Analysis output: all-atom contacts and geometry for MYO7A_60-686H.pdb

Summary statistics

All-Atom Contacts	Clashscore, all atoms:	71.86		1st percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	1	0.18%	Goal: <1%
	Ramachandran outliers	13	2.08%	Goal: <0.05%
	Ramachandran favored	590	94.40%	Goal: >98%
	MolProbity score^	2.71		36th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	9	1.52%	Goal: 0
	Bad backbone bonds:	53 / 5181	1.02%	Goal: 0%
	Bad backbone angles:	108 / 6990	1.55%	Goal: <0.1%

In the two column results, the left column gives the raw count, right column gives the percentage.
* 100th percentile is the best among structures of comparable resolution; 0th percentile is the worst. For clashscore the comparative set of structures was selected in 2004, for MolProbity score in 2006.
^ MolProbity score combines the clashscore, rotamer, and Ramachandran evaluations into a single score, normalized to be on the same scale as X-ray resolution.

By adding H to this model and allowing Asn/Gln/His flips, we could *automatically* improve your clashscore by 1.09 points.

Multi-criterion visualizations

View (639 Kb)

Single-criterion visualizations

- **Clash list** (14 Kb): View
- **Ramachandran plot kinemage** (442 Kb): View in KiNG | Download
- **Ramachandran plot PDF** (1.7 Mb): View
- **Cβ deviation scatter plot** (44 Kb): View in KiNG | Download

Continue >