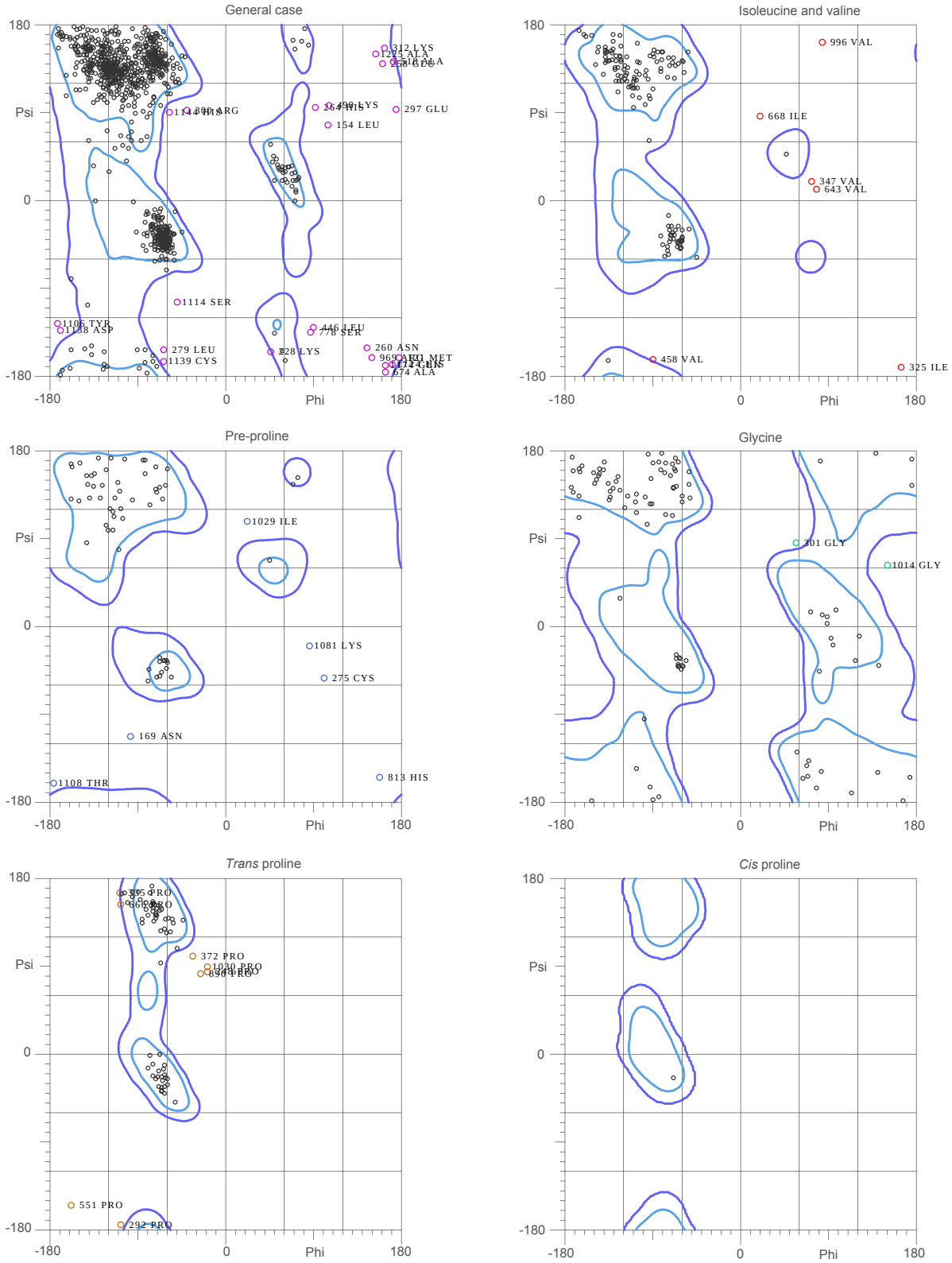
MolProbity Ramachandran analysis

6abu.B99990042.pdb, model 1



91.2% (1188/1302) of all residues were in favored (98%) regions.
96.5% (1256/1302) of all residues were in allowed (>99.8%) regions.

There were 46 outliers (phi, psi):
121 MET (179.6, -161.3)
154 LEU (106.0, 78.3)
169 ASN (-98.5, -113.5)
228 LYS (46.7, -156.0)
248 PRO (-19.1, 85.5)
258 GLU (161.3, -141.0)
260 ASN (145.7, -152.0)
264 HIS (92.9, 96.4)
275 CYS (101.4, -53.3)
279 LEU (-64.5, -153.0)
292 PRO (-109.0, -175.9)
297 GLU (175.3, 94.1)
300 ARG (-40.9, 93.4)
301 GLY (57.3, 86.3)
312 LYS (163.4, 157.9)
325 ILE (165.5, -171.3)
335 PRO (-109.4, 166.1)
347 VAL (73.2, 26.7)
372 PRO (-34.2, -101.9)
446 LEU (90.2, -136.1)
458 VAL (-90.8, -163.6)
490 LYS (106.2, 98.1)
518 ALA (172.8, 143.2)
551 PRO (-159.3, -155.3)
643 VAL (78.3, 13.0)
668 PRO (-108.1, 154.5)
668 ILE (20.6, 87.2)
674 ALA (165.8, -177.0)
778 SER (87.8, -135.6)
813 HIS (158.2, -155.1)
898 PRO (-26.8, 83.5)
969 ARG (150.7, -161.3)
996 VAL (84.3, 163.7)
1014 GLY (151.8, 63.3)
1029 ILE (22.4, 168.8)
1030 PRO (-19.3, 96.6)
1081 LYS (86.6, -20.5)
1106 TYR (-173.7, -127.0)
1108 THR (-178.8, -161.1)
1114 SER (-51.0, -104.8)
1124 HIS (171.1, -168.2)
1138 ASP (-170.4, -133.9)
1139 CYS (-64.5, -166.0)
1144 HIS (-38.5, 91.5)
1174 GLN (164.3, -169.7)
1225 ALA (154.4, 151.4)

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