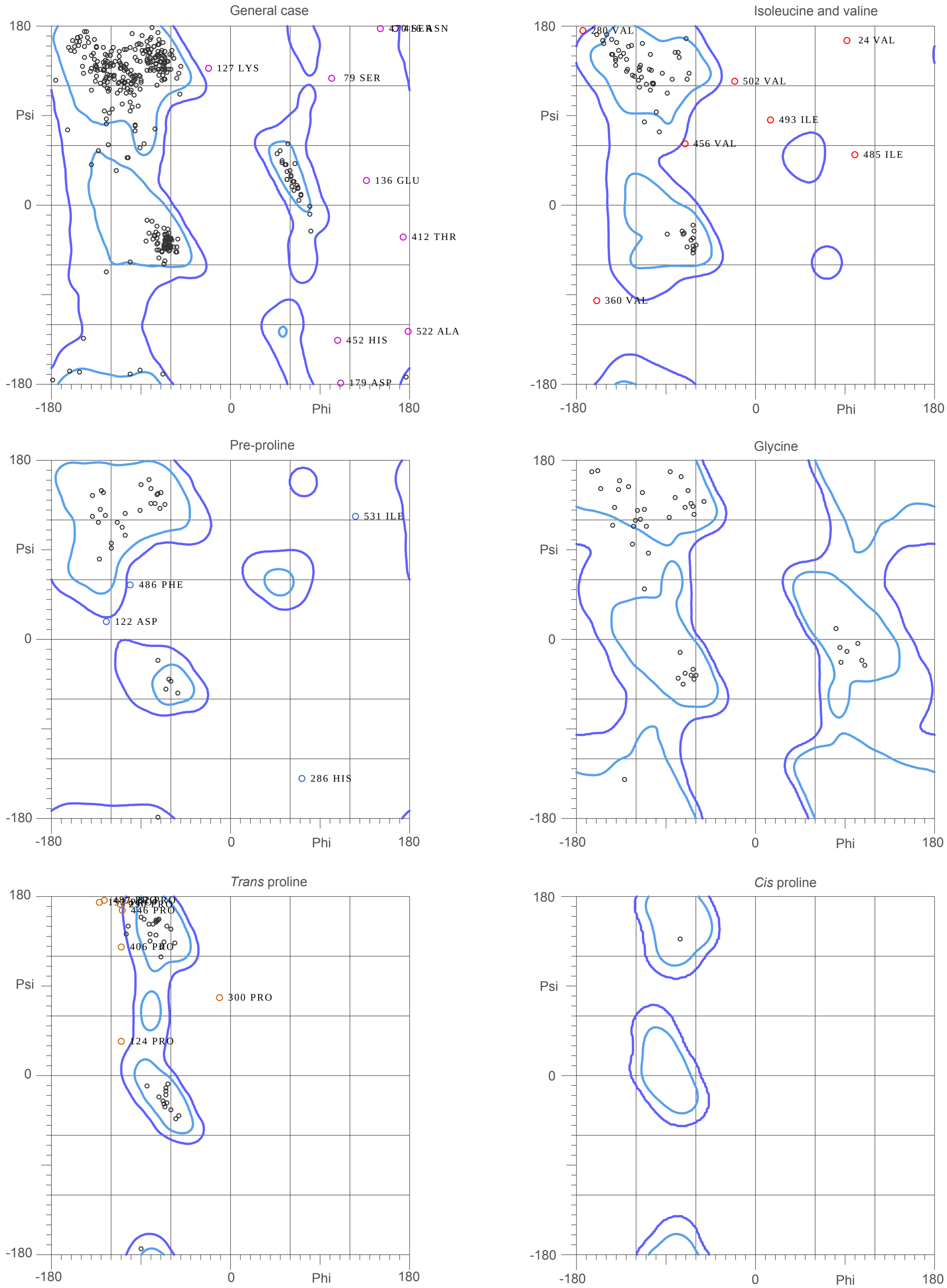
MolProbity Ramachandran analysis

1aozA.B99990012.pdb, model 1



88,2% (485/550) of all residues were in favored (98%) regions.
94,9% (522/550) of all residues were in allowed (>99.8%) regions.

There were 28 outliers (phi, psi):
24 VAL (92,7, 166,2)
32 PRO (-106,0, 177,5)
79 SER (102,3, 128,2)
122 ASP (-125,4, 18,3)
124 PRO (-110,2, 35,0)
127 LYS (-22,1, 138,4)
136 GLU (137,3, 25,3)
179 ASP (111,8, -179,2)
192 PRO (-132,4, 175,2)
280 VAL (-174,3, 176,9)
286 HIS (72,7, -141,0)
290 PRO (-111,5, 173,9)
300 PRO (-11,6, 79,1)
360 VAL (-160,3, -96,5)
406 PRO (-110,3, 130,7)
412 THR (175,0, -32,8)
416 ASN (166,9, 178,3)
446 PRO (-109,7, 167,7)
452 HIS (108,3, -136,9)
456 VAL (-71,7, 62,6)
470 SER (151,6, 178,1)
485 ILE (100,2, 51,7)
486 PHE (-101,9, 55,3)
487 PRO (-127,3, 177,2)
493 ILE (15,9, 86,7)
502 VAL (-21,8, 125,4)
522 ALA (179,4, -127,9)
531 ILE (126,6, 124,1)

http://kinemage.biochem.duke.edu

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