

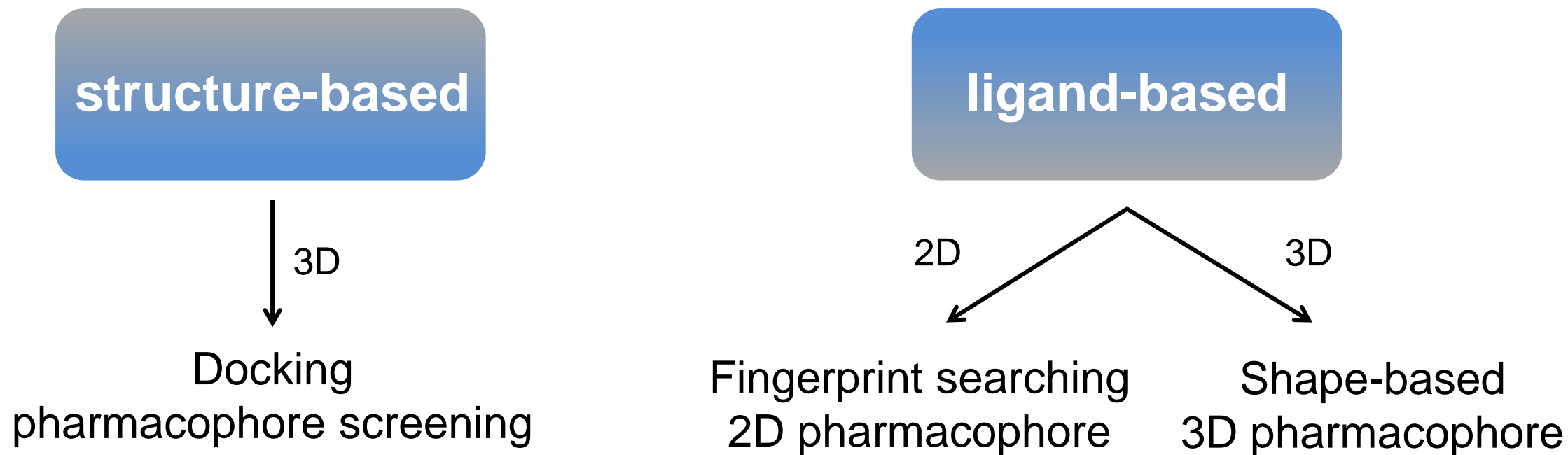


Structure-Based Virtual Screening with Glide

Stephan Ehrlich

Virtual Screening is a Starting Point in CADD

- Uses *in silico* methods to identify molecules that could bind to a target
- These methods are classified as either **structure-based** or **ligand-based**:





Virtual screening with glide: Theory

Ligands are Evaluated in Three Ways

Docking



Scoring



Filtering

What possible poses can my ligand adopt in the binding site?

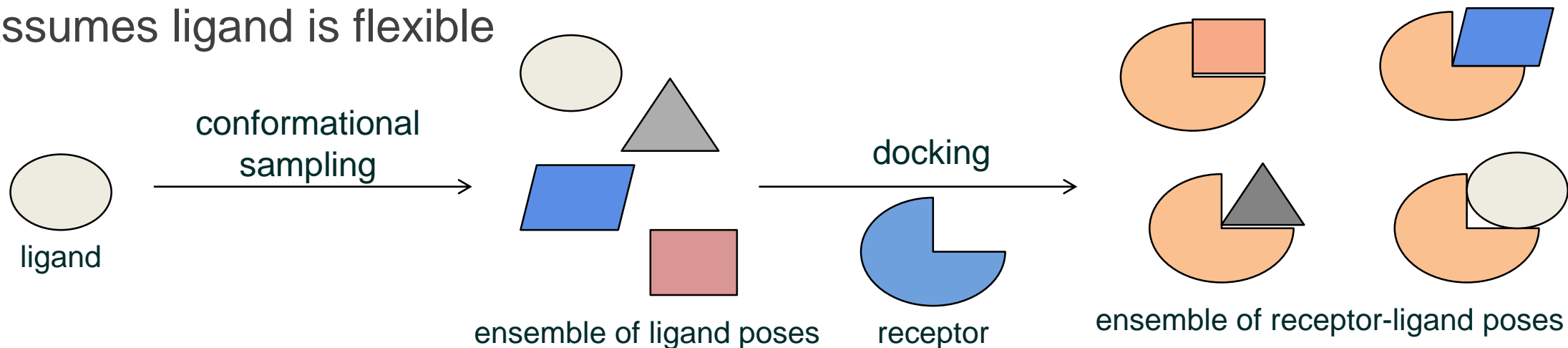
Which of those poses makes the best interactions with the receptor?

