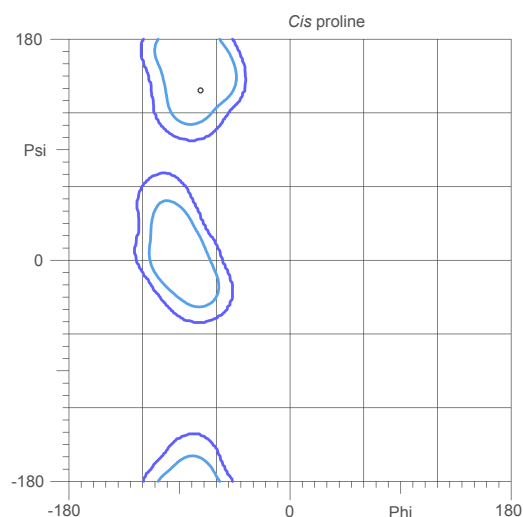
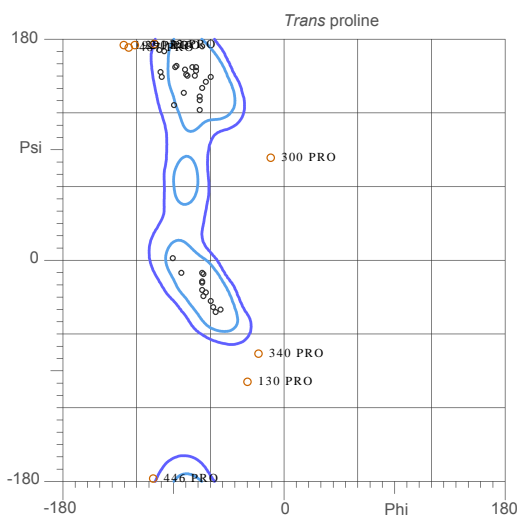
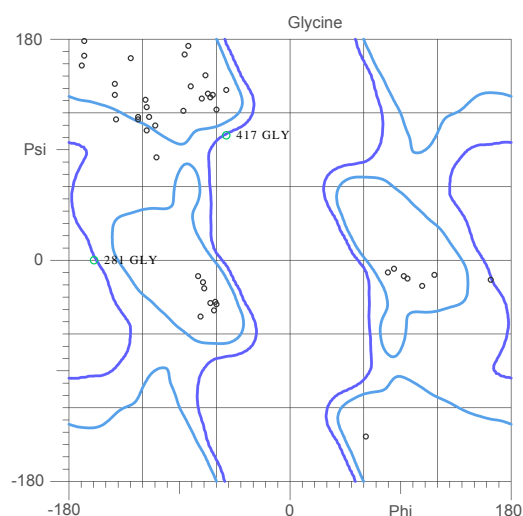
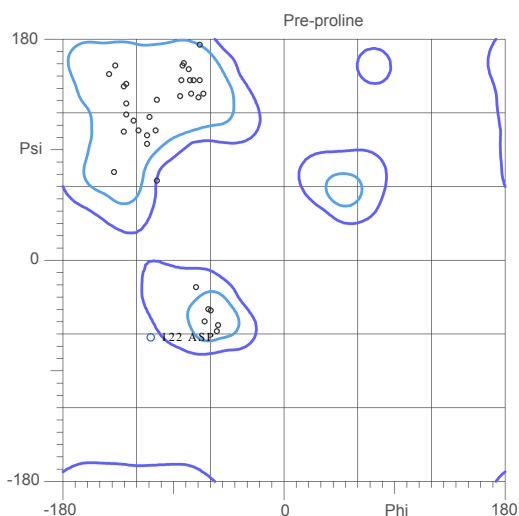
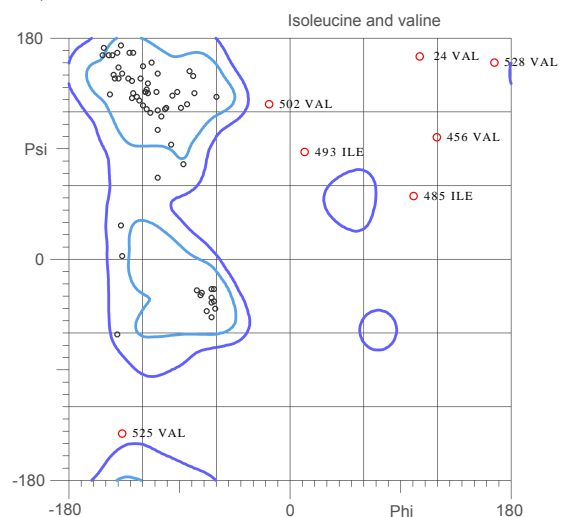
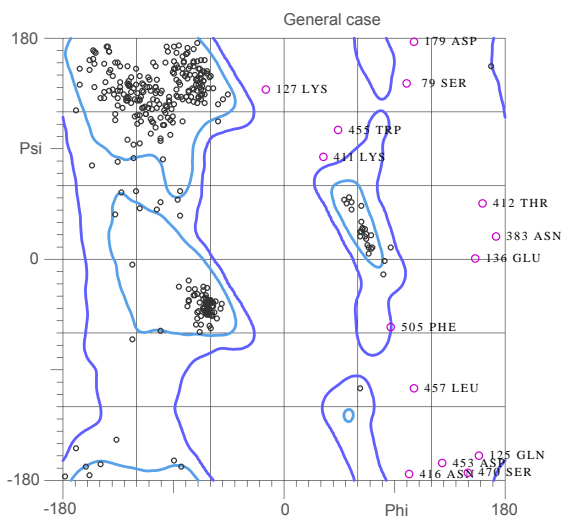


MolProbity Ramachandran analysis

1aozA.B99990005.pdb, model 1



446 (179) of all residues were in favored (90%) regions.

446 (179) of all residues were in allowed (90%) regions.

There were 0 outliers (0%) in the disallowed regions.

127 LYS (127) in the alpha-helical region.

179 ASP (179) in the alpha-helical region.

79 SER (79) in the alpha-helical region.

455 TRP (455) in the alpha-helical region.

411 LYS (411) in the alpha-helical region.

412 THR (412) in the alpha-helical region.

383 ASN (383) in the alpha-helical region.

136 GLU (136) in the alpha-helical region.

505 PHE (505) in the alpha-helical region.

457 LEU (457) in the alpha-helical region.

453 ASN (453) in the alpha-helical region.

425 GLN (425) in the alpha-helical region.

416 ASN (416) in the alpha-helical region.

471 SER (471) in the alpha-helical region.