

# Applications of AI in drug design

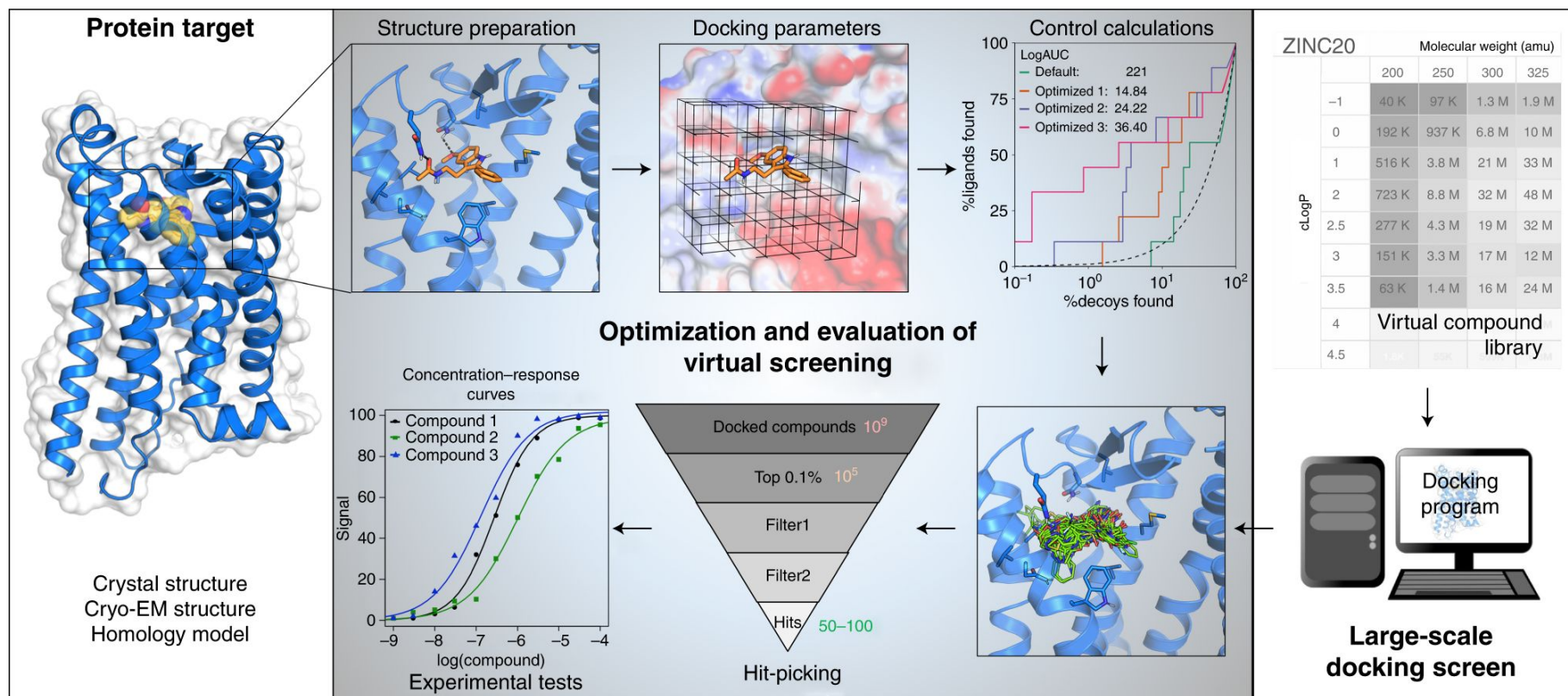
Kenneth Huang

Šali & Echeverria Labs

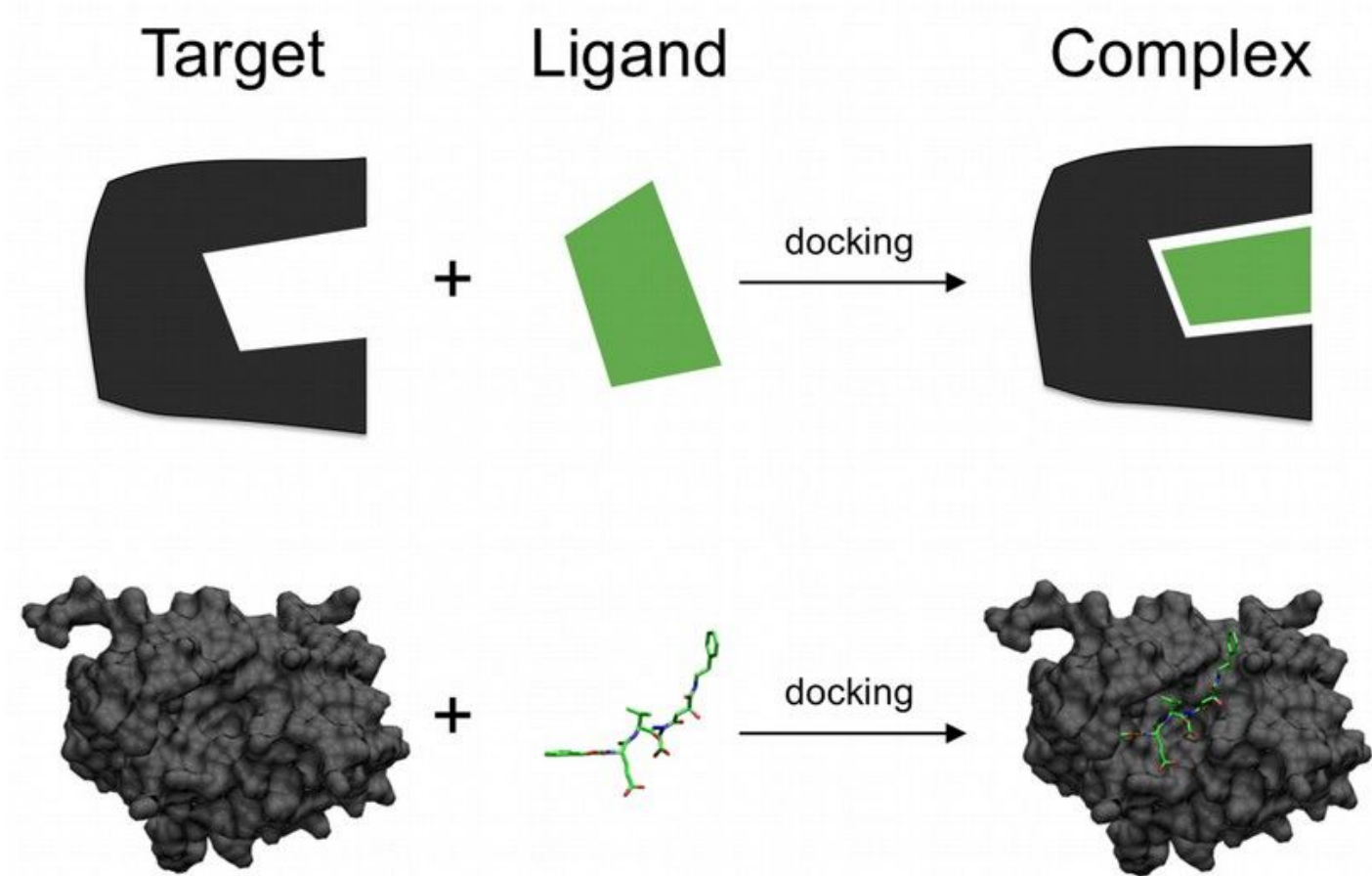