Which of those make the contacts I care about?

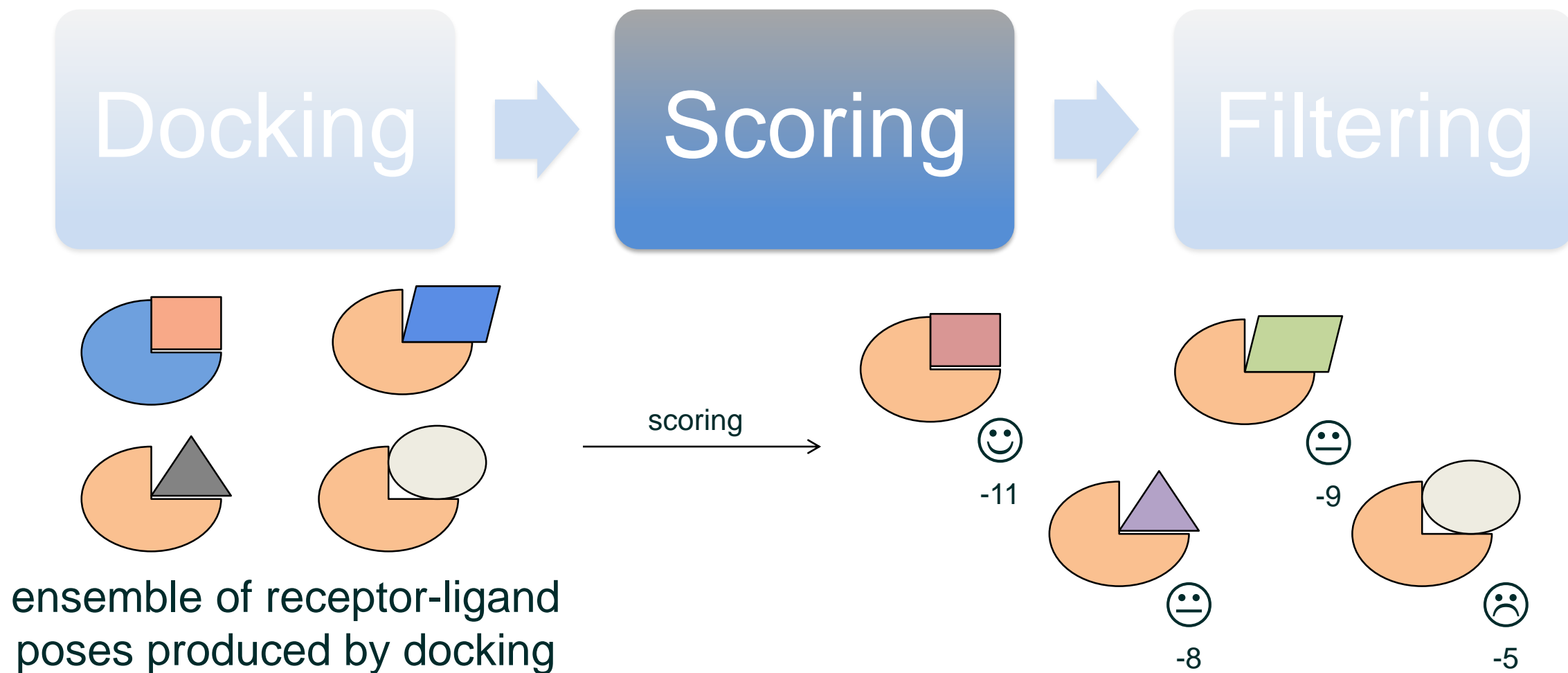
Docking Fits Ligands to a Receptor



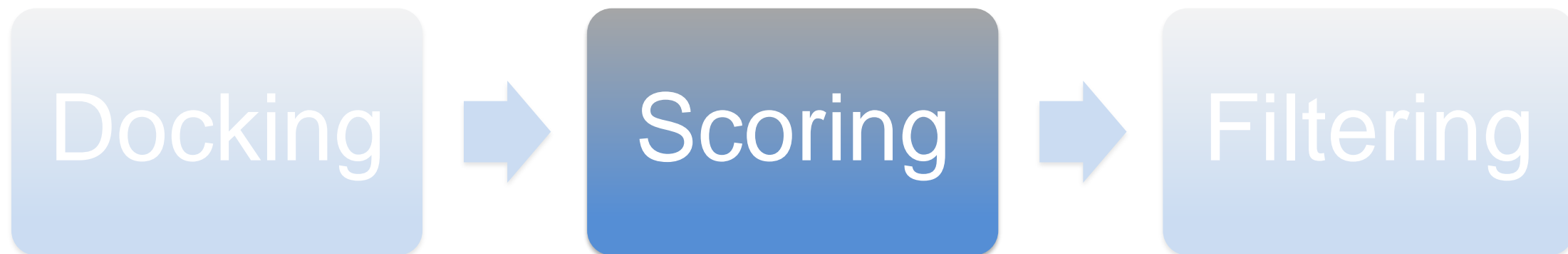
- Assumes receptor is rigid
- Assumes ligand is flexible



Scoring Evaluates the Ligand Fit



Scoring Evaluates the Ligand Fit



Scoring functions:

- **Do not** correlate with IC_{50} , K_d , EC_{50} , etc.
- **Do not** provide a rank-ordering of ligands
- Are optimized to **give good enrichment**
 - Separates “good” ideas from “bad”
 - Limit the number of ligands to be investigated further

Glide has Different Scoring Functions

Scoring Function	Computing Time	When to Use
SP	10 – 30 sec/molecule	First pass virtual screening on large databases/hit generation
