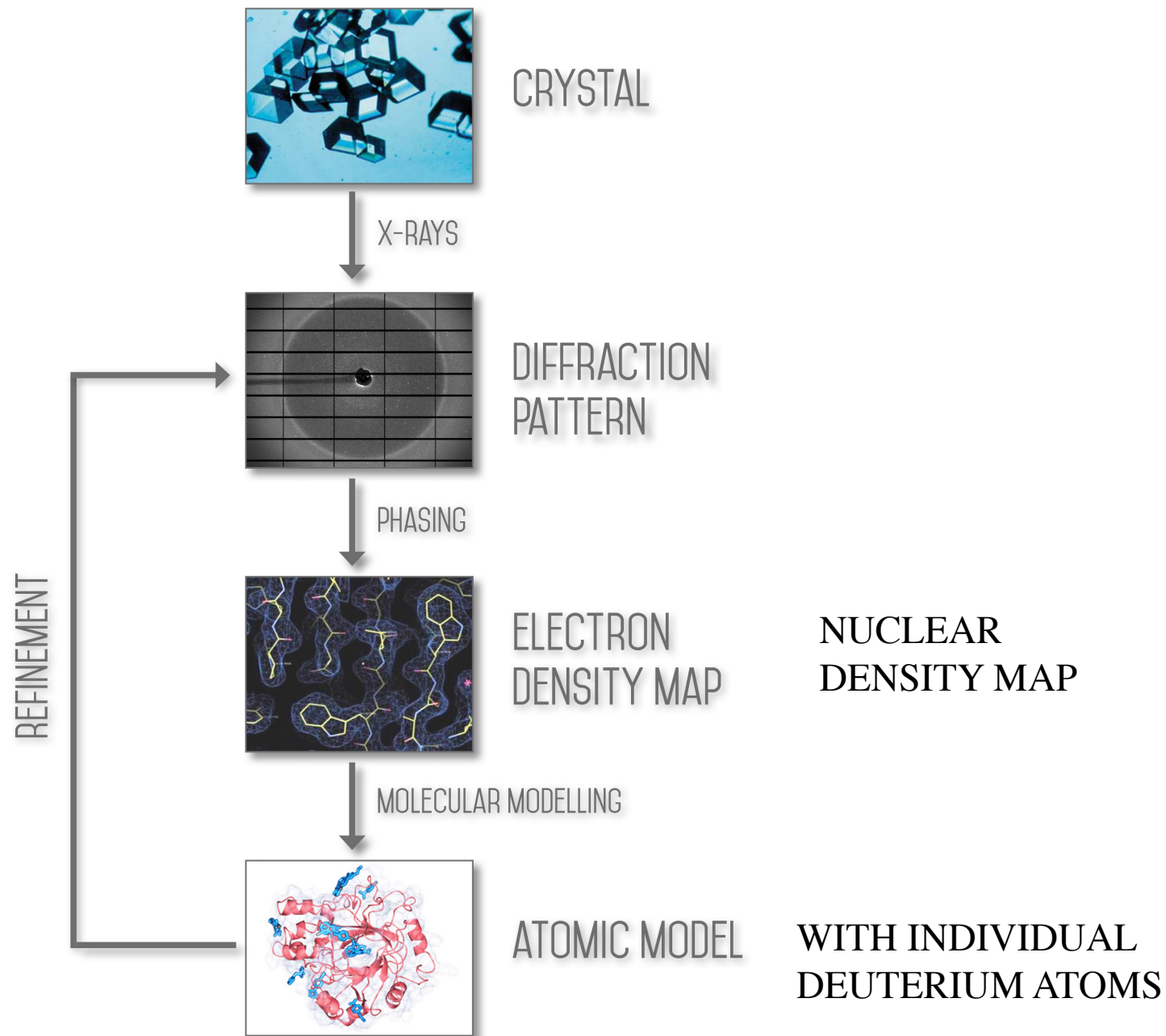


Enhancing refinement with quantum mechanics in neutron protein crystallography

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Crystallographic refinement

Structure refinement is a process of changing a model parameters in order to optimize a goal (target) function:

$$T = F(\textit{Experimental data}, \textit{Model parameters}, \textit{Restrains})$$