University of California, San Francisco



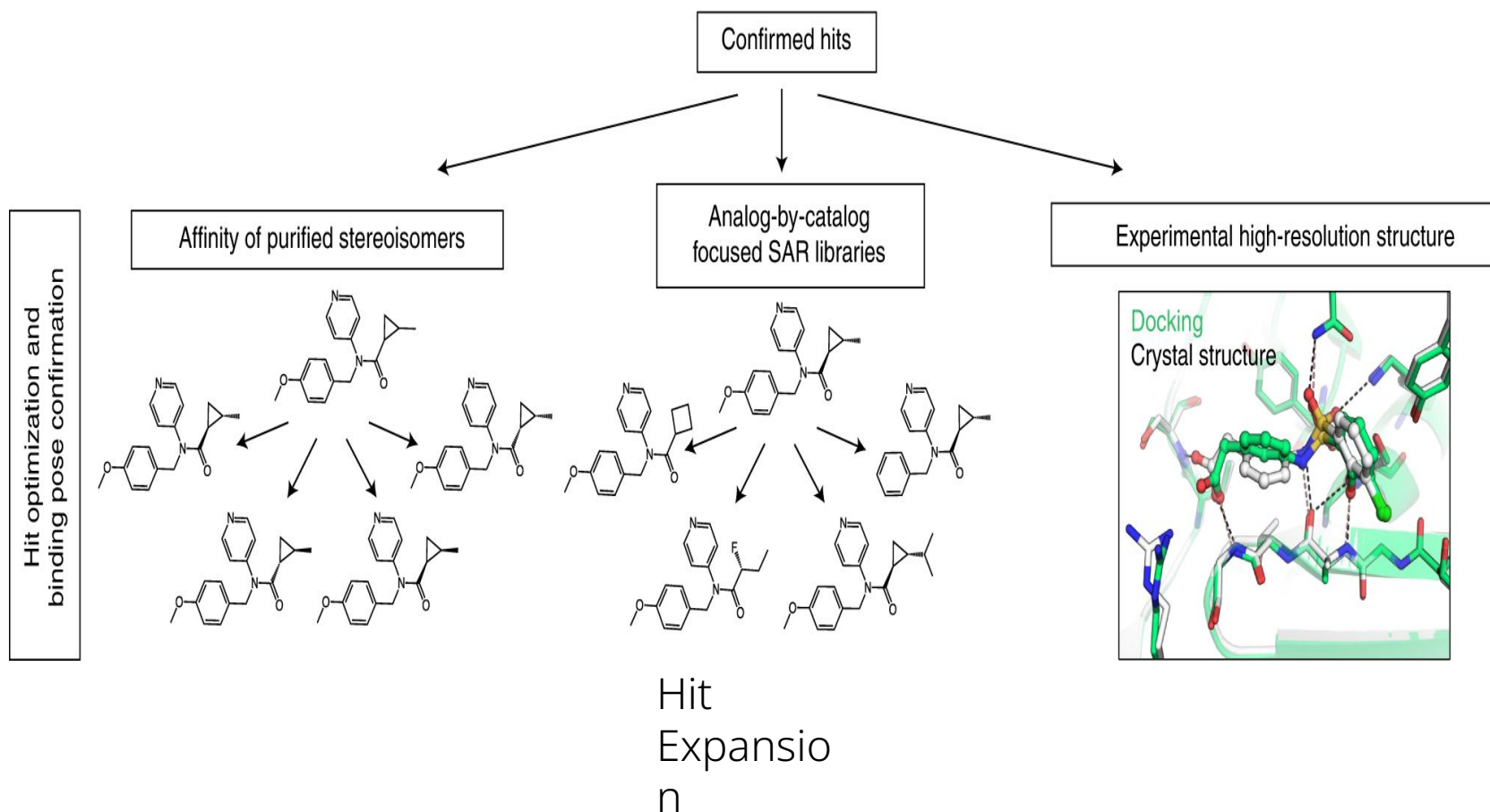
# From desktop to experimental applications