XP	3-5 min/molecule	Refinement of a smaller dataset /lead optimization

- SP seeks to minimize **false negatives** while XP seeks to minimize **false positives**
- The XP scoring function includes more stringent terms for modeling desolvation, hydrophobic effects, and charged interactions

Filtering Refines the Ligand Evaluation

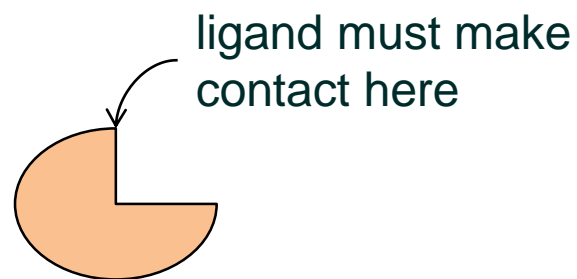
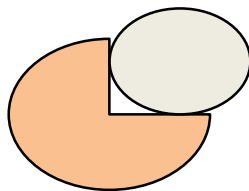
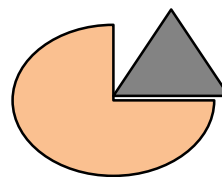
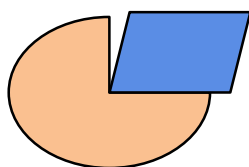
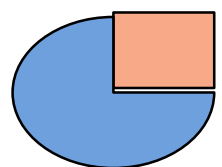
Docking



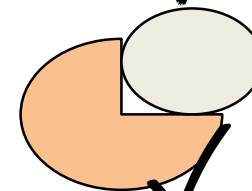
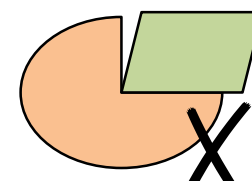
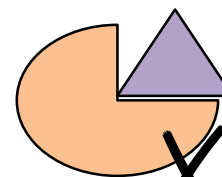
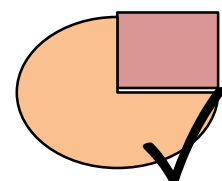
Scoring



