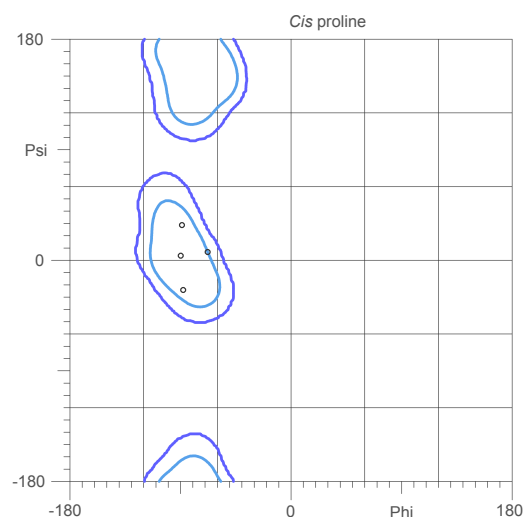
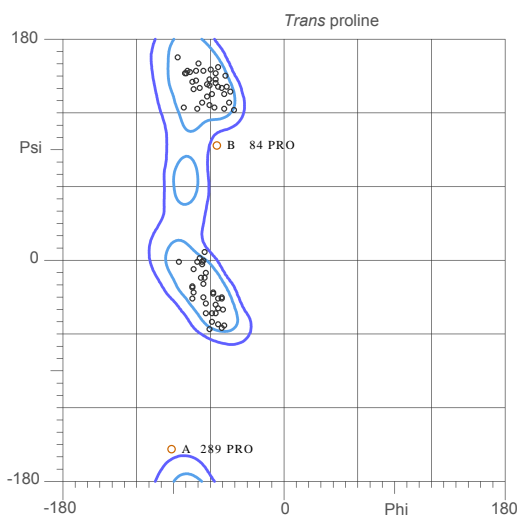
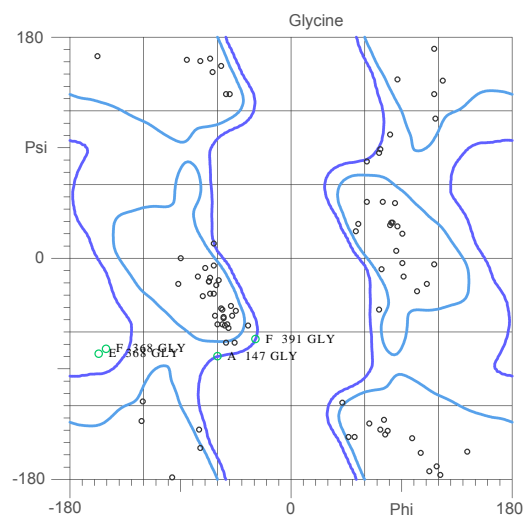
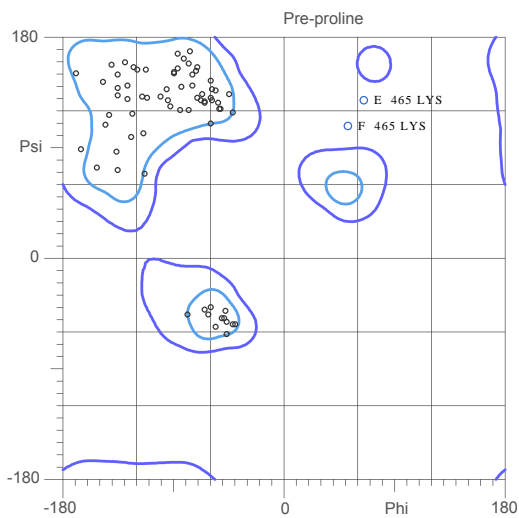
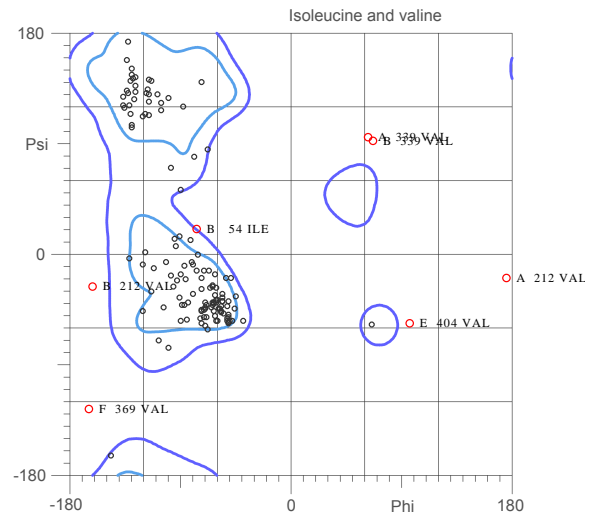
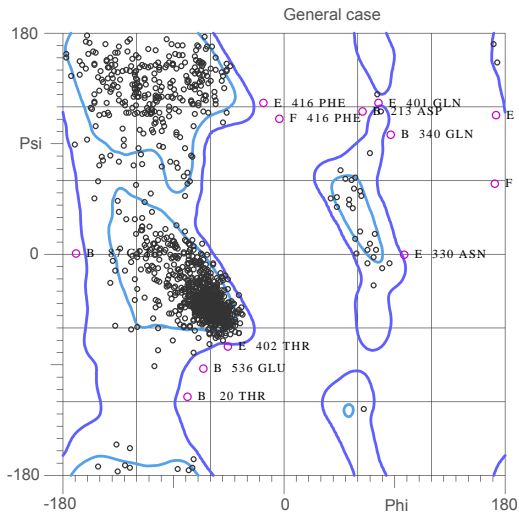


