlay of staurosporine onto the top-ranked e-pharmacophore (5e8w-STU-TGFR1\_HUMAN).



Top-10 ranking of “known-known” DTI pairs of staurosporine (STU)

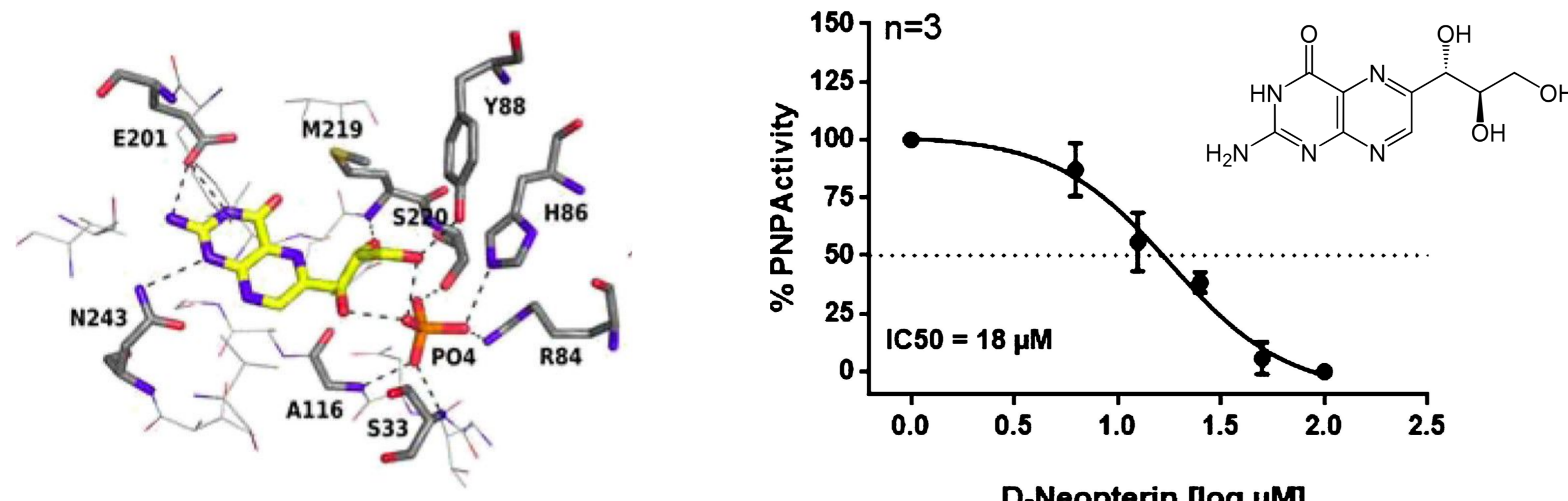
Rank	Target ID <sup>a</sup>	Target Name	Feature types <sup>b</sup>	Feature count	Fitness
1	5e8w-STU-TGFR1_HUMAN	TGF-beta receptor type-1	ADRRR	5	2.901
2	1u59-STU-ZAP70_HUMAN	Tyrosine-protein kinase ZAP-70	ADHRRR	6	2.898
3	3ckx-STU-STK24_HUMAN	Serine/threonine-protein kinase 24	ADHPRRR	7	2.895
4	1e8z-STU-PK3CG_HUMAN	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform	AHRRR	5	2.891
5	2buJ-STU-STK16_HUMAN	Serine/threonine-protein kinase 16	ADHRRR	6	2.889
6	1q3d-STU-GSK3B_HUMAN	Glycogen synthase kinase-3 beta	ADHRRR	6	2.886
7	4u97-STU-IRAK4_HUMAN	Interleukin-1 receptor-associated kinase 4	ADHRRR	6	2.886
8	3bkb-STU-FES_HUMAN	Tyrosine-protein kinase Fes/Fps	ADHRRR	6	2.885
9	1aQ1-STU-CDK2_HUMAN	Cyclin-dependent kinase 2	ADHRRR	6	2.883
10	3a62-STU-KS6B1_HUMAN	Ribosomal protein S6 kinase beta-1	ADHRRR	6	2.883

<sup>a</sup>PDBID-hetID-UniProtEntryName.

<sup>b</sup>A: H-bond acceptor; D: H-bond donor; R: aromatic; H: hydrophobe.

## Prospective Validation

- A scaffold hopping study was carried out with 7735 DrugBank ligands against 27 e-pharmacophores of the human purine nucleoside phosphorylase (hPNP), a validated cancer drug target with no FDA-approved drugs. Four hits (neopterin, tiazofurin, CAN-508, and pseudouridine) were selected for *in vitro* validation by means of a colorimetric assay. Only neopterin (endogenous biomarker) showed significant inhibition of hPNP.



## Summary and Outlook

- ePharmaLib is an open-access library of 15,148 medicinally relevant e-pharmacophores, for use in diverse virtual screening scenarios.
- A good balance was obtained between computational efficiency and predictive accuracy, with an average runtime of an hour/molecule/processor.
- Of note, pharmacophore screening should be combined with molecular docking and/or molecular (meta)dynamics simulations prior to experimental validation.
- The mechanism of action of neopterin (an endogenous immunomodulator) was elucidated to stem from its inhibition of hPNP. Therefore, neopterin could serve as a starting point for the development of a new class of hPNP inhibitors.

<http://www.pharmbioinf.uni-freiburg.de/epharmalib>

<https://training.galaxyproject.org/training-material/topics/computational-chemistry/tutorials/zauberkuigel/tutorial.html>

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