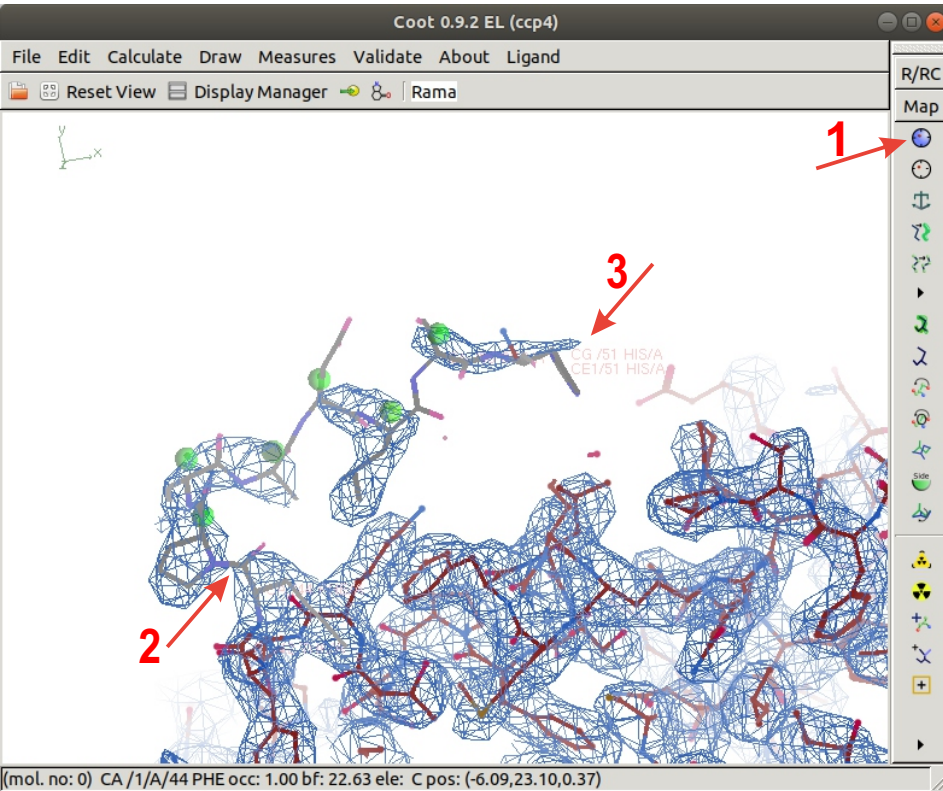


A**B**

Accept Refinement?

Accept Refinement?
Success

Bonds: 0.210
Angles: 0.845
Torsions: 1.417
Planes: 0.561
Chirals: 0.582
Non-bonded: 0.000
Rama Plot: -190.337

Atom Pull Restraint

☒ Auto-clear

Clear Atom Pull Restraint

Active Refinement

Flip This Peptide
Flip Next Peptide
Crankshaft Peptide Optimise
Backrub Rotamer Fit

Accept Reject