Analysis output: all-atom contacts and geometry for GPSM2_20-381.pdb_14_1H.pdb

Summary statistics

All-Atom Contacts	Clashscore, all atoms:	2.34		99th percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	0	0.00%	Goal: <1%
	Ramachandran outliers	0	0.00%	Goal: <0.05%
	Ramachandran favored	356	98.89%	Goal: >98%
	MolProbity score^	1.01		100th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	10	3.03%	Goal: 0
	Bad backbone bonds:	0 / 2868	0.00%	Goal: 0%
	Bad backbone angles:	21 / 3870	0.54%	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 0.18 points.

Multi-criterion visualizations

View (340 Kb)

Single-criterion visualizations

- **Clash list** (679 bytes): View
- **Ramachandran plot kinemage** (425 Kb): View in KiNG | Download
- **Ramachandran plot PDF** (1.7 Mb): View
- **Cβ deviation scatter plot** (32 Kb): View in KiNG | Download

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