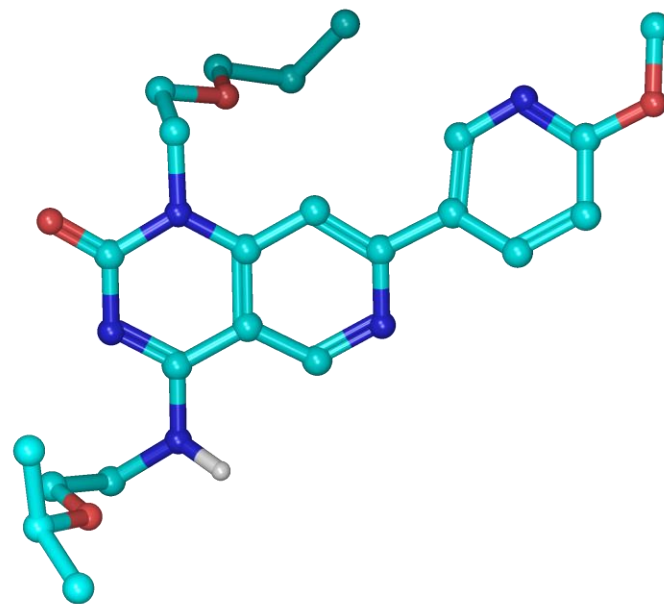
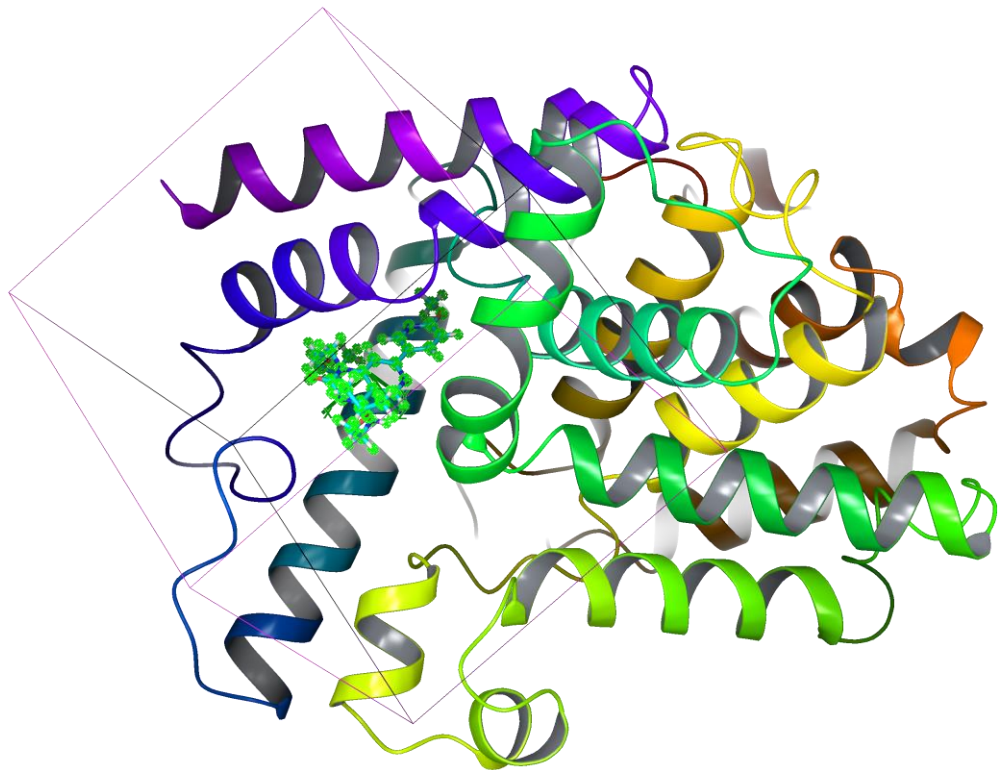
Filtering