# Molecular docking: searching for small molecule design



# Drug design becomes an enumerative problem based on increasing number of combinations

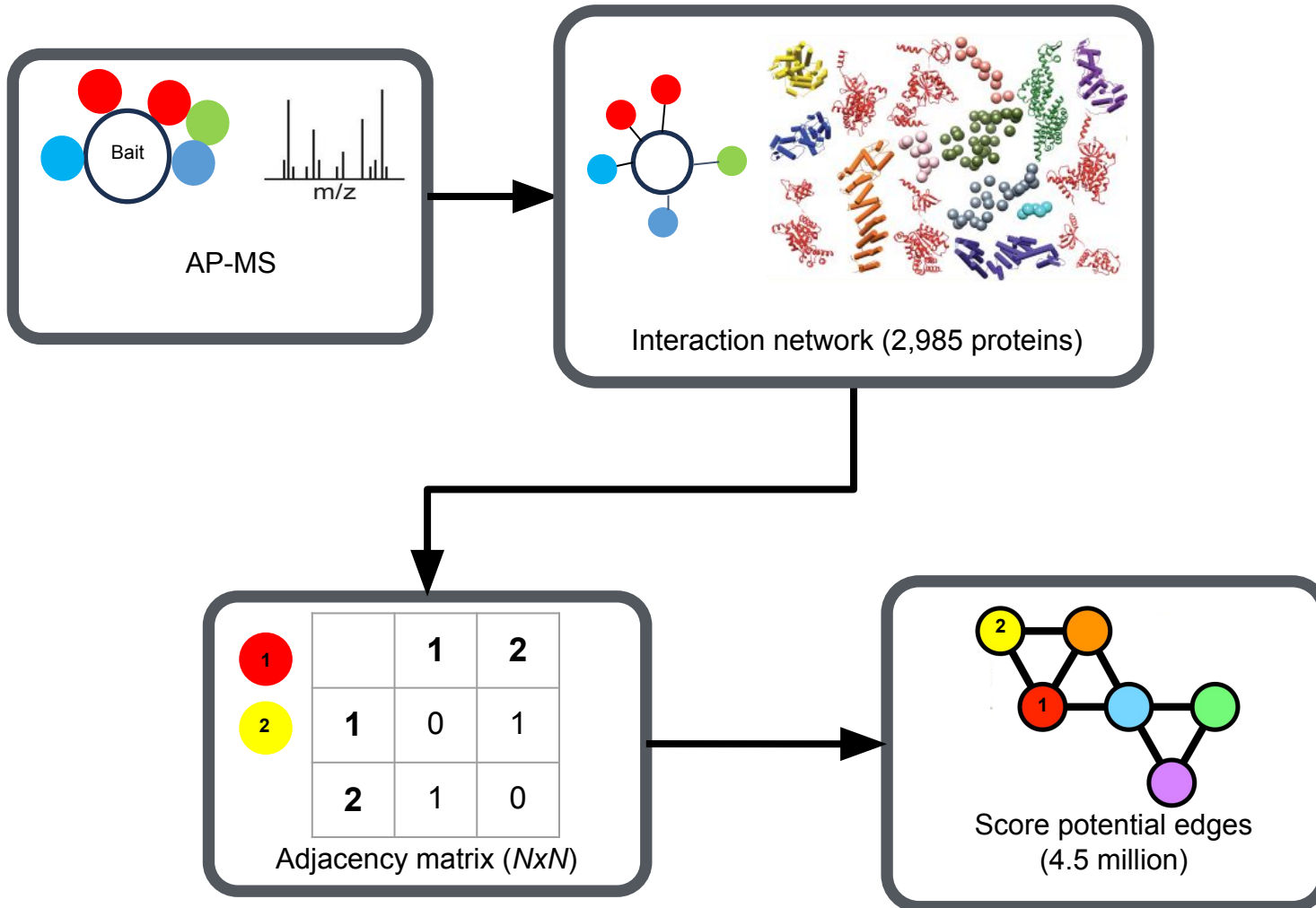


# Does the solution fit the problem?

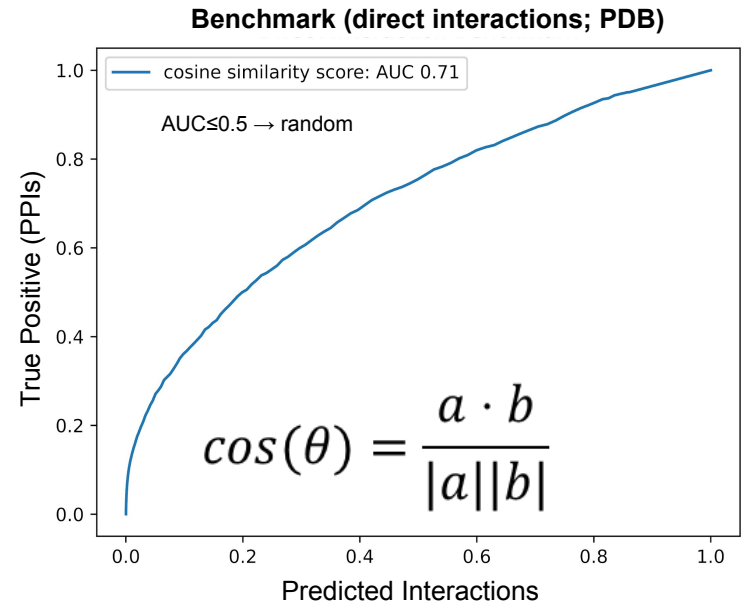
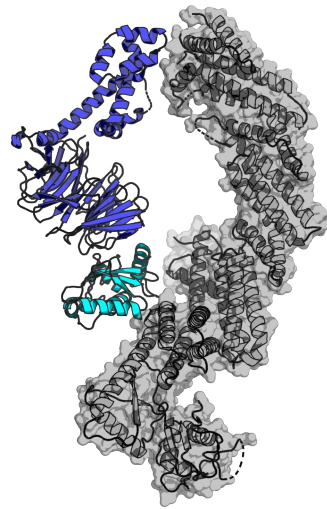
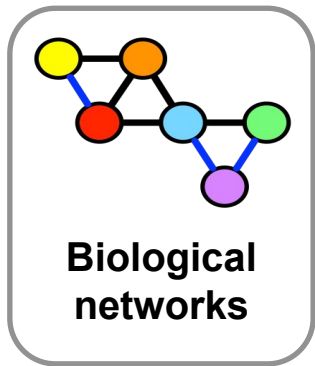


I'LL OFTEN ENCOURAGE RELATIVES TO TRY TO SOLVE  
COMPUTER PROBLEMS THEMSELVES BY TRIAL AND ERROR.  
HOWEVER, I'VE LEARNED AN IMPORTANT LESSON: IF THEY  
SAY THEY'VE SOLVED THEIR PROBLEM, *NEVER* ASK HOW.

# Machine learning: pattern searching and dimensional reduction of the data



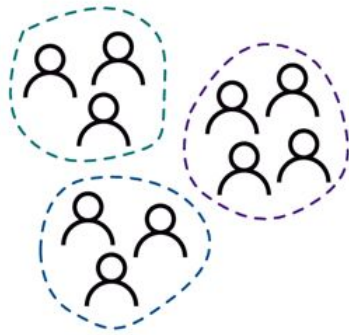
# Machine learning: pattern searching and dimensional reduction of the data





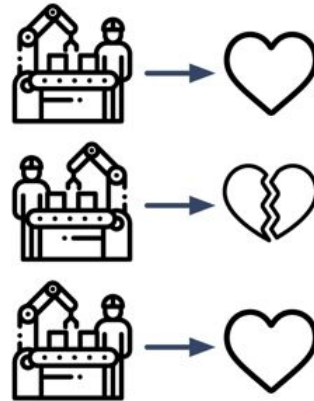
# The triad of machine learning approaches