Experimental data – a set of diffraction amplitudes F_{obs}

Model parameters: coordinates, ADP, occupancies

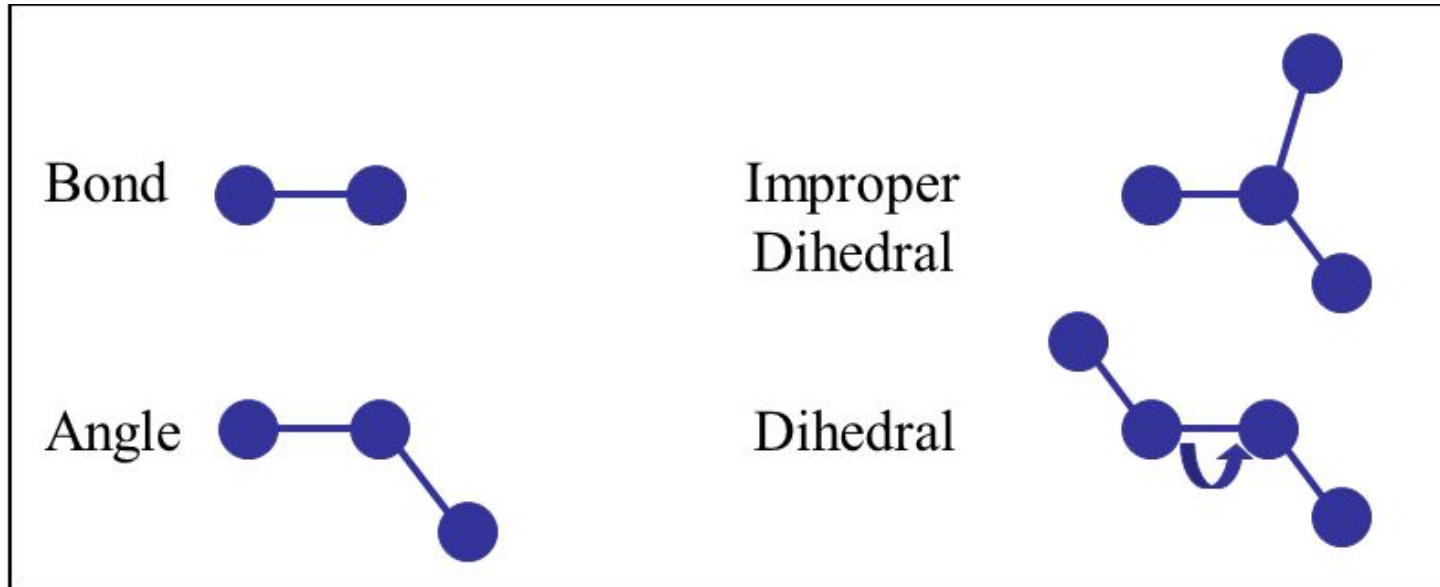
Restrains – additional information to compensate for the insufficiency of experimental data

$$E = W * E_{\text{DATA}} + E_{\text{RESTRAINTS}}$$

$$E = W (w_x * E_{\text{XRAY}} + w_N * E_{\text{NEUTRON}}) + E_{\text{EH}}$$

Restraints used in crystallographic refinement

Engh & Huber restraints – statistical force-field

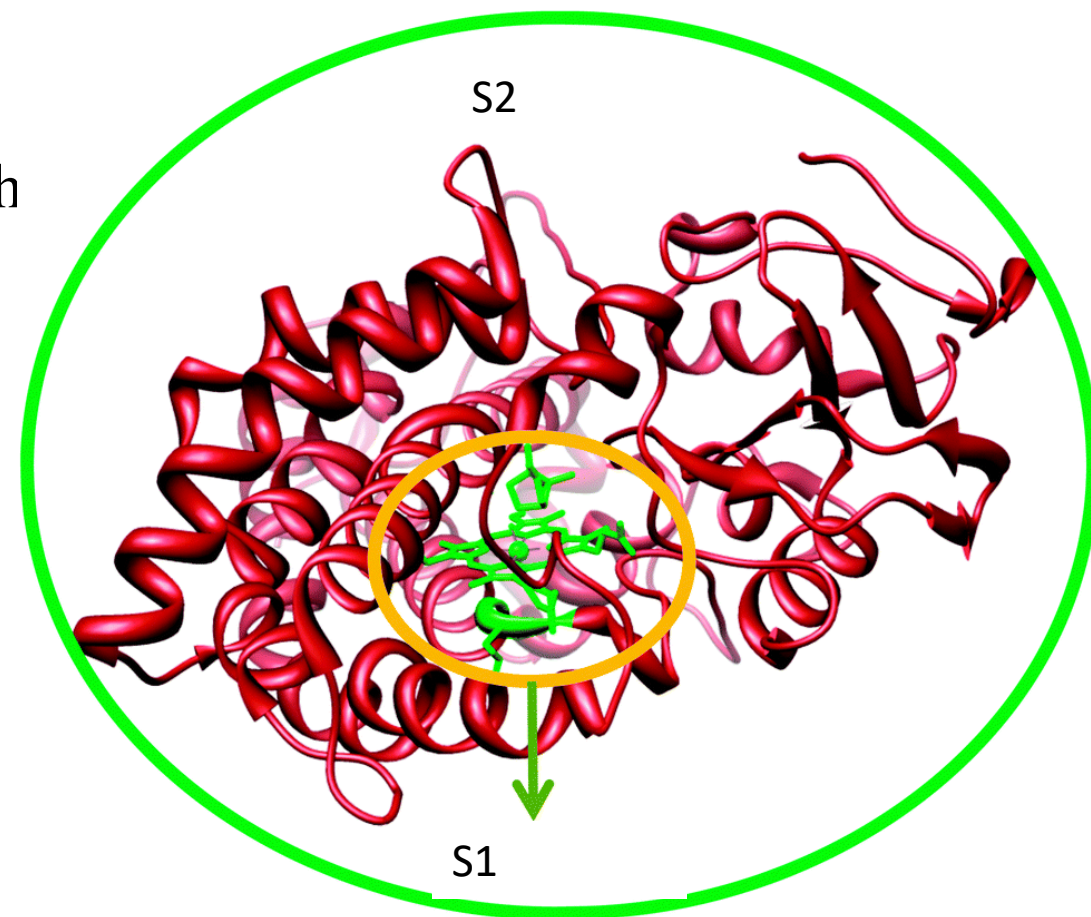


Quantum refinement – how does it work?

