

## Analysis output: all-atom contacts and geometry for KCNJ10\_27-338\_FFX1H.pdb

## **Summary statistics**

All-Atom Contacts	Clashscore, all atoms:	0.45		99 <sup>th</sup> percentile* (N=1784, all resolutions)
	Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms.			
Protein Geometry	Poor rotamers	38	3.47%	Goal: <0.3%
	Favored rotamers	945	86.22%	Goal: >98%
	Ramachandran outliers	21	1.69%	Goal: <0.05%
	Ramachandran favored	1082	87.26%	Goal: >98%
	MolProbity score <sup>^</sup>	1.68		90 <sup>th</sup> percentile* (N=27675, 0Å - 99Å)
	Cβ deviations >0.25Å	37	3.14%	Goal: 0
	Bad bonds:	0 / 10140	0.00%	Goal: 0%
	Bad angles:	116 / 13792	0.84%	Goal: <0.1%
Peptide Omegas	Cis Prolines:	0 / 48	0.00%	Expected: ≤1 per chain, or ≤5%
	Cis nonProlines:	6 / 1196	0.50%	Goal: <0.05%
	Twisted Peptides:	2 / 1244	0.16%	Goal: 0

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

## **Multi-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.

## **Single-criterion visualizations**

- Clash list (553 bytes): View
- Ramachandran plot kinemage (486 Kb): View in KiNG | Download
- Ramachandran plot PDF (1.7 Mb): View
- **C**β **deviation scatter plot** (84 Kb): View in KiNG | Download

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