Protocol Viewer: PhenixProtRunMolprobityViewer Protocol: phenix - MolProbity viewer C Cite Volume and models | MolProbity results | Real-space correlation | Atomic properties MolProbity results Summary MolProbity MolProbity Basic Statistics @ (2) Open in Coot @ Basic Geometry: Bond Length Restraints Basic Geometry: Bond Angle Restraints Basic Geometry: Dihedral Angle Restraints Basic Geometry: Chirality Restraints Basic Geometry: Planarity Restraints Protein Select plot: Ramachandran plot View plot @ @ No Ramachandran outliers detected ถ Rotamer outliers: Rotamer outliers: O No C-beta position outliers detected Recommended Asn/Gin/His sidechain flips: (2) No non-trans peptides detected 0 Clashes All atom-contact analysis @ @

Close