



Analysis output: all-atom contacts and geometry for SNAI2_158- 264H.pdb

Summary statistics

All-Atom Contacts	Clashscore, all atoms:	18.8		36 th percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	6	6.19%	Goal: <0.3%
	Favored rotamers	90	92.78%	Goal: >98%
	Ramachandran outliers	4	3.81%	Goal: <0.05%
	Ramachandran favored	96	91.43%	Goal: >98%
	MolProbity score [^]	2.88		28 th percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	1	0.98%	Goal: 0
	Bad bonds:	18 / 879	2.05%	Goal: 0%
	Bad angles:	11 / 1178	0.93%	Goal: <0.1%
Peptide Omegas	Cis Prolines:	1 / 4	25.00%	Expected: ≤1 per chain, or ≤5%
	Cis nonProlines:	1 / 102	0.98%	Goal: <0.05%

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 2.35 points.

Multi-criterion visualizations



Multi-criterion chart

[View](#) (123 Kb)

Single-criterion visualizations

- **Clash list** (1.5 Kb): [View](#)
- **Ramachandran plot kinemage** (411 Kb): [View in KiNG](#) | [Download](#)
- **Ramachandran plot PDF** (1.7 Mb): [View](#)
- **C β deviation scatter plot** (16 Kb): [View in KiNG](#) | [Download](#)

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