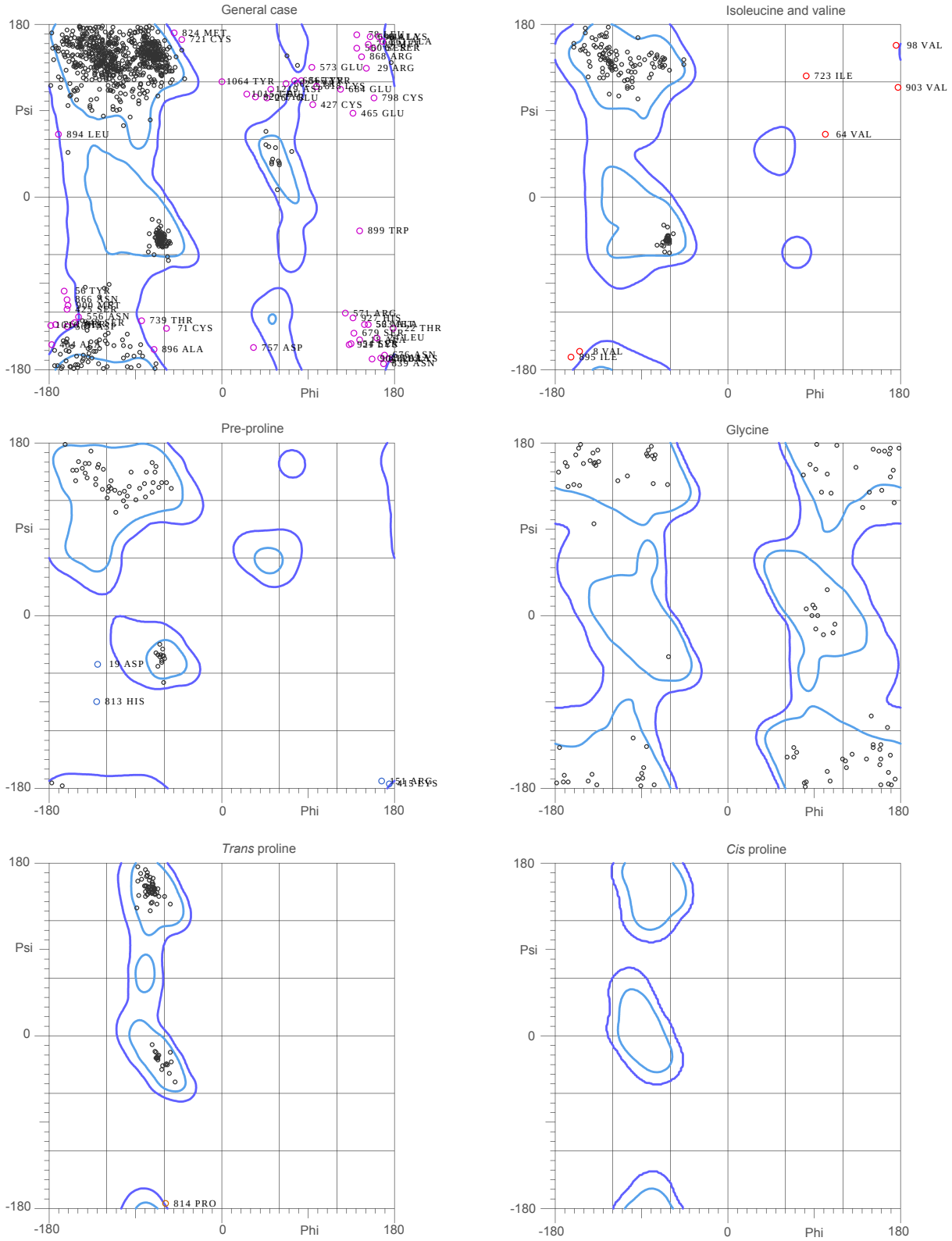
MolProbity Ramachandran analysis

6abu.B99990012.pdb, model 1



88.2% (1148/1302) of all residues were in favored (98%) regions.
96.9% (1235/1302) of all residues were in allowed (+98.8%) regions.

Three worst 67 outliers (phi, psi):
B 9 HIS (-155.1, -165.4)
B 10 ALA (144.2, -148.1)
B 19 ASP (-138.6, -31.1)
B 32 THR (179.5, -137.4)
B 34 ARG (162.7, -147.4)
B 39 ARG (151.3, 135.1)
B 50 ASN (-138.6, -153.9)
B 54 SER (155.1, -153.9)
B 56 TYR (-165.4, -66.3)
B 74 VAL (162.2, 95.0)
B 87 SER (158.7, 150.1)
B 71 CYS (-56.3, -157.1)
B 78 ARG (142.7, 178.5)
B 98 VAL (-156.1, 178.5)
B 131 ARG (167.2, -179.4)
B 261 SER (-174.5, -155.1)
B 267 ALD (47.5, 154.4)
B 484 ALA (-178.2, -154.8)
B 415 VAL (175.1, -179.4)
B 420 SER (-162.8, -157.8)
B 441 ARG (-64.1, 179.4)
B 444 LYS (164.5, 168.5)
B 485 GLU (157.8, 98.4)
B 556 ASN (-159.6, -135.8)
B 560 SER (141.4, 150.8)
B 561 ARG (-159.6, 150.8)
B 565 TYR (85.9, 115.8)
B 567 ASP (-163.9, -131.8)
B 571 ARG (159.2, -110.7)
B 572 GLN (96.8, 178.7)
B 602 TYR (67.7, 119.5)
B 676 ASN (174.8, -145.8)
B 679 SER (138.3, -142.5)
B 681 TYR (76.7, 122.3)
B 695 ILE (-159.6, 150.8)
B 696 ALA (155.8, 168.4)
B 721 CYS (-62.2, 165.1)
B 723 ILE (85.8, 127.8)
B 729 THR (-84.4, -129.5)
B 757 ASP (55.8, -157.1)
B 798 CYS (159.4, 164.1)
B 812 ARG (-159.6, 150.8)
B 813 HIS (-155.7, -98.5)
B 814 PRO (-59.8, -175.3)
B 818 LYS (96.5, 116.4)
B 820 LYS (175.1, -169.7)
B 824 MET (-56.1, 175.2)
B 835 ALA (166.5, -168.5)
B 861 ARG (-159.6, 150.8)
B 863 ALA (108.2, 162.5)
B 866 ASN (-162.1, -107.9)
B 868 ARG (140.4, 147.9)
B 894 LEU (-173.8, 68.5)
B 895 ILE (-164.5, -167.9)
B 896 ALA (-175.8, -159.3)
B 897 ASN (-159.6, 150.8)
B 900 MET (-161.7, -115.3)
B 903 VAL (178.8, 115.9)
B 904 ALA (127.5, -149.0)
B 920 TYR (91.6, 106.8)
B 921 ASN (-159.6, 150.8)
B 927 HIS (117.6, -156.5)
B 948 SER (-154.9, -151.9)
B 1015 LEU (25.9, 108.6)
B 1018 HIS (-179.6, -154.6)
B 1064 TYR (-6.8, 151.3)
B 1219 ASP (51.8, 113.2)

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