Resolution stays the same and rotation about the z-axis occurs when using a tight mask

Mon, 05/07/2018 - 16:33 #1

anp2054

Resolution stays the same and rotation about the z-axis occurs when using a tight mask

When I use a tight mask when doing manual refinement, I notice that the resolution stays the same and the structure rotates about the z-axis instead. Why does this happen and how can I avoid it?

Mon, 05/07/2018 - 16:44

#2

timgrant

Hi,

Hi,

Any tight mask you apply is not used for the resolution estimation. In cisTEM the "masking" for resolution estimation is handled by a scaling factor based on the molecular weight, the reconstructions are never masked, so resolutions will not necessarily improve when you mask.

In terms of things rotating, if your molecule is not constrained by symmetry, there is no reason that it shouldn't "move" during refinement. If you don't want the angles to change, you can turn off their refinement by unclicking Psi, Theta and Phi from the Parameters to refine section in the expert options.

I hope this answers your question?

Tim

Mon, 05/07/2018 - 17:04 (Reply to #2)

anp2054

Thanks, it helped.

Thanks, it helped.

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