Analysis output: all-atom contacts and geometry for COL11A1_1596-1805_FFX1H.pdb

Summary statistics

All-Atom Contacts	Clashscore, all atoms:	0.92		99th percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	7	3.76%	Goal: <0.3%
	Favored rotamers	169	90.86%	Goal: >98%
	Ramachandran outliers	0	0.00%	Goal: <0.05%
	Ramachandran favored	183	87.98%	Goal: >98%
	MolProbity score^	1.81		85th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	2	1.04%	Goal: 0
	Bad bonds:	0 / 1713	0.00%	Goal: 0%
	Bad angles:	13 / 2318	0.56%	Goal: <0.1%
Peptide Omegas	Cis Prolines:	1 / 11	9.09%	Expected: ≤1 per chain, or ≤5%
	Cis nonProlines:	2 / 198	1.01%	Goal: <0.05%
	Twisted Peptides:	2 / 209	0.96%	Goal: 0

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.

Multi-criterion visualizations

View (224 Kb)

Single-criterion visualizations

- **Clash list** (301 bytes): View
- **Ramachandran plot kinemage** (417 Kb): View in KiNG | Download
- **Ramachandran plot PDF** (1.7 Mb): View
- **Cβ deviation scatter plot** (24 Kb): View in KiNG | Download

Continue >