filtering



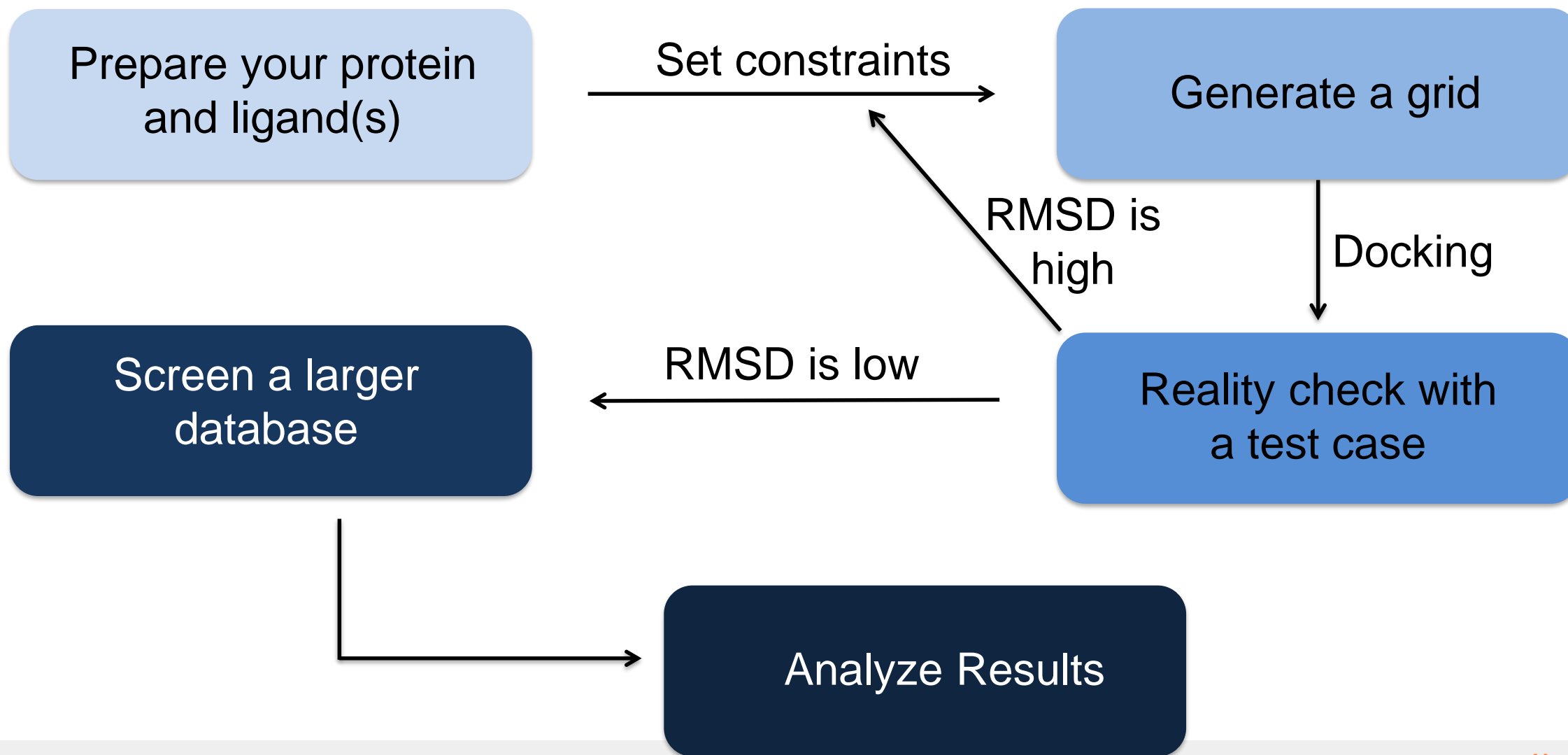
Glide Docking is Run in Two Steps



A 3D molecular docking visualization. A protein structure is shown as a grey ribbon against a dark background. A ligand molecule, depicted with orange spheres and a stick model, is docked into the protein's binding pocket. The text "Virtual screening with Glide: Application" is overlaid in white.