# MolProbity Ramachandran analysis

3d0g.H.pdb, model 1



85.7% (136/157) of all residues were in favored (98%) regions.  
10.7% (168/157) of all residues were in allowed (100%) regions.

There were 27 outliers (phi, psi):

- A 137 GLY (136.1, 104.4)
- A 138 VAL (136.1, 104.4)
- A 139 VAL (136.1, 104.4)
- A 140 VAL (136.1, 104.4)
- A 141 VAL (136.1, 104.4)
- A 142 VAL (136.1, 104.4)
- A 143 VAL (136.1, 104.4)
- A 144 VAL (136.1, 104.4)
- A 145 VAL (136.1, 104.4)
- A 146 VAL (136.1, 104.4)
- A 147 GLY (136.1, 104.4)
- A 148 VAL (136.1, 104.4)
- A 149 VAL (136.1, 104.4)
- A 150 VAL (136.1, 104.4)
- A 151 VAL (136.1, 104.4)
- A 152 VAL (136.1, 104.4)
- A 153 VAL (136.1, 104.4)
- A 154 VAL (136.1, 104.4)
- A 155 VAL (136.1, 104.4)
- A 156 VAL (136.1, 104.4)
- A 157 VAL (136.1, 104.4)
- A 158 VAL (136.1, 104.4)
- A 159 VAL (136.1, 104.4)
- A 160 VAL (136.1, 104.4)
- A 161 VAL (136.1, 104.4)
- A 162 VAL (136.1, 104.4)
- A 163 VAL (136.1, 104.4)
- A 164 VAL (136.1, 104.4)
- A 165 VAL (136.1, 104.4)
- A 166 VAL (136.1, 104.4)
- A 167 VAL (136.1, 104.4)
- A 168 VAL (136.1, 104.4)
- A 169 VAL (136.1, 104.4)
- A 170 VAL (136.1, 104.4)
- A 171 VAL (136.1, 104.4)
- A 172 VAL (136.1, 104.4)
- A 173 VAL (136.1, 104.4)
- A 174 VAL (136.1, 104.4)
- A 175 VAL (136.1, 104.4)
- A 176 VAL (136.1, 104.4)
- A 177 VAL (136.1, 104.4)
- A 178 VAL (136.1, 104.4)
- A 179 VAL (136.1, 104.4)
- A 180 VAL (136.1, 104.4)