

Analysis output: all-atom contacts and geometry for EPS8L2_494-555H.pdb

Summary statistics

All-Atom Contacts	Clashscore, all atoms:	18.27		37 th percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	3	5.88%	Goal: <0.3%
	Favored rotamers	40	78.43%	Goal: >98%
	Ramachandran outliers	0	0.00%	Goal: <0.05%
	Ramachandran favored	56	93.33%	Goal: >98%
	MolProbity score [^]	2.78		32 nd percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	0	0.00%	Goal: 0
	Bad bonds:	0 / 506	0.00%	Goal: 0%
	Bad angles:	0 / 684	0.00%	Goal: <0.1%
Peptide Omegas	Cis Prolines:	0/2	0.00%	Expected: ≤1 per chain, or ≤5%

In the two column results, the left column gives the raw count, right column gives the percentage.

Multi-criterion visualizations



View (70 Kb)

Single-criterion visualizations

- Clash list (932 bytes): View
- Ramachandran plot kinemage (408 Kb): View in KiNG | Download
- Ramachandran plot PDF (1.7 Mb): View
- Cβ deviation scatter plot (14 Kb): View in KiNG | Download

^{* 100&}lt;sup>th</sup> 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.

