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Supporting information for article:

Tah1 helix-swap dimerization prevents mixed Hsp90 co-chaperone complexes

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MolProbity Ramachandran analysis

4CQG, model 1

97.4% (299/307) of all residues were in favored (98%) regions.
100.0% (307/307) of all residues were in allowed (>99.8%) regions.

There were no outliers.

http://kinemage.biochem.duke.edu

Lovell, Davis, et al. Proteins 50:437 (2003)

Figure S1  Ramachandran plot.