

# MolProbity Ramachandran analysis

3scj.H.pdb, model 1



82.9% (234/281) of all residues were in favored (98%) regions.

16.7% (47/281) of all residues were in allowed (1.0%) regions.

There were 0 outliers (0%):

0.00% (0/281) in the 5% region.

0.00% (0/281) in the 1% region.

0.00% (0/281) in the 0.5% region.

0.00% (0/281) in the 0.1% region.

0.00% (0/281) in the 0.05% region.

0.00% (0/281) in the 0.01% region.

0.00% (0/281) in the 0.005% region.

0.00% (0/281) in the 0.001% region.

0.00% (0/281) in the 0.0005% region.

0.00% (0/281) in the 0.0001% region.

0.00% (0/281) in the 0.00005% region.

0.00% (0/281) in the 0.00001% region.

0.00% (0/281) in the 0.000005% region.

0.00% (0/281) in the 0.000001% region.

0.00% (0/281) in the 0.0000005% region.

0.00% (0/281) in the 0.0000001% region.

0.00% (0/281) in the 0.00000005% region.

0.00% (0/281) in the 0.00000001% region.

0.00% (0/281) in the 0.000000005% region.

0.00% (0/281) in the 0.000000001% region.

0.00% (0/281) in the 0.0000000005% region.

0.00% (0/281) in the 0.0000000001% region.

0.00% (0/281) in the 0.00000000005% region.

0.00% (0/281) in the 0.00000000001% region.

0.00% (0/281) in the 0.000000000005% region.

0.00% (0/281) in the 0.000000000001% region.

0.00% (0/281) in the 0.0000000000005% region.

0.00% (0/281) in the 0.0000000000001% region.

0.00% (0/281) in the 0.00000000000005% region.

0.00% (0/281) in the 0.00000000000001% region.

0.00% (0/281) in the 0.000000000000005% region.

0.00% (0/281) in the 0.000000000000001% region.

0.00% (0/281) in the 0.0000000000000005% region.

0.00% (0/281) in the 0.0000000000000001% region.

0.00% (0/281) in the 0.00000000000000005% region.

0.00% (0/281) in the 0.00000000000000001% region.

0.00% (0/281) in the 0.000000000000000005% region.

0.00% (0/281) in the 0.000000000000000001% region.

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0.00% (0/281) in the 0.000000000000000000005% region.

0.00% (0/281) in the 0.000000000000000000001% region.