Combines nCNS (crystallographic refinement) with
Turbomole (QM calculations)

Refinement steps:

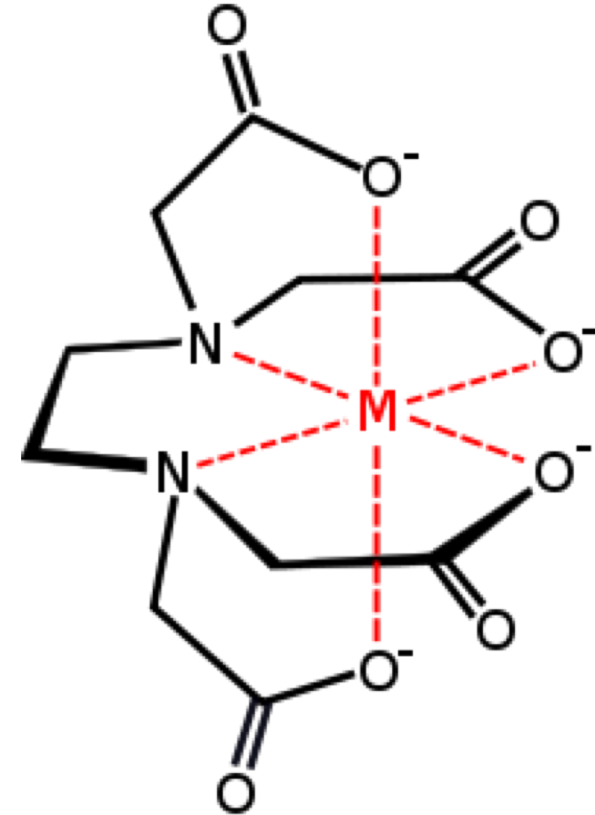
- Evaluate QM wavefunction
- Relax the geometry of S1
- Crystallographic refinement of S2 with S1
fixed
- ADP refinement



$$\mathbf{E} = \mathbf{w} (\mathbf{w}_X * \mathbf{E}_{X\text{-RAY}} + \mathbf{w}_N * \mathbf{E}_{\text{NEUTRON}}) + \mathbf{E}_{\text{QM1}} + \mathbf{w}_{\text{EH}} (\mathbf{E}_{\text{EH12}} - \mathbf{E}_{\text{EH1}})$$

How can quantum chemistry help in neutron protein crystallography?

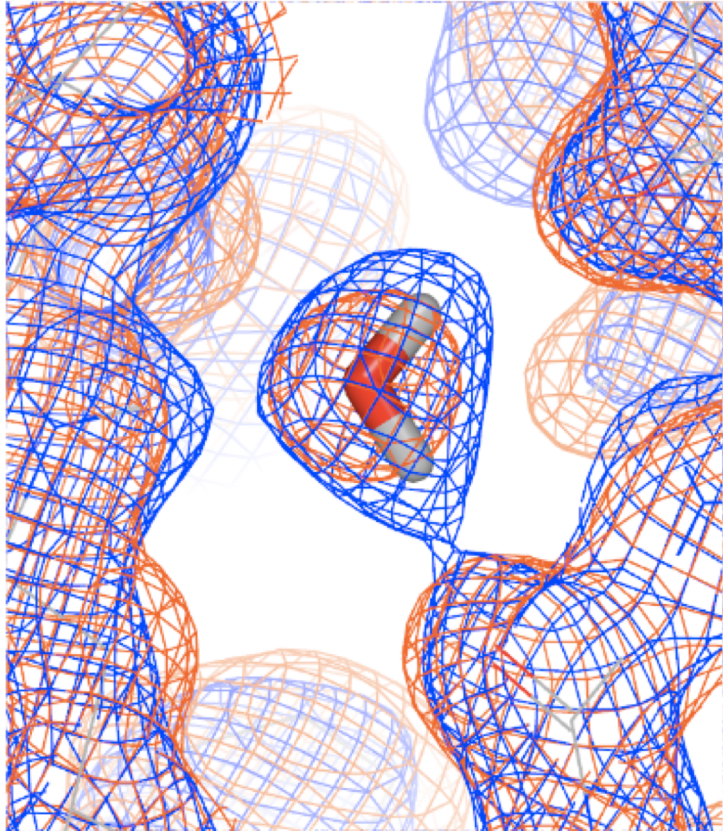
- Poor ligand parametrization
- Poor metal parametrization
- X-H/X-D distances not optimized
- Hydrogen bonding terms



