



Analysis output: all-atom contacts and geometry for ref1_1H.pdb

Summary statistics

All-Atom Contacts	Clashscore, all atoms:	0		100 th percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	5	2.98%	Goal: <0.3%
	Favored rotamers	147	87.50%	Goal: >98%
	Ramachandran outliers	7	3.63%	Goal: <0.05%
	Ramachandran favored	165	85.49%	Goal: >98%
	MolProbity score [^]	1.51		95 th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	3	1.68%	Goal: 0
	Bad bonds:	0 / 1572	0.00%	Goal: 0%
	Bad angles:	19 / 2124	0.89%	Goal: <0.1%
Peptide Omegas	Cis Prolines:	0 / 5	0.00%	Expected: ≤1 per chain, or ≤5%
	Twisted Peptides:	2 / 194	1.03%	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](#) (207 Kb)

Single-criterion visualizations

- **Clash list** (175 bytes): [View](#)
- **Ramachandran plot kinemage** (416 Kb): [View in KiNG](#) | [Download](#)
- **Ramachandran plot PDF** (1.7 Mb): [View](#)
- **C β deviation scatter plot** (20 Kb): [View in KiNG](#) | [Download](#)

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