## Unsupervised Learning



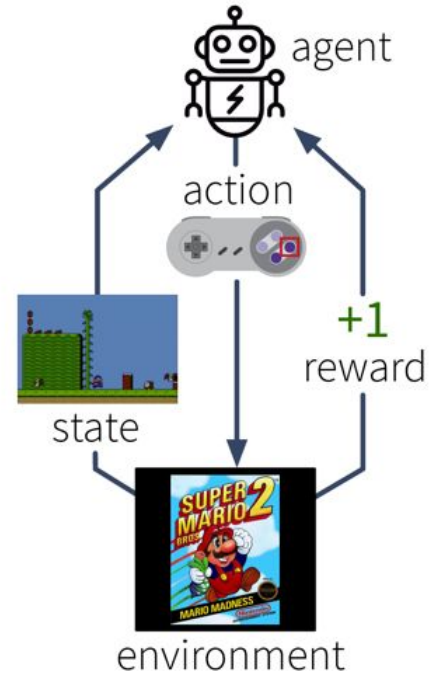
discover patterns  
in the data

## Supervised Learning



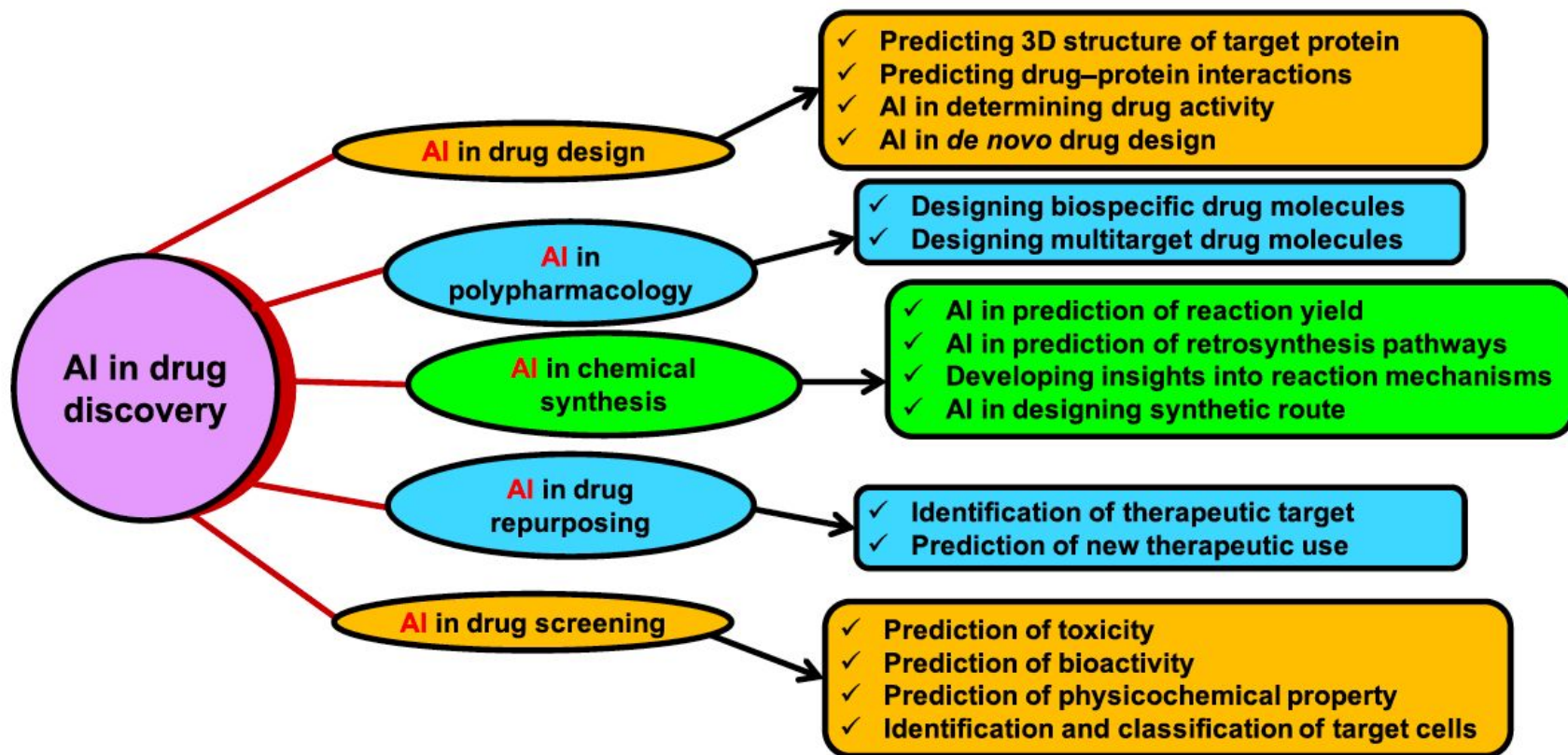
