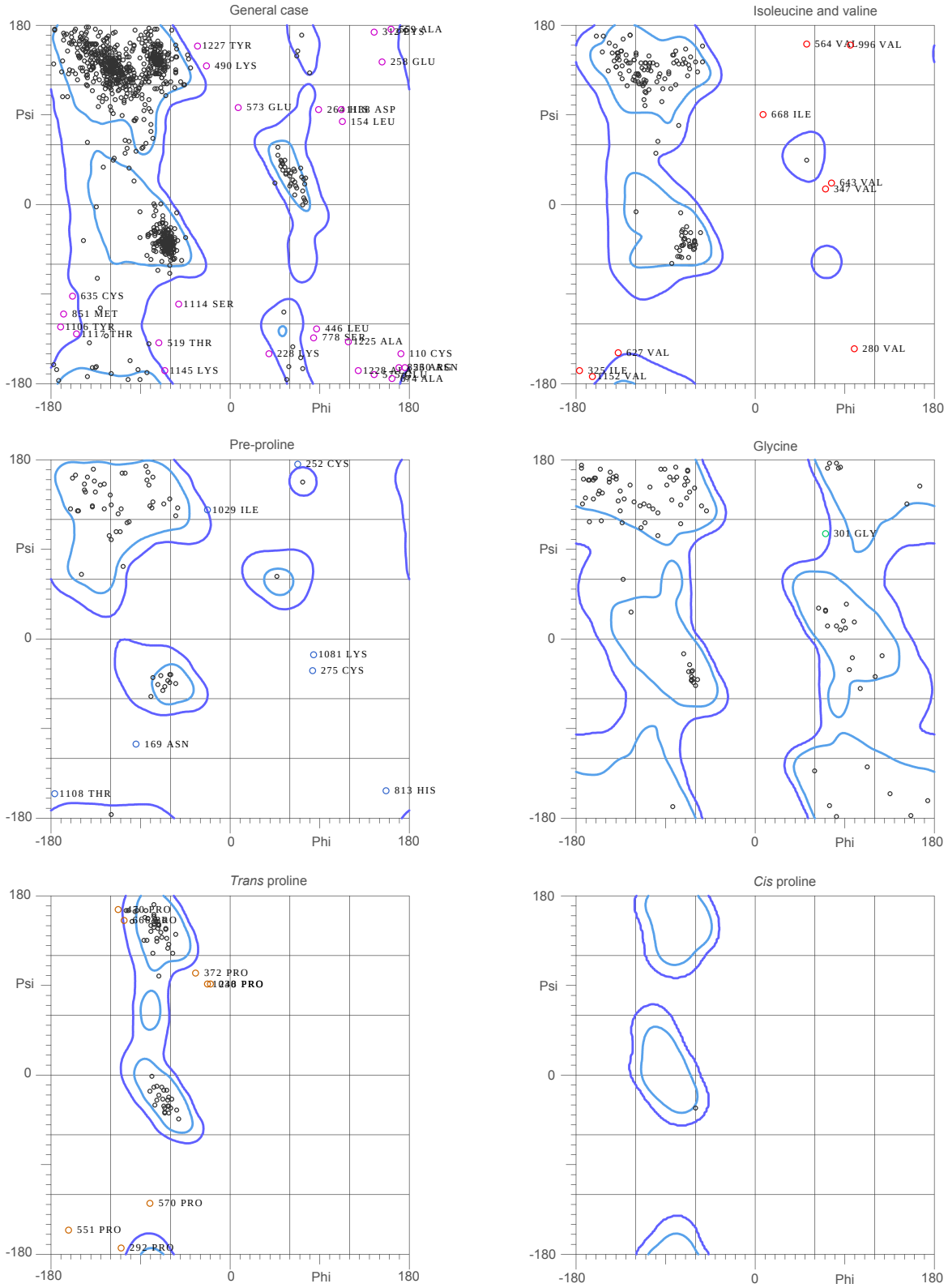
MolProbity Ramachandran analysis

6abu.B99990023.pdb, model 1



90.6% (1172/1302) of all residues were in favored (98%) regions.
96.1% (1251/1302) of all residues were in allowed (>99.8%) regions.

There were 51 outliers (phi, psi):
110 CYS (172.2, -150.0)
154 LEU (113.7, 84.8)
169 ASN (-95.4, -104.3)
228 LYS (39.9, -150.2)
248 PRO (-20.3, 52.7)
252 CYS (68.1, 176.0)
258 GLU (153.1, 145.0)
260 ASN (176.6, -164.6)
264 HIS (89.1, 96.7)
275 CYS (83.7, -32.1)
280 VAL (108.2, -165.8)
292 PRO (-110.2, -174.7)
301 GLY (71.5, 106.2)
312 LYS (145.1, 174.2)
325 ILE (-177.9, -167.6)
347 VAL (71.1, 16.3)
372 PRO (-35.1, 103.0)
446 LEU (87.7, -125.8)
470 PRO (-113.8, 167.7)
490 LYS (-24.1, 140.9)
519 THR (-72.8, -139.8)
551 PRO (-163.3, -156.5)
559 ALA (163.0, 177.6)
564 VAL (52.4, 162.2)
570 PRO (-81.7, -129.8)
573 GLU (8.7, 98.1)
575 GLU (145.1, -171.1)
627 VAL (-138.2, -148.7)
635 CYS (-159.0, -92.5)
643 VAL (77.3, 22.8)
666 PRO (-107.8, 154.1)
668 ILE (8.8, 91.8)
674 ALA (163.7, -175.9)
778 SER (84.2, -134.4)
813 HIS (157.4, -153.2)
851 MET (-168.2, -110.0)
853 ARG (170.8, -164.5)
996 VAL (96.8, 161.5)
1029 ILE (-23.5, 138.7)
1038 PRO (-23.5, 92.9)
1081 LYS (85.6, -16.5)
1106 TYR (-171.5, -123.7)
1108 THR (-177.8, -154.3)
1114 SER (-52.3, -100.3)
1117 THR (-151.9, -138.0)
1138 ASP (112.6, 96.9)
1145 LYS (-66.1, -167.9)
1152 VAL (-164.2, -173.5)
1225 ALA (119.3, -138.9)
1227 TYR (-33.0, 166.7)
1228 ALA (129.3, -167.2)

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