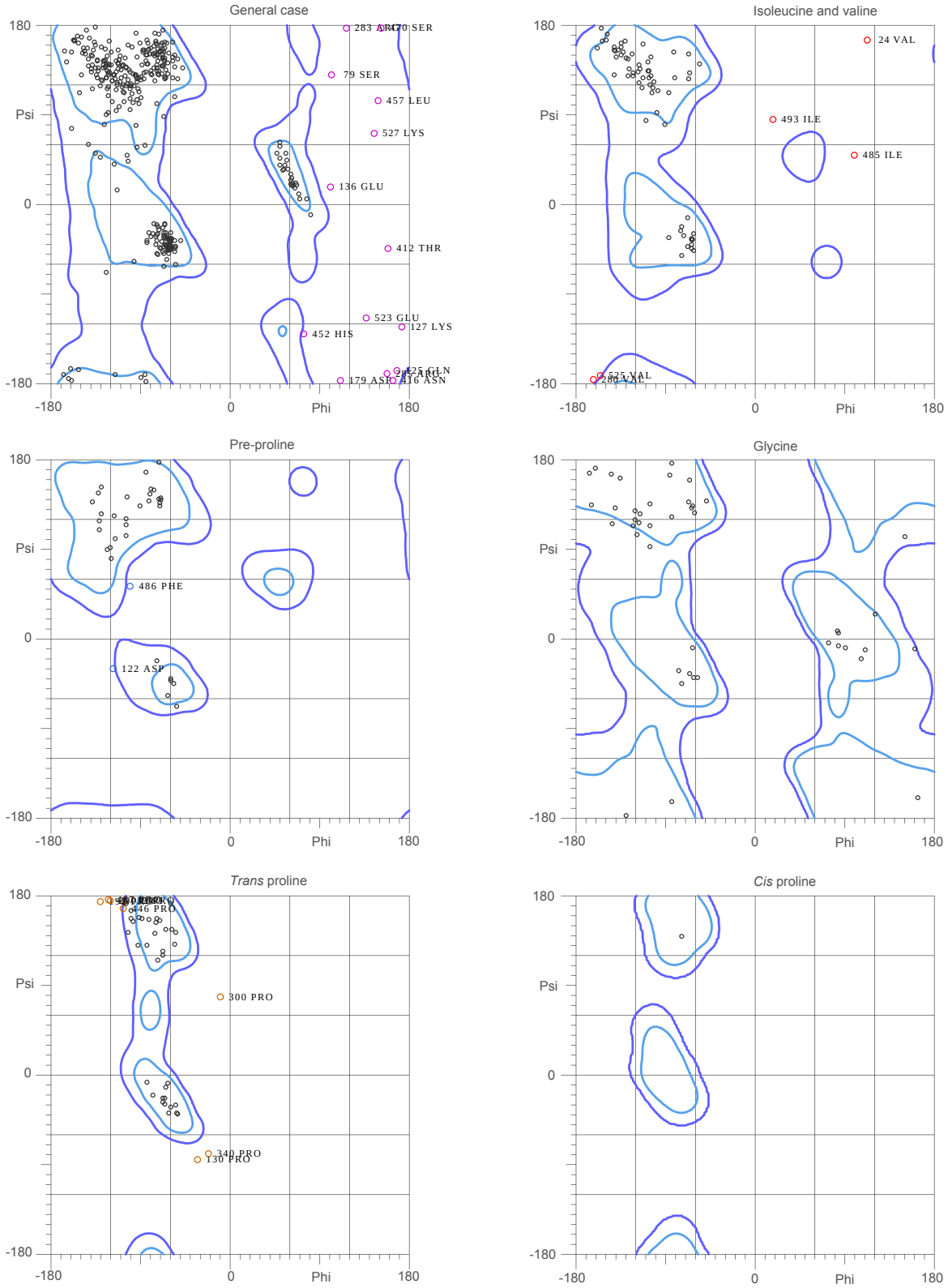
MolProbity Ramachandran analysis

1aozA.B99990047.pdb, model 1



88.9% (409/553) of all residues were in favored (98%) regions.
96.7% (533/553) of all residues were in allowed (>99.8%) regions.

Three worst 20 outliers (phi, psi):
24 VAL (113.8, 100.0)
32 PRO (-106.6, -178.9)
79 SER (102.3, 151.2)
122 ASP (-63.1, -178.9)
125 GLN (108.5, -167.6)
127 LYS (175.5, -123.5)
130 PRO (-55.5, -85.3)
136 GLU (101.5, 18.4)
179 ASP (111.5, -177.1)
192 PRO (-111.7, 175.4)
280 VAL (-163.4, -179.2)
203 ARG (117.6, 178.8)
285 ARG (130.1, -179.9)
290 PRO (-121.9, 177.8)
300 PRO (-56.8, 79.5)
340 PRO (-52.9, -78.4)
412 THR (-63.8, 143.1)
416 ASN (108.6, -177.5)
446 PRO (-108.5, 168.6)
452 HIS (74.7, -138.3)
457 LEU (149.8, 105.0)
470 SER (152.8, 178.6)
485 ILE (100.8, 51.8)
486 PHE (-101.6, 55.9)
487 PRO (-122.9, 177.9)
493 ILE (58.2, 66.7)
523 GLU (137.4, -114.9)
525 VAL (-116.2, -177.2)
527 LYS (143.8, 72.6)

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