

### RDKit UGM 2015

Aligning ideas to bound ligands in PyMOL



# Helping chemists be (even more) creative

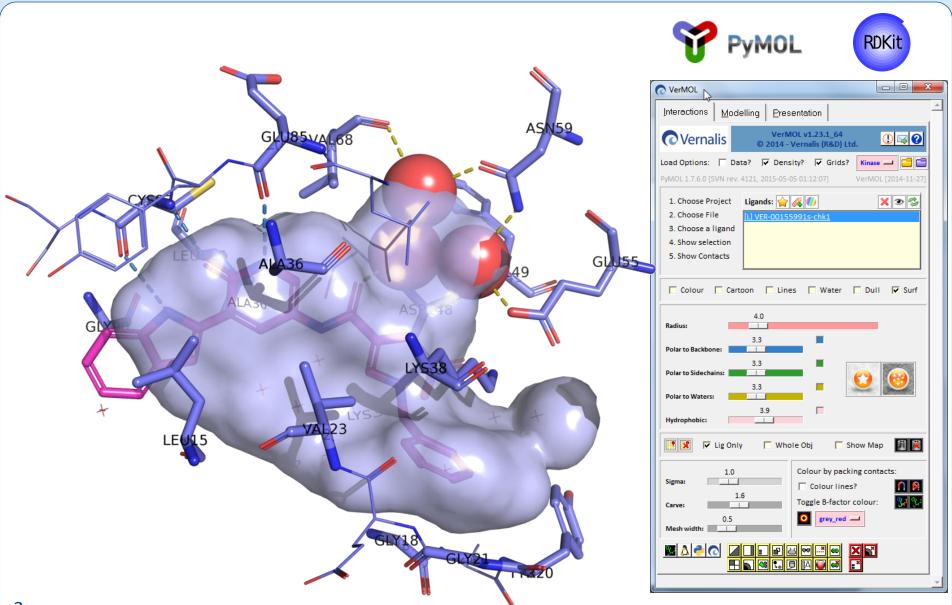


- Goal all our chemists should be able to:
  - Explore details of ligand-bound crystal structures
  - Assess and prioritise their own structure-based hypotheses
  - Share ideas with expert computational chemists for higher-level calculations