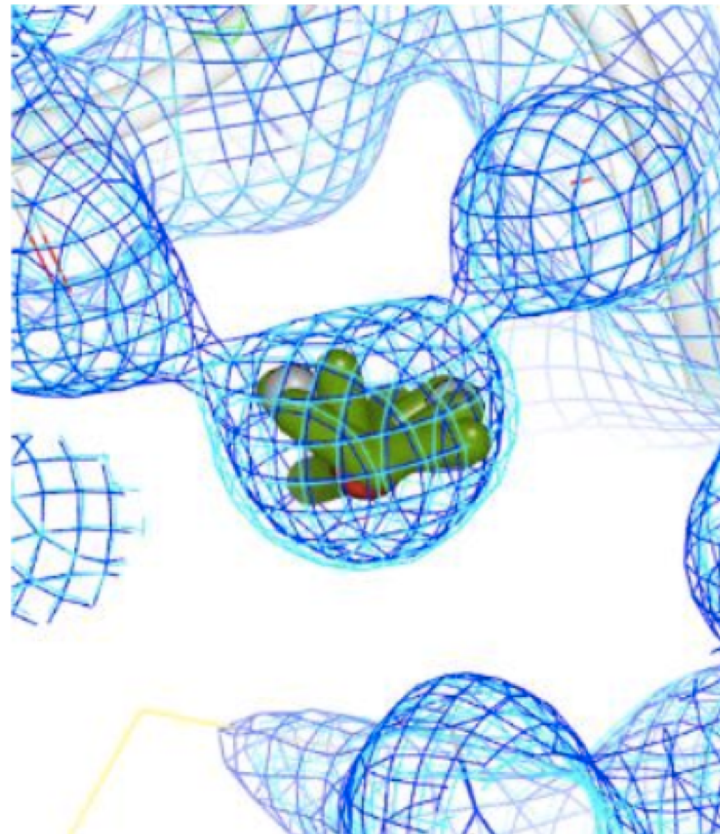


Applications

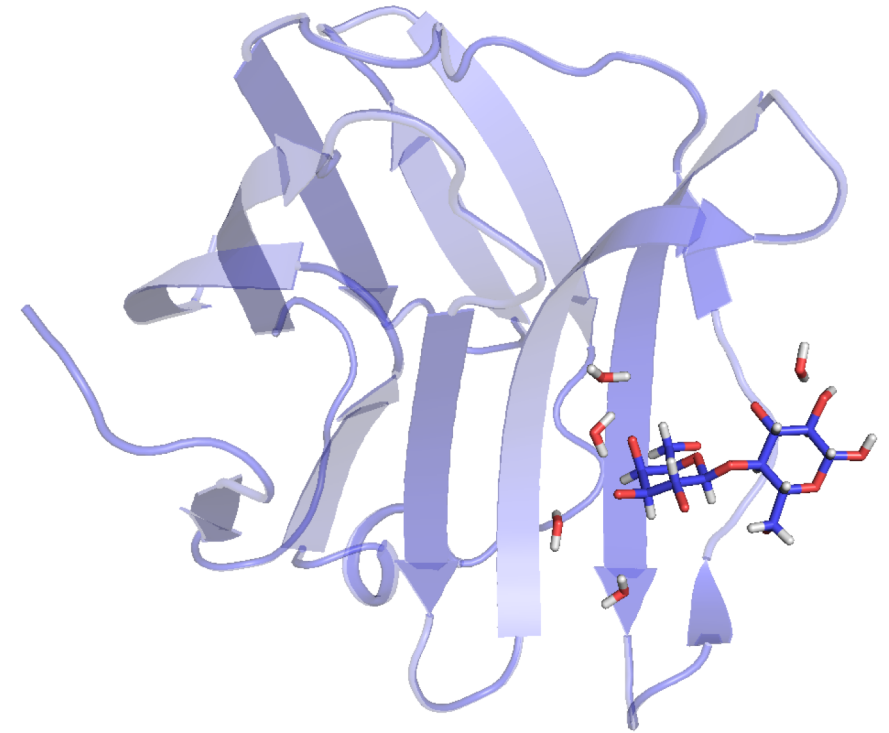
Orientation of water molecules



Orange – electron density
