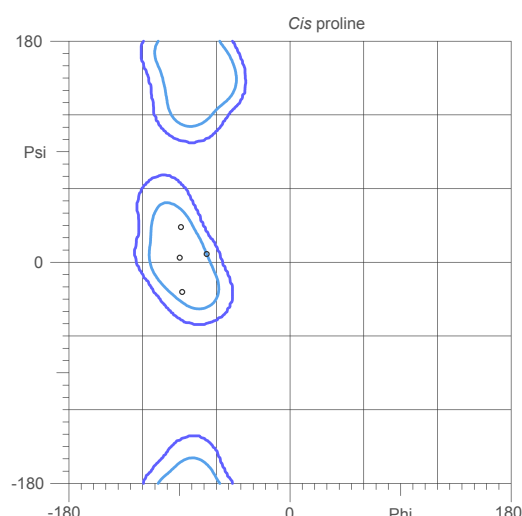
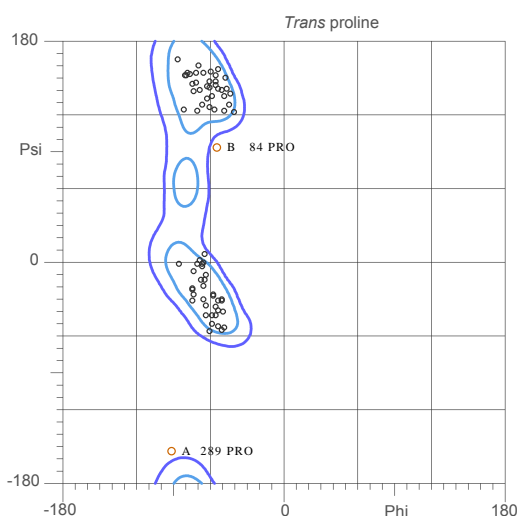
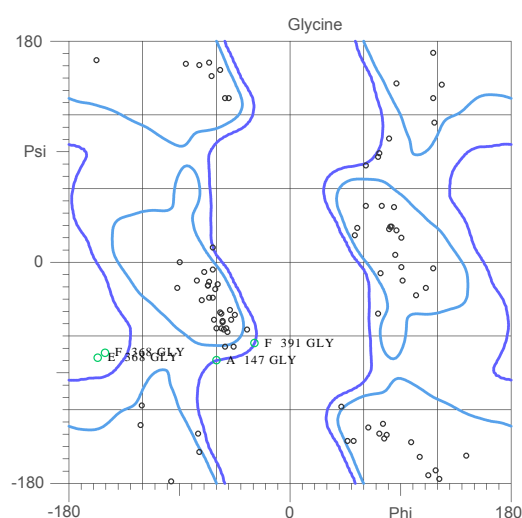
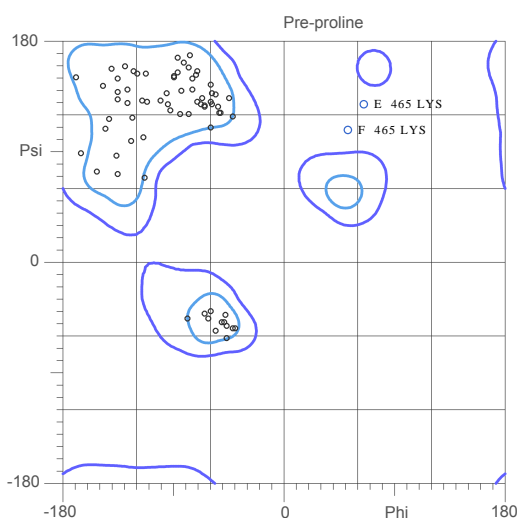
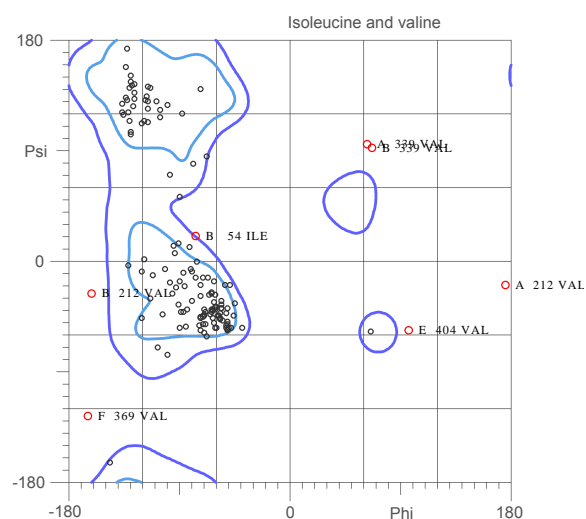
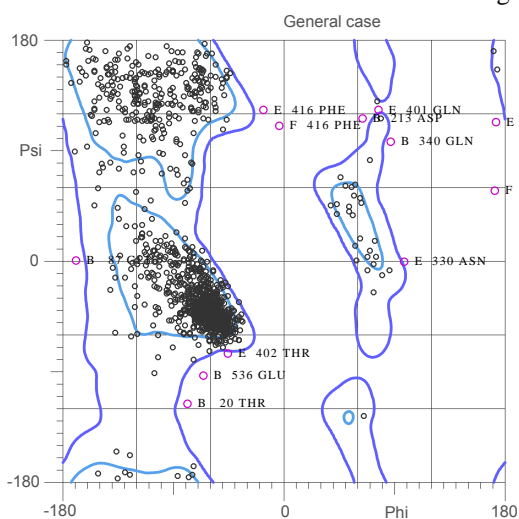


# MolProbity Ramachandran analysis

3d0g.H.pdb, model 1



85.7% (136/157) of all residues were in favored (90%) regions.  
92.7% (136/146) of all residues were in allowed (95%) regions.

There were 27 outliers (phi, psi):

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