Analysis output: all-atom contacts and geometry for CDH23_586-817H.pdb

You cannot use your browser's back button in MolProbity, and you cannot have multiple windows of the same working session (except for kinemage views, charts, and the like).

Please continue on from here; no damage was done to your session.

Summary statistics

All-Atom Contacts	Clashscore, all atoms:	65.85		1st percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	7	3.43%	Goal: <1%
	Ramachandran outliers	29	12.61%	Goal: <0.05%
	Ramachandran favored	163	70.87%	Goal: >98%
	MolProbity score^	3.53		8th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	7	3.23%	Goal: 0
	Bad backbone bonds:	10 / 1824	0.55%	Goal: 0%
	Bad backbone angles:	31 / 2500	1.24%	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 2 points.

Multi-criterion visualizations

View (241 Kb)

Single-criterion visualizations

- **Clash list** (5.6 Kb): View
- **Ramachandran plot kinemage** (421 Kb): View in KiNG | Download
- **Ramachandran plot PDF** (1.7 Mb): View
- **Cβ deviation scatter plot** (23 Kb): View in KiNG | Download

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