Blue – nuclear density

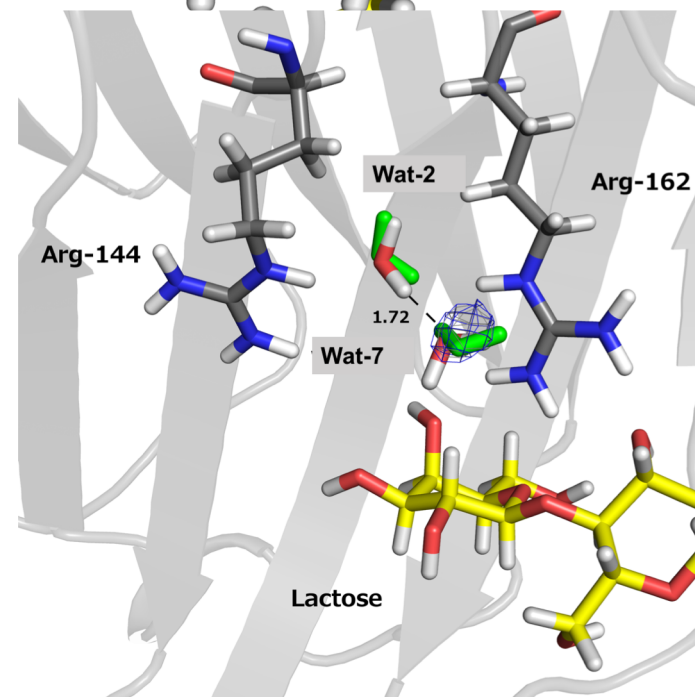
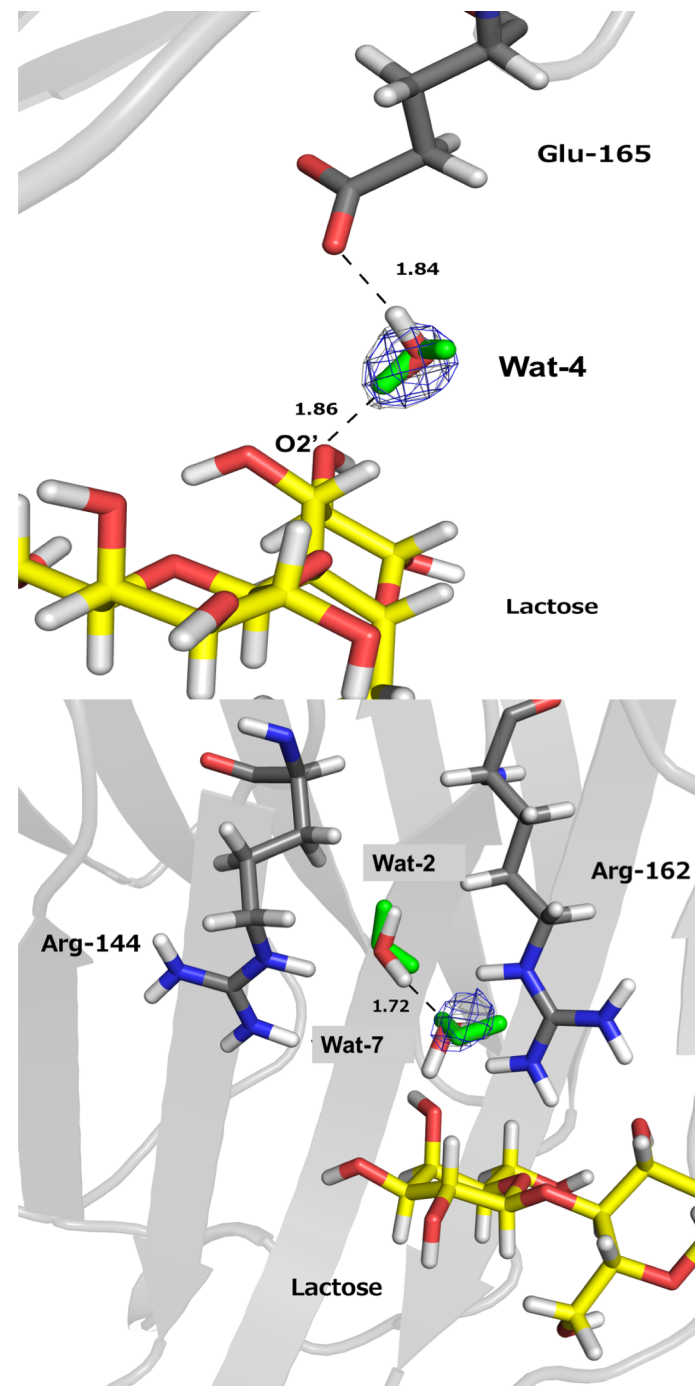
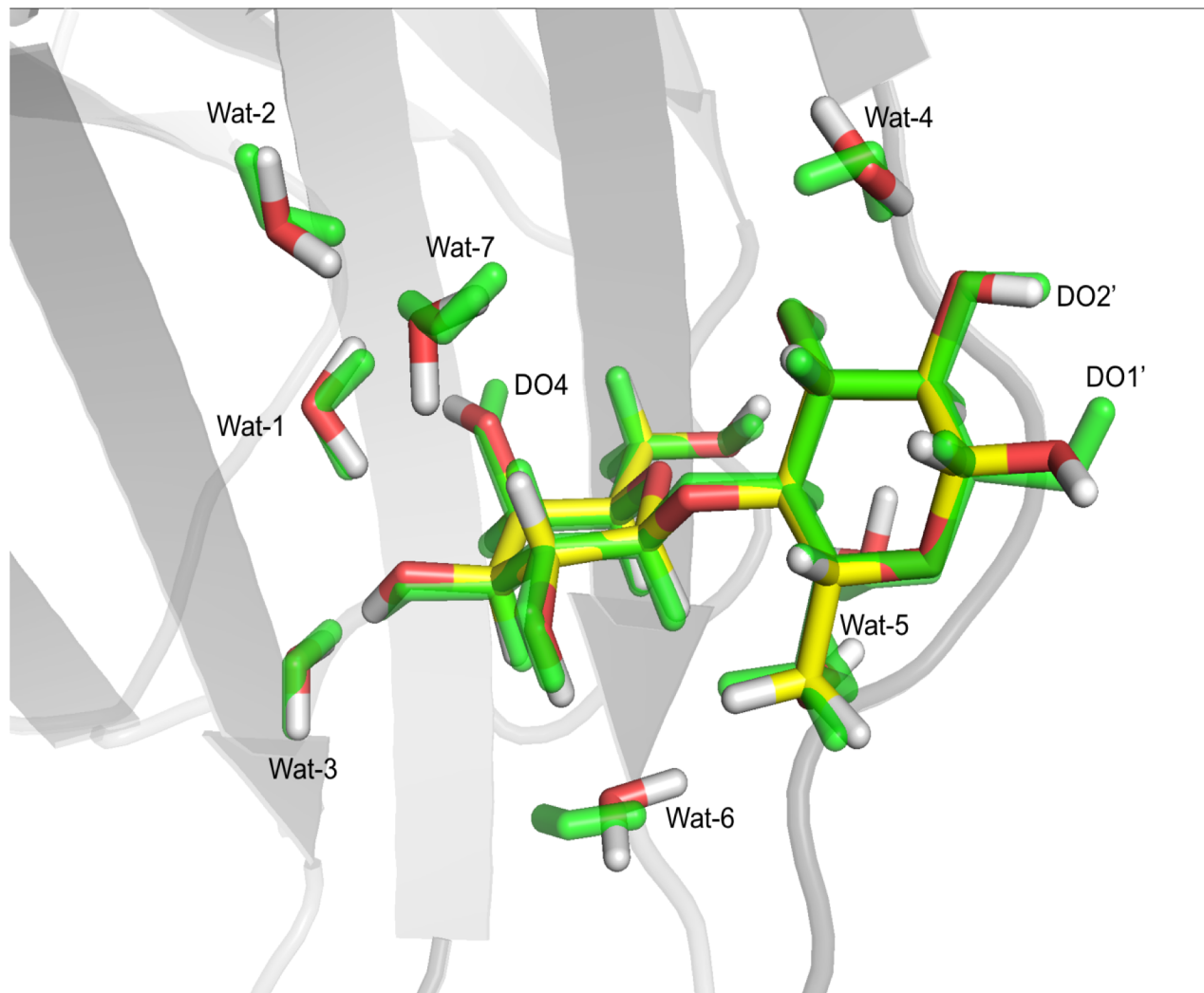


