# Analysis output: all-atom contacts and geometry for KCNQ4_174-332H.pdb

## Summary statistics

| | | | | |
|---|---|---|---|---|
| All-Atom Contacts | Clashscore, all atoms: | 68.91 | | 1st 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 | 10 | 6.80% | Goal: <0.05% |
| | Ramachandran favored | 120 | 81.63% | Goal: >98% |
| | MolProbity score^ | 3.02 | | 22nd percentile* (N=27675, 0Å - 99Å) |
| | Cβ deviations >0.25Å | 1 | 0.75% | Goal: 0 |
| | Bad backbone bonds: | 6 / 1186 | 0.51% | Goal: 0% |
| | Bad backbone angles: | 11 / 1612 | 0.68% | 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.

## Multi-criterion visualizations


View (154 Kb)

## Single-criterion visualizations

- **Clash list** (4 Kb): View
- **Ramachandran plot kinemage** (414 Kb): View in KiNG | Download

- **Ramachandran plot PDF** (1.7 Mb): View
- **Cβ deviation scatter plot** (18 Kb): View in KiNG | Download

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