# **Automatically annotate binding sites**

**VerMOL** – PyMOL plugin to help our chemists

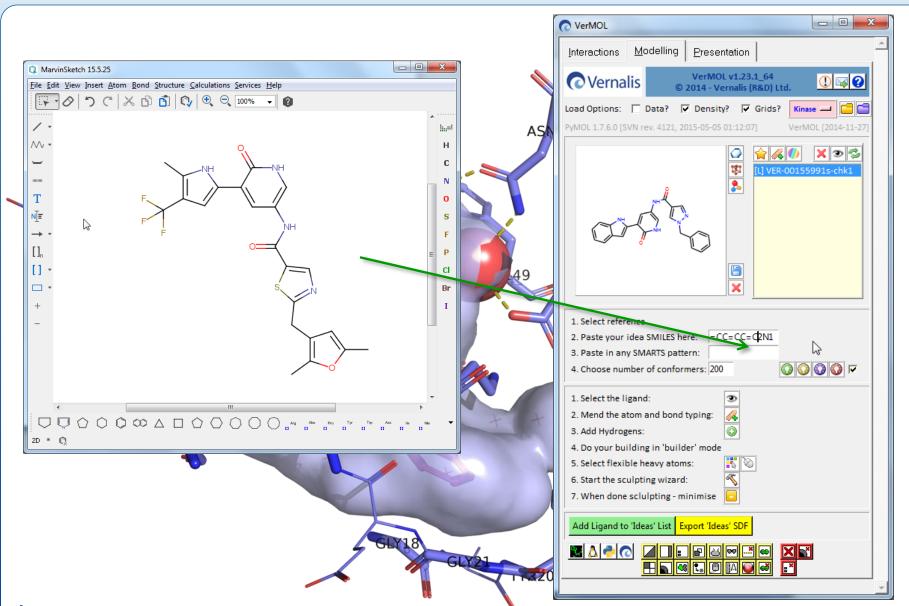




## Assessing a new idea

Sketch, copy, paste, score

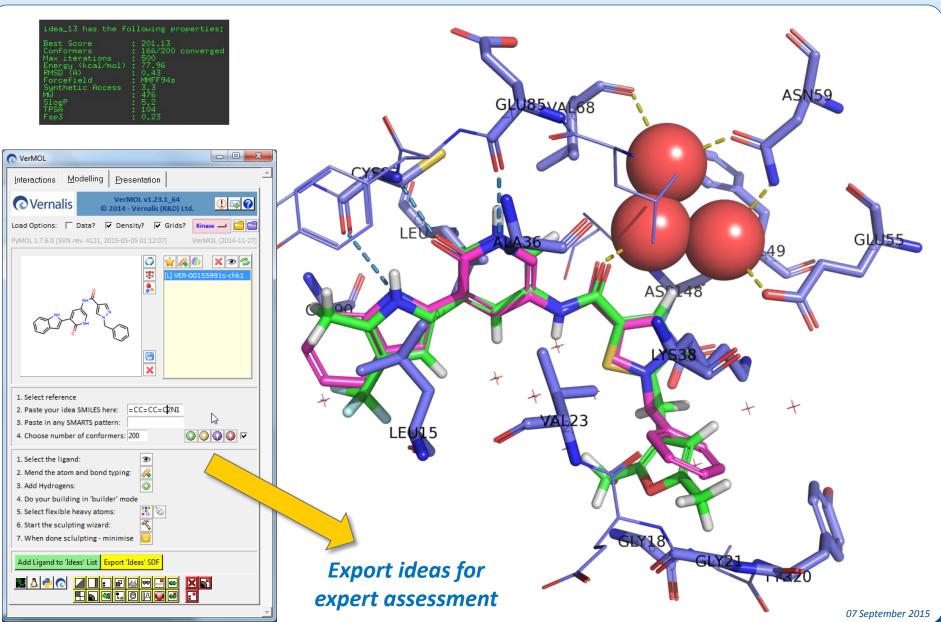




#### Scored idea

#### Based on best ligand overlay



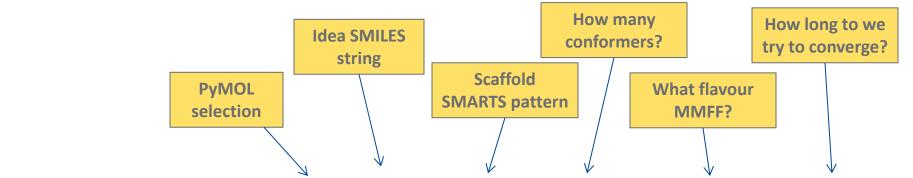


## Implementation steps (and demo)



Actually, for the live demo we'll use the **2C3K** PDB structure

RESEARCH part of Vernalis plc



1. generateIdeaConformers(sele, smiles, smarts, numConfs, mmFFVariant, maxIters, numThreads)

This is the 'orchestrating' function

2. pymolSelectionToRDKit(sele)

Returns RDKit molecule for the reference ligand

multiConfFromSmiles(smiles, nConfs, maxIters, mmFFVariant, numThreads)

AllChem.EmbedMultipleConfs(idea, numConfs, numThreads)

AllChem.MMFFOptimizeMoleculeConfs(idea, numThreads, maxIters, mmffVariant)

Returns multi-conformer RDKit molecule

4. alignMultiConfToRef(multiConfMol, ref)

AllChem.GetO3AForProbeConfs(multiConfMol, ref, prbPyMMFFMolProperties, refPyMMFFMolProperties, constraintMap, numThreads)

Returns pandas dataframe

5. dataframeToPyMOLloadSDF(dataframe)

Loads the object back into PyMOL as an SDF (so that we can step through, etc)