MolProbity Ramachandran analysis

1a8y_.B99990008.pdb, model 1

General case

○ 280 LEU
○ 328 GLU
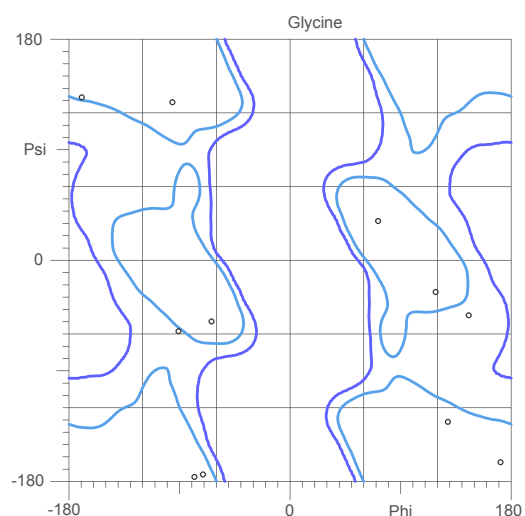○ 226 SER
○ 243 ASP
○ 84 LYS
○ 82 ALA
○ 8 ASP
○ 227 THR
○ 88 THR
○ 75 SER
○ 77 LYS

Psi / Phi axes: -180, 0, 180

Isoleucine and valine

Psi / Phi axes: -180, 0, 180

Pre-proline

○ 172 ILE
○ 169 HIS
○ 209 LYS
○ 232 LYS

Glycine

Trans proline

○ 325 PRO
○ 233 PRO
○ 170 PRO

Cis proline
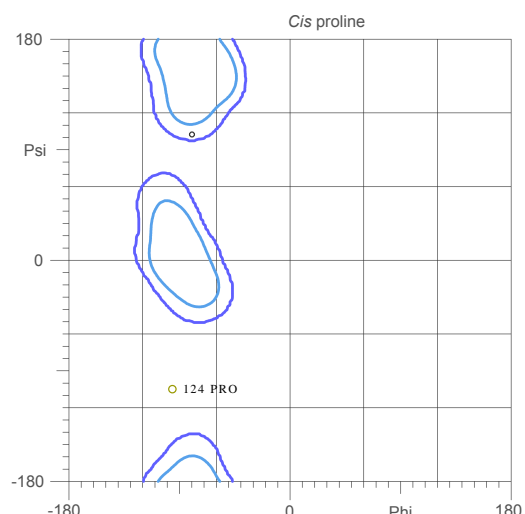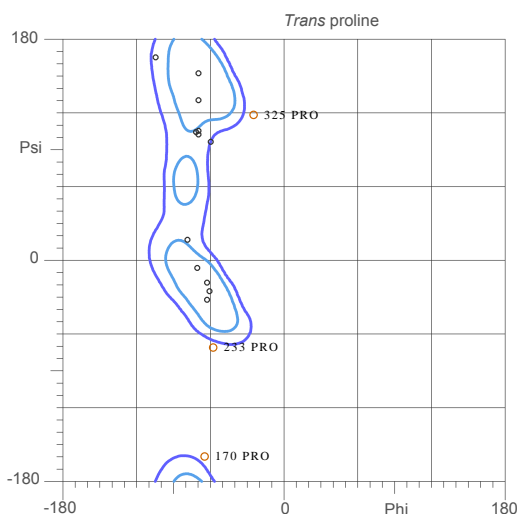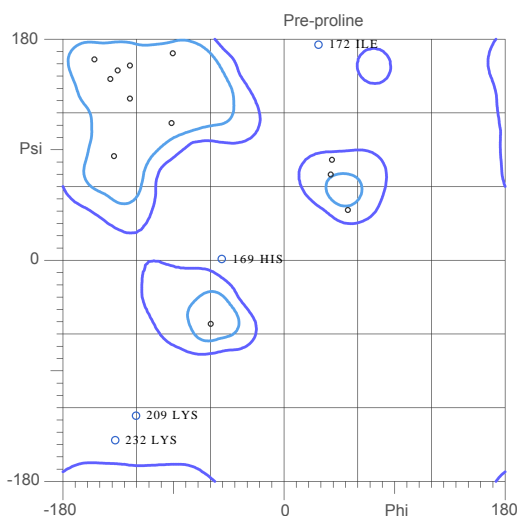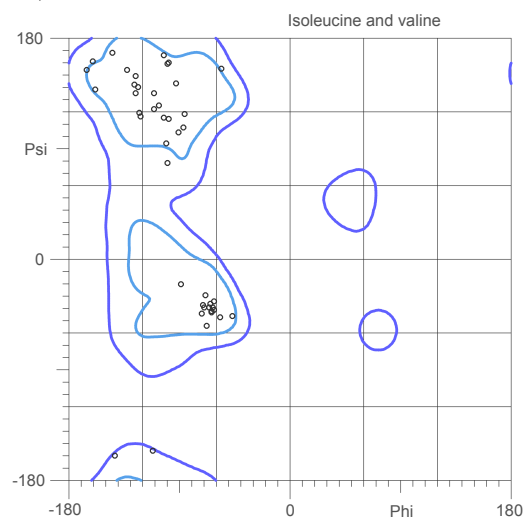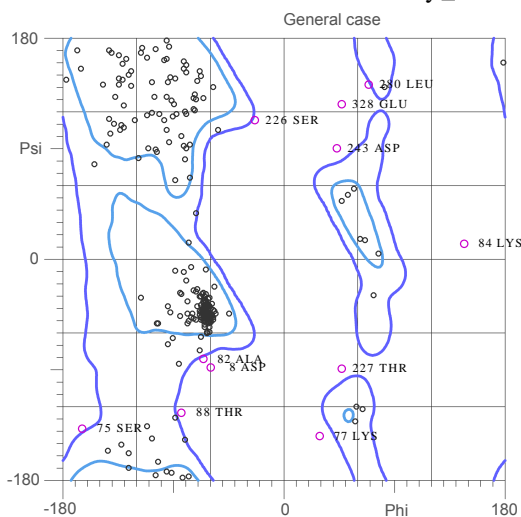
○ 124 PRO

81.8% (275/336) of all residues were in favored (98%) regions.
94.3% (317/336) of all residues were in allowed (>99.8%) regions.

There were 19 outliers (phi, psi):
8 ASP (-80.7, -88.3)
75 SER (-165.2, -138.7)
77 LYS (29.3, -144.1)
82 ALA (-66.3, -81.1)
84 LYS (147.5, 15.5)
88 THR (-84.9, -125.5)
124 PRO (-96.1, -105.8)
169 HIS (-51.5, 1.2)
170 PRO (-65.2, -160.2)
172 ILE (28.2, 176.3)
209 LYS (-121.1, -127.1)
226 SER (-24.8, 114.9)
227 THR (47.2, -89.5)
232 LYS (-138.4, -147.4)
233 PRO (-58.6, -71.2)
243 ASP (43.0, 91.5)
280 LEU (69.8, 143.1)
325 PRO (-26.0, 119.5)
328 GLU (48.0, 127.8)

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