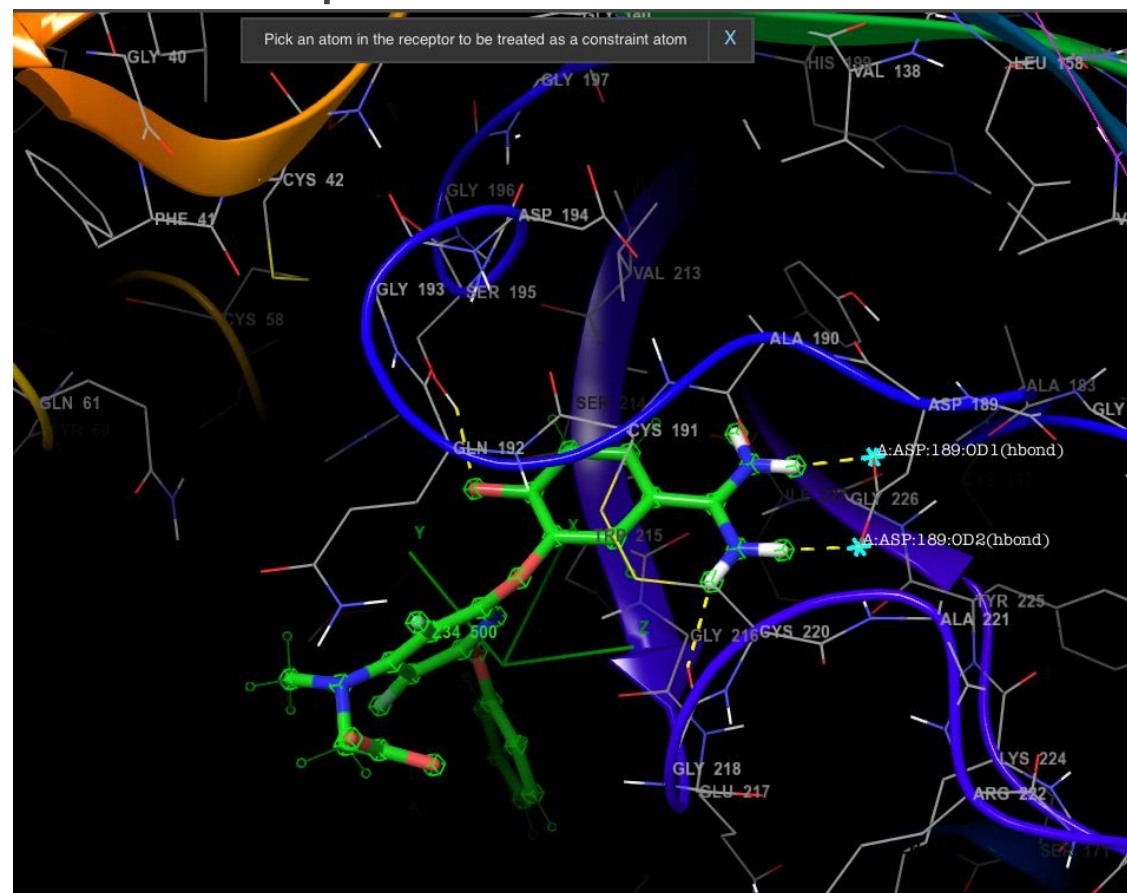
Virtual screening with Glide: Application

An Ideal Workflow for a Virtual Screen using Glide



Constraints Can Add Information

- Evaluate evidence that a ligand should bind in a specific area or make a particular contact
 - crystal structure data
 - site-directed mutagenesis data
 - biological data
- Types of constraints:
 - Positional and NOE
 - Hydrogen-bonding and metal
 - Metal coordination
 - Core



Useful Video Links Related to Today's Workshop

- Ligand Preparation

<https://www.schrodinger.com/training/videos/ligand-preparation>

- Receptor Grid Generation

<https://www.schrodinger.com/training/videos/docking-receptor-grid-generation-docking-virtual-screening/glide-receptor-grid>

- Docking

<https://www.schrodinger.com/training/videos/docking-ligand-docking>

- Applying Constraints in Docking

<https://www.schrodinger.com/training/videos/docking-ligand-docking/using-h-bond-and-positional-constraints>

Other Education Resources are Available Online

- Knowledge Base: <https://www.schrodinger.com/kb/>
- Support Center: <https://www.schrodinger.com/supportcenter>
- Training Center: <https://www.schrodinger.com/training>
- Schrödinger Seminar Series:
<https://www.schrodinger.com/seminars/current>
<https://www.schrodinger.com/seminars/archives>
- Script Center: <https://www.schrodinger.com/scriptcenter/>

Thanks for Joining Us!

Scientific and Technical Support

help@schrodinger.com