a model generates  
a specific output  
given some input

## Reinforcement Learning

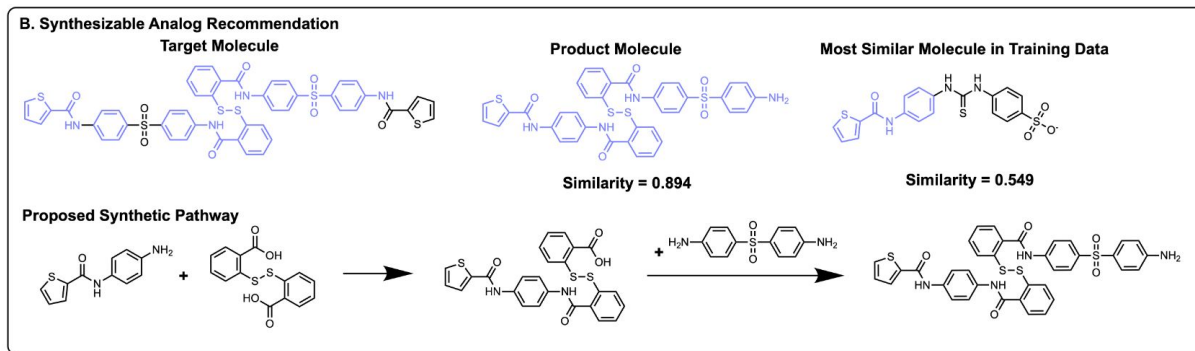
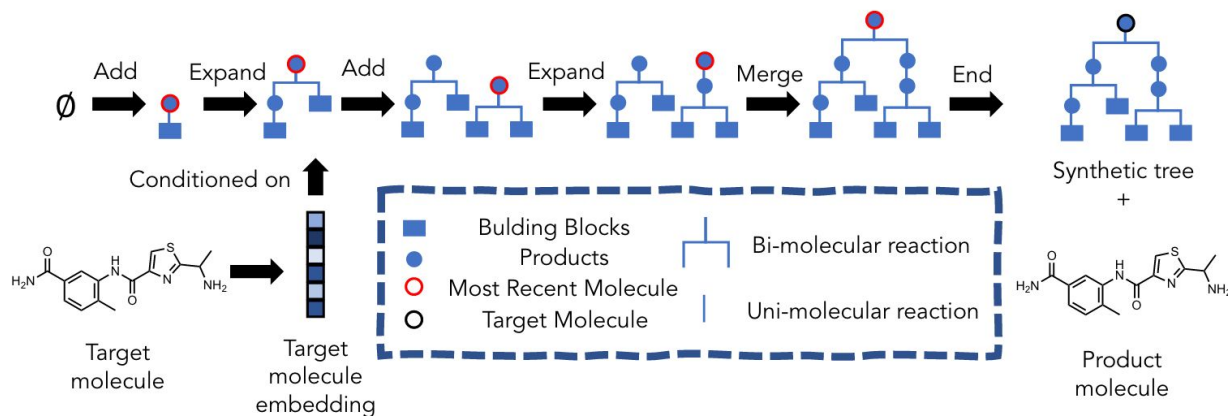




