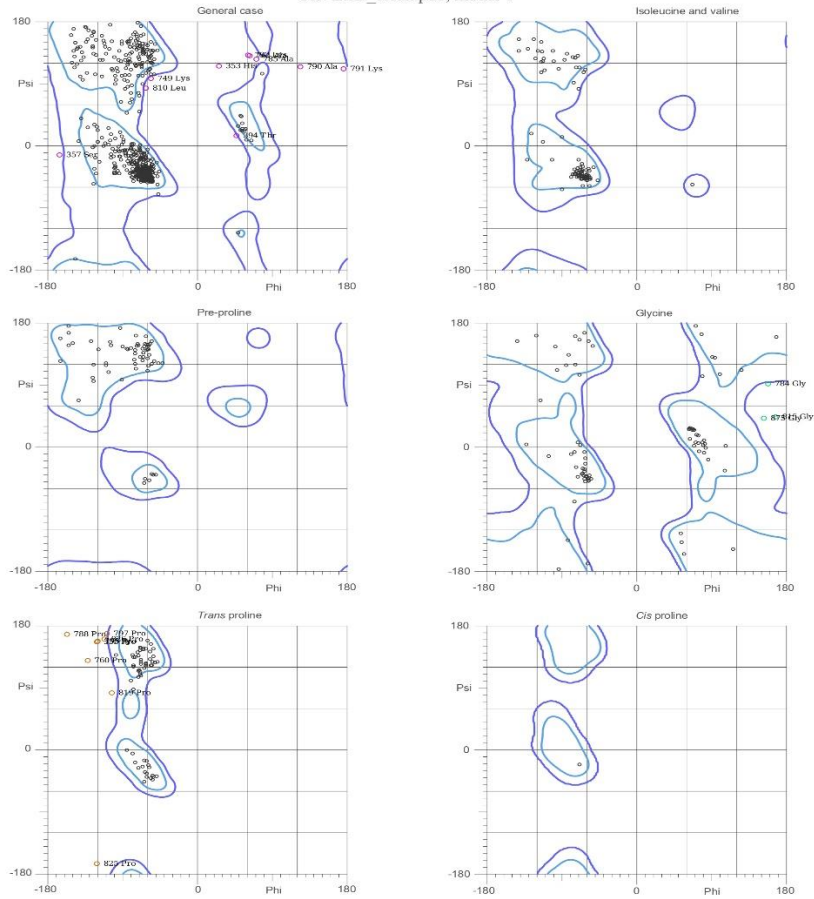


S2 Fig. MolProbity Ramachandran plot.

MolProbity Ramachandran analysis

AF-EtID_clean.pdb, model 1



93.0% (818/880) of all residues were in favored (98%) regions.
 97.6% (859/880) of all residues were in allowed (>99.8%) regions.

There were 21 outliers (phi, psi):

353 His (27.0, 116.4)	785 Ala (71.3, 126.1)	815 Gly (167.9, 41.5)
355 Pro (-121.2, 157.4)	788 Pro (-157.9, 168.9)	819 Pro (-103.9, 83.1)
357 Ser (-166.6, -13.7)	790 Ala (124.9, 115.1)	825 Pro (-121.5, -165.4)
394 Thr (47.5, 15.1)	791 Lys (176.4, 112.5)	826 Pro (-112.2, 161.6)
749 Lys (-56.3, 98.4)	792 Lys (61.9, 132.4)	875 Gly (153.2, 42.1)
760 Pro (-132.2, 130.1)	795 Pro (-120.8, 158.6)	
761 Ala (63.4, 131.8)	797 Pro (-109.6, 169.3)	
784 Gly (158.7, 93.0)	810 Leu (-62.9, 84.2)	

<http://kinemage.biochem.duke.edu>

Lovell, Davis, et al. Proteins 50:437 (2003)