

# MolProbity Ramachandran analysis

6m17.H.pdb, model 1



89.7% (2746/3060) of all residues were in favored (90%) regions.  
99.4% (3012/3060) of all residues were in allowed (≥95%) regions.

There were 48 outliers (Phi, Psi):

A 146 GLU (-45.5, -95.7)	E 483 VAL (60.9, -42.2)
A 147 PRO (-51.5, 88.8)	E 485 ILE (-59.5, -49.8)
C 108 HIS (71.5, 88.8)	F 429 THR (-151.1, 142.8)
C 147 PRO (-51.5, 87.8)	F 474 GLN (42.8, 114.2)
D 394 GLU (-18.1, -105.8)	F 478 THR (161.9, 135.9)
D 397 GLY (-48.8, 31.5)	F 480 CYS (166.3, 168.6)
D 401 VAL (-18.1, 140.8)	F 483 VAL (60.9, -42.2)
D 411 LYS (164.9, 9.7)	F 485 GLY (-59.5, -49.8)
D 421 LEU (-108.1, 8.9)	
D 478 THR (161.9, 135.9)	
E 429 PHE (-45.5, -16.0)	
E 474 GLN (42.8, 114.2)	
E 478 THR (161.9, 135.9)	
E 480 CYS (166.3, 168.6)	
E 483 VAL (60.9, -42.2)	
E 485 ILE (-59.5, -49.8)	
F 429 THR (-151.1, 142.8)	
F 474 GLN (42.8, 114.2)	
F 478 THR (161.9, 135.9)	
F 480 CYS (166.3, 168.6)	
F 483 VAL (60.9, -42.2)	
F 485 GLY (-59.5, -49.8)	