# Drug design is a problem/environment largely denoted by a large amount of noise

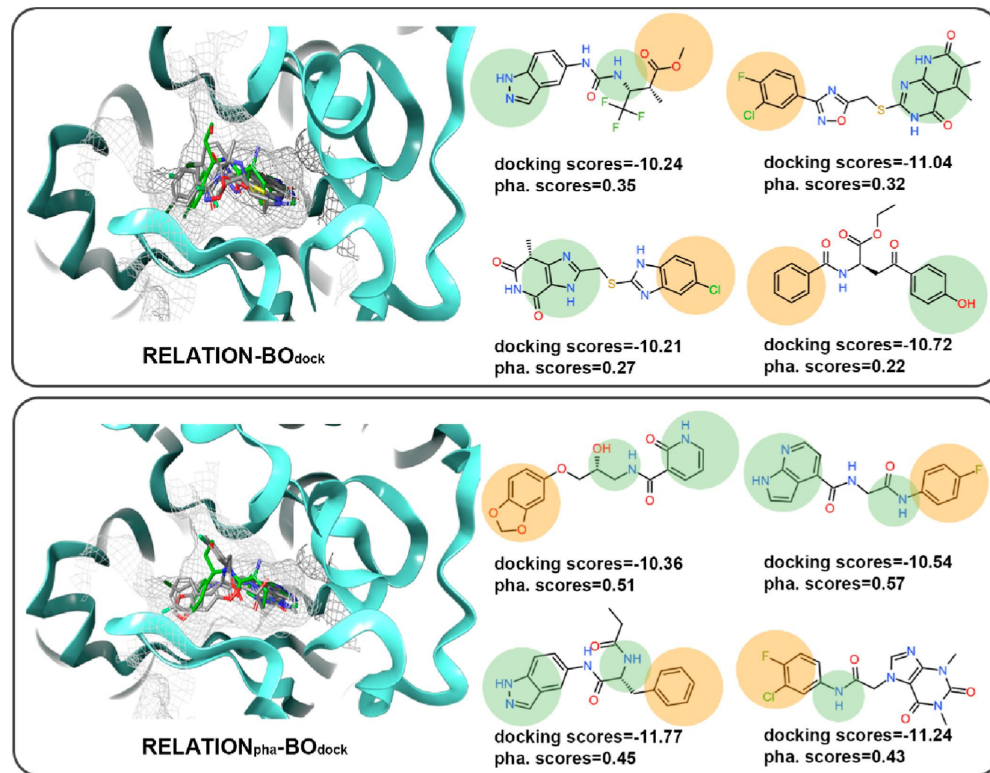


# De novo drug design by exploration of alternative synthetic pathways

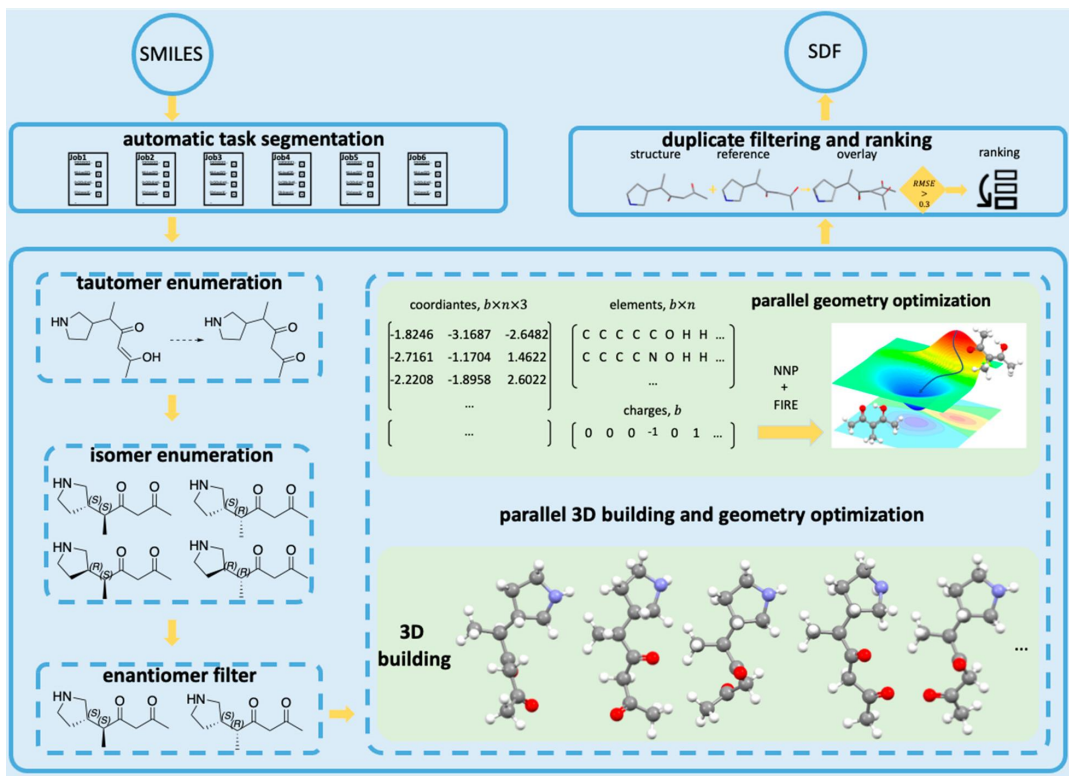


# De novo drug design by exploration of alternative synthetic pathways

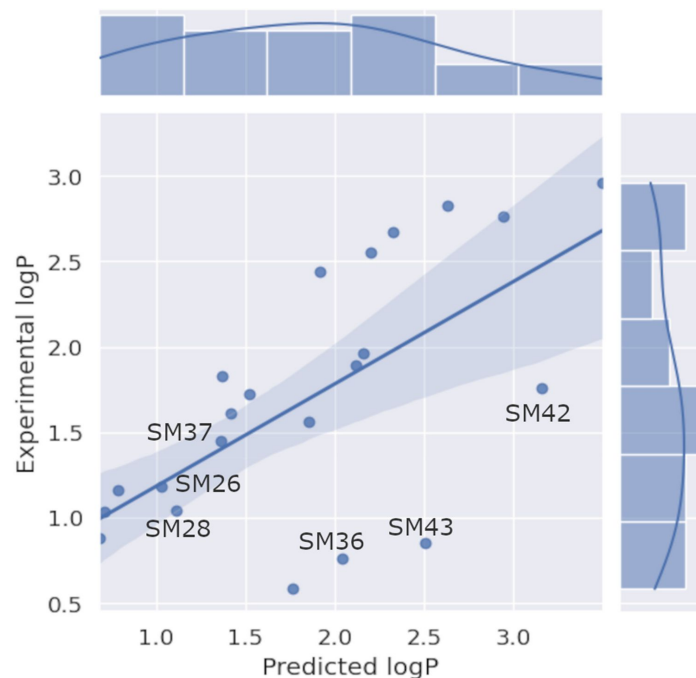
## RELATION: A Deep Generative Model for Structure-Based De Novo Drug Design



# 3D conformer generation to assist in prediction of molecular properties



## Auto3D: Automatic Generation of the Low-energy 3D Structures with ANI Neural Network Potentials



Liu, Z.; Zubatiuk, T.; Roitberg, A.; Isayev, O. *J. Chem. Inf. Model.* **2022**, 62 (22), 5373–5382.

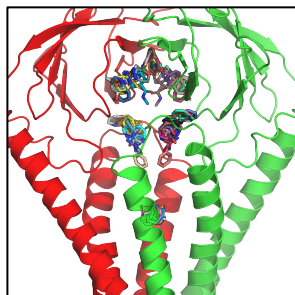
[https://github.com/isayevlab/Auto3D\\_pkg](https://github.com/isayevlab/Auto3D_pkg)

Lenselink, Eelke B., and Pieter FW Stouten. *Journal of Computer-Aided Molecular Design* 35, no. 8 (2021): 901-909.

