Analysis output: all-atom contacts and geometry for LOXL3_56-144H.pdb

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Summary statistics

All-Atom Contacts	Clashscore, all atoms:	33.06		13th 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: <0.3%
	Favored rotamers		0.00%	Goal: >98%
	Ramachandran outliers	9	4.31%	Goal: <0.05%
	Ramachandran favored	178	85.17%	Goal: >98%
	MolProbity score^	2.66		38th percentile* (N=27675, 0Å - 99Å)
	Bad bonds:	24 / 844	2.84%	Goal: 0%
	Bad angles:	39 / 1054	3.70%	Goal: <0.1%
Peptide Omegas	Cis Prolines:	0 / 7	0.00%	Expected: ≤1 per chain, or ≤5%
	Twisted Peptides:	3 / 210	1.43%	Goal: 0
Low-resolution Criteria	CaBLAM outliers	5	2.40%	Goal: <1.0%
	CA Geometry outliers	10	4.81%	Goal: <0.5%

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 (2.7 Kb)

Single-criterion visualizations

- **Clash list** (1.7 Kb): View
- **Ramachandran plot kinemage** (418 Kb): View in KiNG | Download
- **Ramachandran plot PDF** (1.7 Mb): View
- **Cβ deviation scatter plot** (11 Kb): View in KiNG | Download

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