



Analysis output: all-atom contacts and geometry for MYO3A_16-287H.pdb

Summary statistics

| | | | | |
|-------------------|---|-----------|--|--------------|
| All-Atom Contacts | Clashscore, all atoms: | 33.82 | 12 th percentile* (N=1784, all resolutions) | |
| | Clashscore is the number of serious steric overlaps (> 0.4 Å) per 1000 atoms. | | | |
| Protein Geometry | Poor rotamers | 0 | 0.00% | Goal: <1% |
| | Ramachandran outliers | 5 | 1.85% | Goal: <0.05% |
| | Ramachandran favored | 250 | 92.59% | Goal: >98% |
| | MolProbity score^ | 2.48 | 48 th percentile* (N=27675, 0Å - 99Å) | |
| | Cβ deviations >0.25Å | 4 | 1.58% | Goal: 0 |
| | Bad backbone bonds: | 19 / 2218 | 0.86% | Goal: 0% |
| | Bad backbone angles: | 16 / 3006 | 0.53% | Goal: <0.1% |

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.

By adding H to this model and allowing Asn/Gln/His flips, we could *automatically* improve your clashscore by 1.15 points.

Multi-criterion visualizations



[View](#) (272 Kb)

Single-criterion visualizations

- **Clash list** (4.2 Kb): [View](#)
- **Ramachandran plot kinemage** (421 Kb): [View in KiNG](#) | [Download](#)
- **Ramachandran plot PDF** (1.7 Mb): [View](#)
- **C β deviation scatter plot** (25 Kb): [View in KiNG](#) | [Download](#)

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