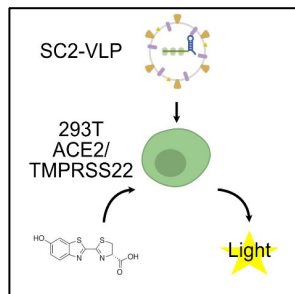


# Case 1: Plurality of binding sites

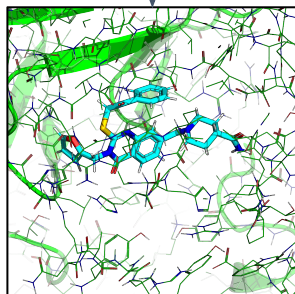
Identify ligand pocket



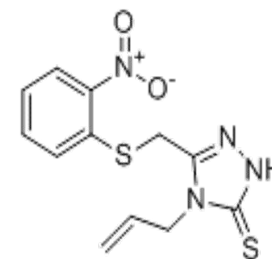
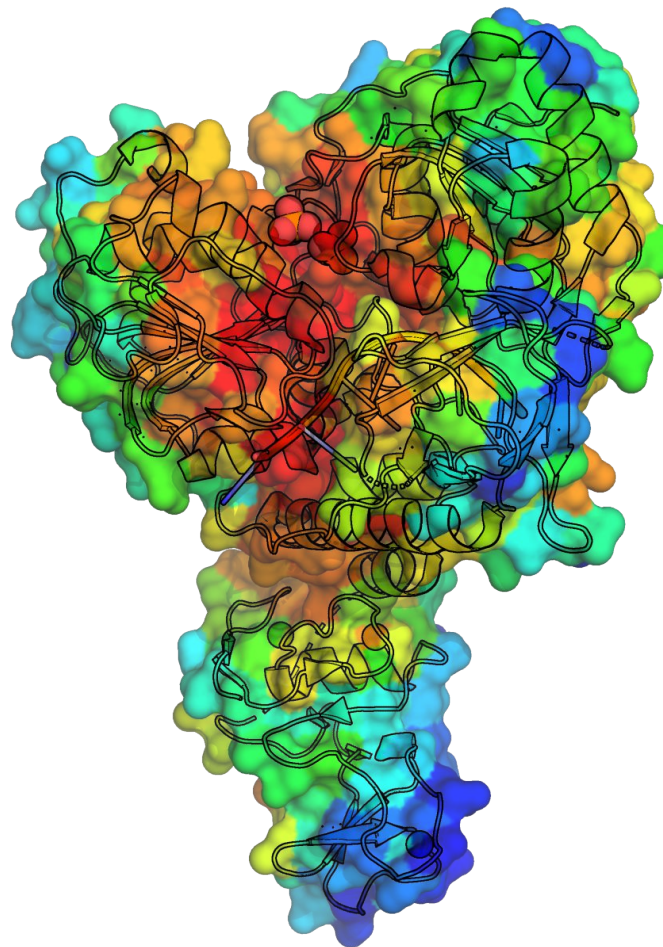
Verify activity with assays



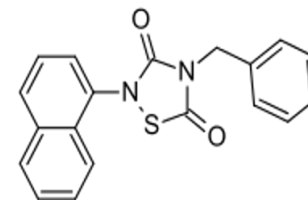
Optimize ligand design



Multi-functionality of viral proteins  $\Rightarrow$  multiple pockets



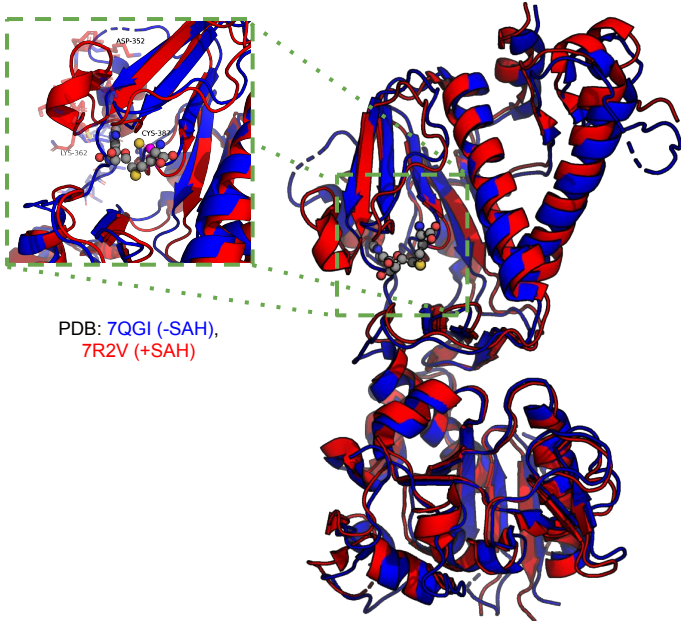
SSYA-10-001  
IC50 = 0.6uM



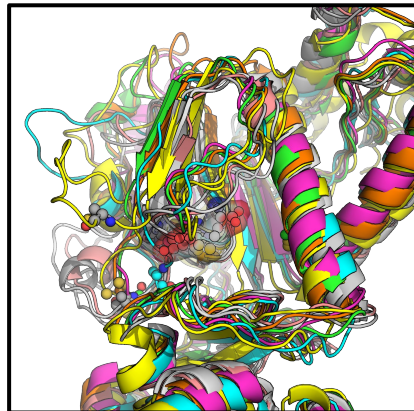
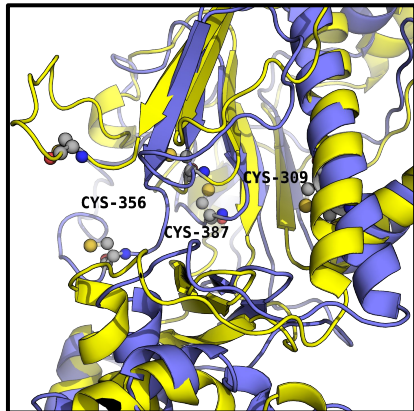
Tideglusib  
IC50 = 25-50uM

# Case 2: Multi-state proteins increase search space for ligand discovery

Additional conformations in ligand pocket(s)



PDB: 7QGI (-SAH),  
7R2V (+SAH)



Expanding range of potential ligand pockets

