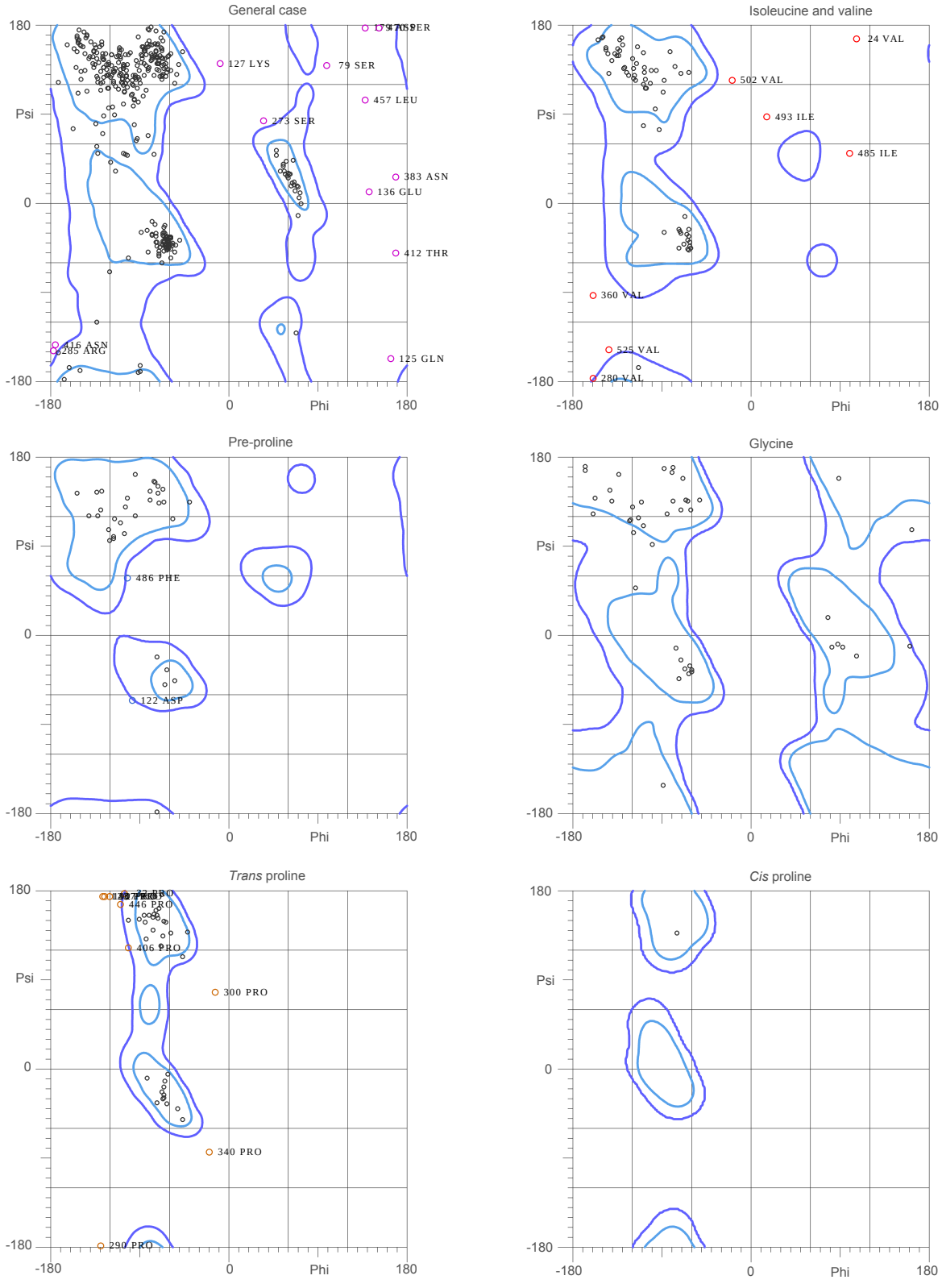
MolProbity Ramachandran analysis

1aozA.B99990018.pdb, model 1



88.2% (485/550) of all residues were in favored (98%) regions.
96.5% (520/550) of all residues were in allowed (>99.8%) regions.

There were 30 outliers (pb, psi):

24 VAL (107.5, 107.7)
52 PRO (-108.6, 178.1)
79 SER (99.8, 148.9)
122 ASP (-86.7, -86.9)
122 PRO (-128.6, 175.3)
125 GLN (-103.6, -107.3)
127 LYS (-8.6, 142.8)
136 GLU (142.5, 52.1)
179 ASP (-108.6, 178.1)
192 PRO (-126.7, 175.4)
273 SER (93.6, 84.5)
280 VAL (-166.5, -178.8)
285 ARG (-178.5, -168.9)
290 PRO (-135.6, -179.4)
300 PRO (-14.6, 78.8)
340 PRO (-135.6, -84.5)
360 VAL (-141.6, -95.1)
383 ASN (100.5, 27.4)
406 PRO (-102.9, 125.1)
412 THR (109.9, -58.1)
416 ASN (-176.2, -143.5)
446 PRO (-111.6, 147.7)
457 LEU (-135.5, 108.9)
479 SER (152.2, 178.9)
485 ILE (100.6, 51.0)
486 PHE (-103.0, 58.4)
487 PRO (-121.4, 175.6)
493 ILE (94.6, 88.5)
502 VAL (-176.6, 123.6)
525 VAL (-144.6, -148.9)

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