

## Analysis output: all-atom contacts and geometry for FGF3\_36-183H.pdb

## **Summary statistics**

All-Atom Contacts	Clashscore, all atoms:	68.69		1st percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	7	5.65%	Goal: <0.3%
	Favored rotamers	111	89.52%	Goal: >98%
	Ramachandran outliers	5	3.42%	Goal: <0.05%
	Ramachandran favored	121	82.88%	Goal: >98%
	MolProbity score <sup>^</sup>	3.57		7 <sup>th</sup> percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	10	7.41%	Goal: 0
	Bad bonds:	20 / 1224	1.63%	Goal: 0%
	Bad angles:	43 / 1648	2.61%	Goal: <0.1%
Peptide Omegas	Cis Prolines:	0/6	0.00%	Expected: ≤1 per chain, or ≤5%
	Cis nonProlines:	1 / 141	0.71%	Goal: <0.05%
	Twisted Peptides:	1 / 147	0.68%	Goal: 0

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

By adding H to this model and allowing Asn/Gln/His flips, we could *automatically* improve your clashscore by 2.08 points.

## **Multi-criterion visualizations**



View (172 Kb)

## Single-criterion visualizations

<sup>\* 100&</sup>lt;sup>th</sup> percentile is the best among structures of comparable resolution; 0<sup>th</sup> percentile is the worst. For clashscore the comparative set of structures was selected in 2004, for MolProbity score in 2006.

<sup>^</sup> MolProbity score combines the clashscore, rotamer, and Ramachandran evaluations into a single score, normalized to be on the same scale as X-ray resolution.

- Clash list (7.1 Kb): View
- Ramachandran plot kinemage (413 Kb): View in KiNG | Download
  Ramachandran plot PDF (1.7 Mb): View
- Cβ deviation scatter plot (18 Kb): View in KiNG | Download

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