Teal – electron density
Blue – nuclear density

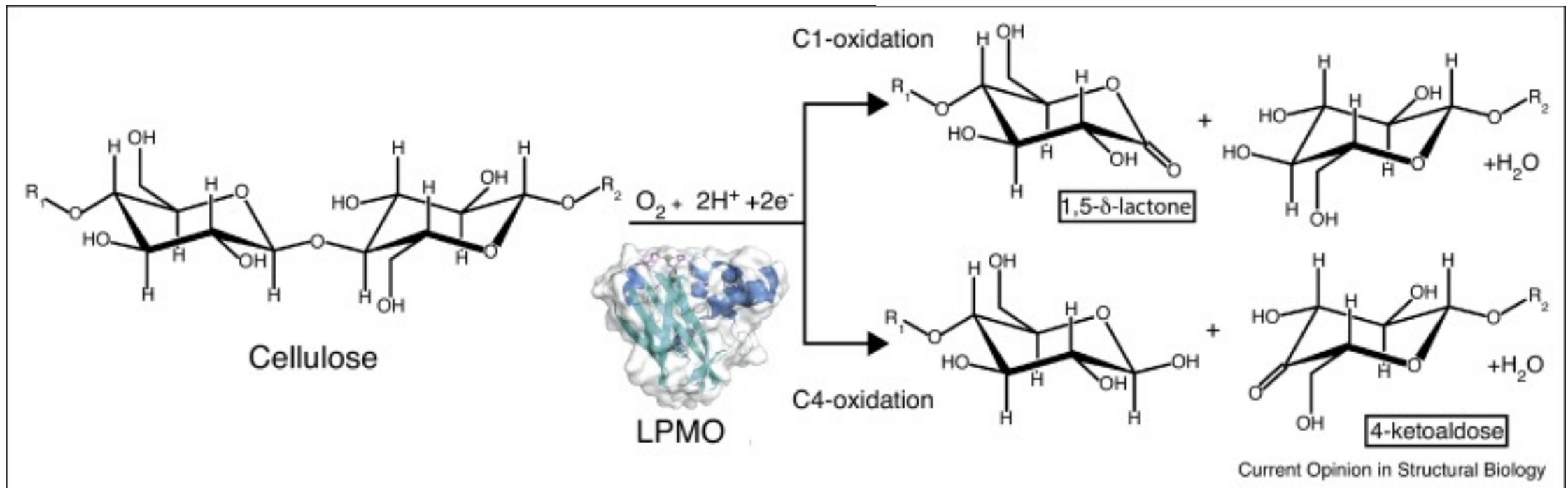
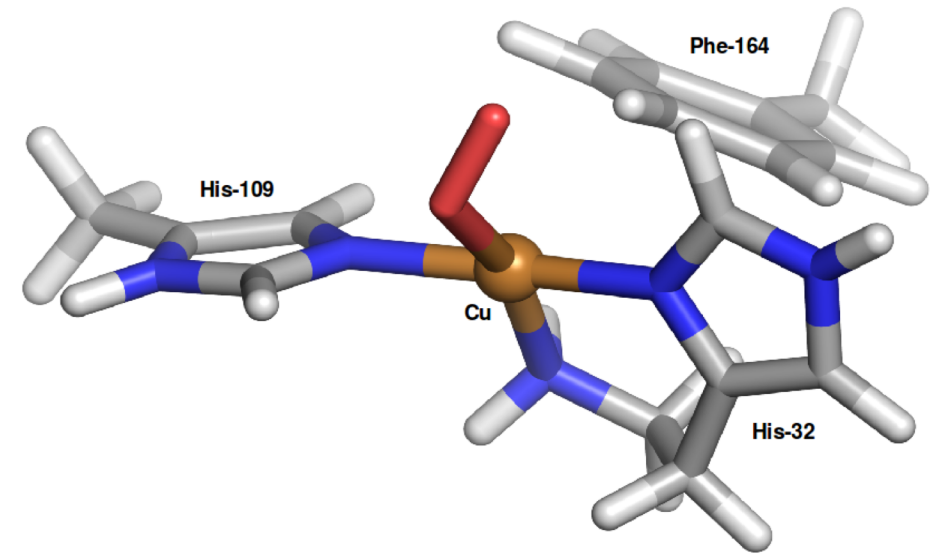


