

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 (≥99.8%) 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, -145.8)
C 147 PRO (-51.5, 88.8)	F 430 THR (-151.1, -145.8)
D 394 GLU (-136.1, -105.8)	F 431 THR (-151.1, -145.8)
D 395 GLY (-48.8, 31.5)	F 432 THR (-151.1, -145.8)
D 396 VAL (-28.8, 110.3)	F 433 THR (-151.1, -145.8)
D 423 LEU (-108.1, 8.9)	F 434 THR (-151.1, -145.8)
D 431 LYS (164.9, 9.7)	F 435 THR (-151.1, -145.8)
D 478 THR (88.8, 8.9)	F 436 THR (-151.1, -145.8)
E 733 ASN (186.2, 172.3)	F 437 THR (-151.1, -145.8)
E 734 GLN (186.2, 172.3)	F 438 THR (-151.1, -145.8)
F 738 PRO (-99.7, 34.0)	F 439 THR (-151.1, -145.8)
F 739 VAL (-108.1, -16.3)	F 440 THR (-151.1, -145.8)
G 429 PRO (-45.5, -16.0)	F 441 THR (-151.1, -145.8)
G 447 GLY (-151.1, -87.7)	F 442 THR (-151.1, -145.8)
H 448 ASN (-44.5, 140.5)	F 443 THR (-151.1, -145.8)
H 472 ILE (-44.5, 140.5)	F 444 THR (-151.1, -145.8)
I 474 GLN (42.8, 114.2)	F 445 THR (-151.1, -145.8)
I 475 GLY (20.8, 122.9)	F 446 THR (-151.1, -145.8)
I 476 THR (161.9, 135.9)	F 447 THR (-151.1, -145.8)
I 477 PRO (-47.4, -108.1)	F 448 THR (-151.1, -145.8)
I 480 CYS (166.3, 168.6)	F 449 THR (-151.1, -145.8)
	F 450 THR (-151.1, -145.8)