# Analysis output: all-atom contacts and geometry for EPS8L2_46-175_FFX1H.pdb

## Summary statistics

| | | | | |
|---|---|---|---|---|
| All-Atom Contacts | Clashscore, all atoms: | 0.96 | | 99th percentile* (N=1784, all resolutions) |
| | Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms. | | | |
| Protein Geometry | Poor rotamers | 4 | 3.23% | Goal: <0.3% |
| | Favored rotamers | 109 | 87.90% | Goal: >98% |
| | Ramachandran outliers | 3 | 2.34% | Goal: <0.05% |
| | Ramachandran favored | 107 | 83.59% | Goal: >98% |
| | MolProbity score^ | 1.86 | | 83rd percentile* (N=27675, 0Å - 99Å) |
| | Cβ deviations >0.25Å | 3 | 2.31% | Goal: 0 |
| | Bad bonds: | 0 / 1073 | 0.00% | Goal: 0% |
| | Bad angles: | 13 / 1455 | 0.89% | Goal: <0.1% |
| Peptide Omegas | Cis Prolines: | 0 / 4 | 0.00% | Expected: ≤1 per chain, or ≤5% |
| | Twisted Peptides: | 1 / 129 | 0.78% | Goal: 0 |

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 (141 Kb)

# Single-criterion visualizations

- **Clash list** (259 bytes): View
- **Ramachandran plot kinemage** (412 Kb): View in KiNG | Download
- **Ramachandran plot PDF** (1.7 Mb): View
- **Cβ deviation scatter plot** (19 Kb): View in KiNG | Download

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