



# Analysis output: all-atom contacts and geometry for ESPN\_9-336.pdb\_20\_1H.pdb

## Summary statistics

All-Atom Contacts	Clashscore, all atoms:	1.66	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	1	0.40%	Goal: <1%
	Ramachandran outliers	10	3.07%	Goal: <0.05%
	Ramachandran favored	281	86.20%	Goal: >98%
	MolProbity score^	1.55	94 <sup>th</sup> percentile* (N=27675, 0Å - 99Å)	
	Cβ deviations >0.25Å	7	2.36%	Goal: 0
	Bad backbone bonds:	0 / 2518	0.00%	Goal: 0%
	Bad backbone angles:	30 / 3433	0.87%	Goal: <0.1%

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

\* 100<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.

## Multi-criterion visualizations



[View](#) (309 Kb)

## Single-criterion visualizations

- **Clash list** (469 bytes): [View](#)
- **Ramachandran plot kinemage** (424 Kb): [View in KiNG](#) | [Download](#)
- **Ramachandran plot PDF** (1.7 Mb): [View](#)
- **C $\beta$  deviation scatter plot** (29 Kb): [View in KiNG](#) | [Download](#)

Continue >

---

About [MolProbity](#) | Website for [the Richardson Lab](#) | Using ecloud x-H | Internal reference 4.1-537