Lactose bound to Galectin-3C

Structure before (green) and after (yellow) the QM refinement

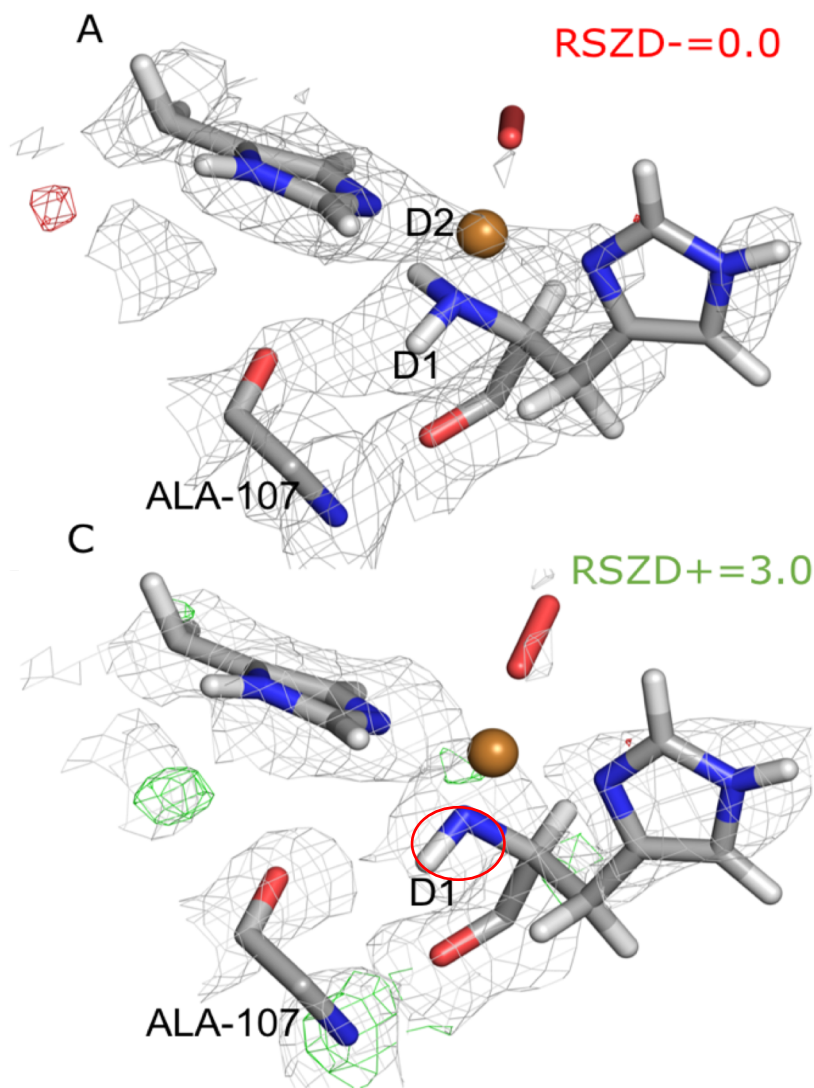


Interpretation of difficult data - Lytic polysaccharide monooxygenase

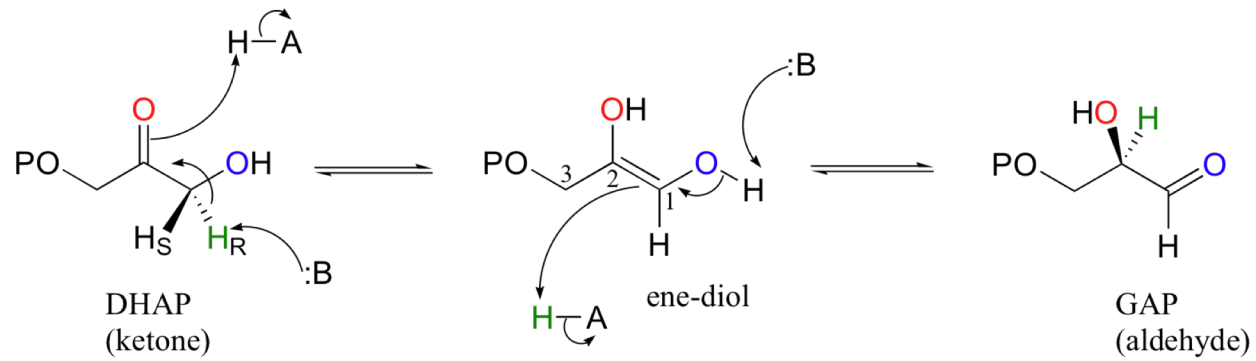


Subunit A

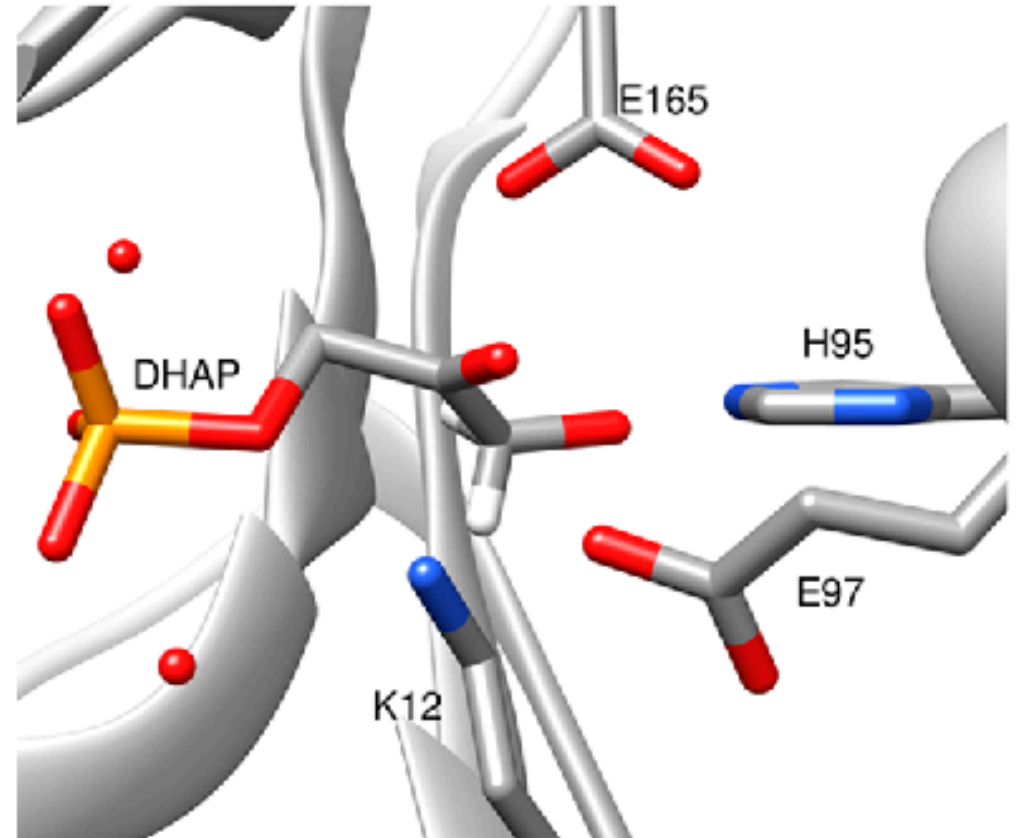
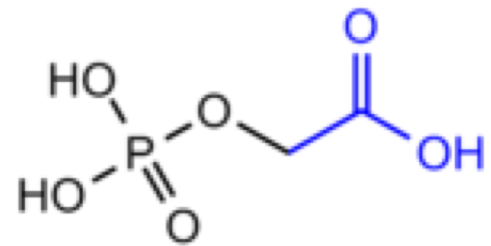
Subunit B



