



Analysis output: all-atom contacts and geometry for EPS8_1- 154_FFX1H.pdb

Summary statistics

| | | | | |
|----------------------|---|----------|--|--------------------------------|
| All-Atom Contacts | Clashscore, all atoms: | 0.4 | 99 th percentile* (N=1784, all resolutions) | |
| | Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms. | | | |
| Protein Geometry | Poor rotamers | 5 | 3.68% | Goal: <0.3% |
| | Favored rotamers | 116 | 85.29% | Goal: >98% |
| | Ramachandran outliers | 1 | 0.66% | Goal: <0.05% |
| | Ramachandran favored | 136 | 89.47% | Goal: >98% |
| | MolProbity score^ | 1.64 | 91 st percentile* (N=27675, 0Å - 99Å) | |
| | Cβ deviations >0.25Å | 3 | 2.00% | Goal: 0 |
| | Bad bonds: | 0 / 1245 | 0.00% | Goal: 0% |
| | Bad angles: | 6 / 1682 | 0.36% | Goal: <0.1% |
| Peptide Omegas | Cis Prolines: | 0 / 4 | 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.

* 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](#) (163 Kb)

Single-criterion visualizations

- **Clash list** (217 bytes): [View](#)
- **Ramachandran plot kinemage** (413 Kb): [View in KiNG](#) | [Download](#)
- **Ramachandran plot PDF** (1.7 Mb): [View](#)
- **C β deviation scatter plot** (19 Kb): [View in KiNG](#) | [Download](#)