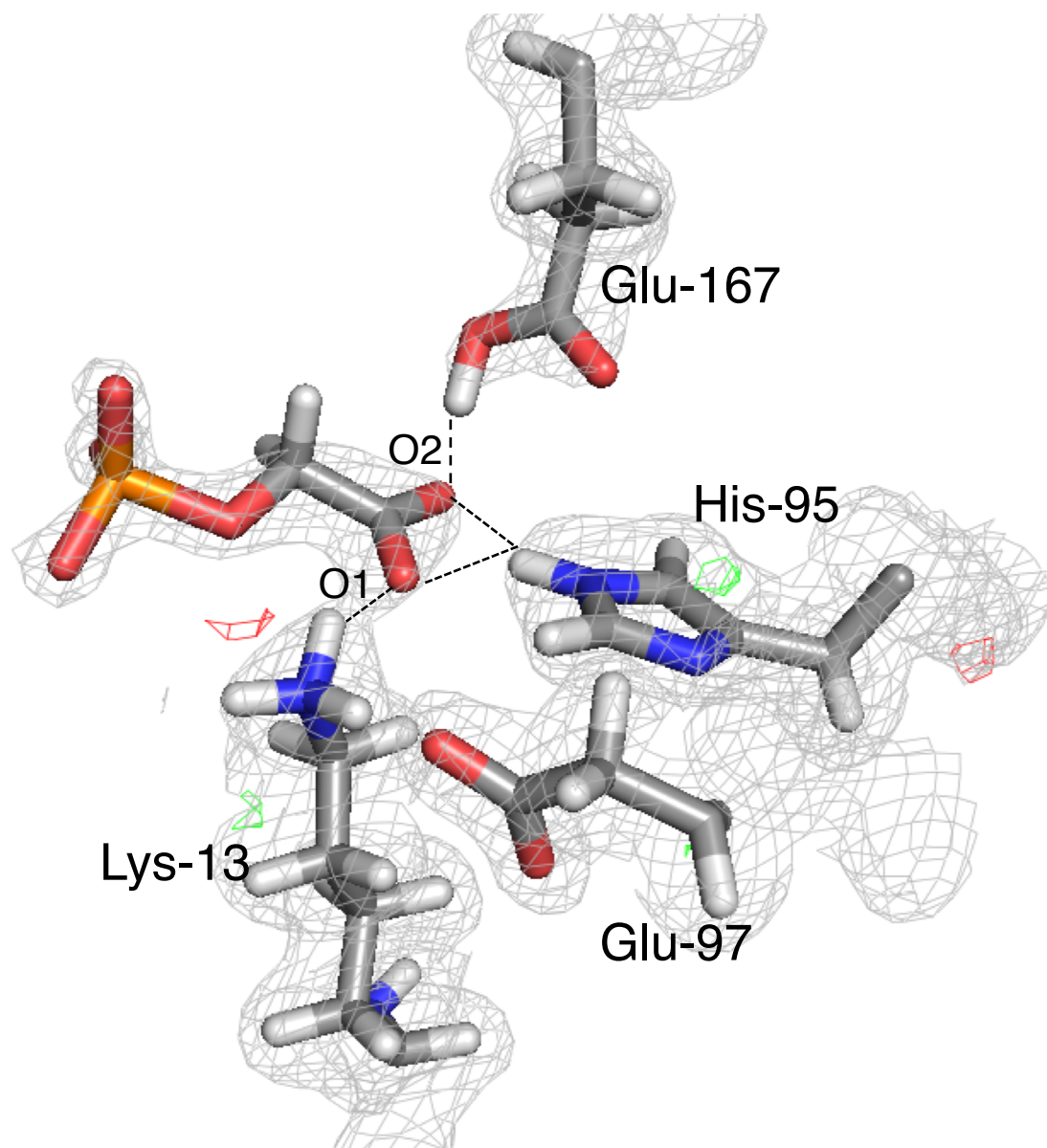
Proton transfer – TIM



2-Phosphoglycolate
Transition state analog



PGA-TIM active site after quantum refinement



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