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# updated apoferritin tutorial for 2.0.0 alpha

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Eugene

updated apoferritin tutorial for 2.0.0 alpha

When can we expect an updated tutorial for version 2.0.0? I can only achieve an 8Å resolution compared with 3Å on version 1.0.0. as per the documentation.

Thanks





davidgenemorgan

updated apoferritin tutorial for 2.0.0 alpha

I totally agree that a new tutorial would be nice.







davidgenemorgan

question about ab initio models

Hi,

I'm working with a bacteriophage procapsid that is prolate and has "broken D5 symmetry" meaning that one end of the procapsid is different from the other. I should be able to reconstruct this using C5 symmetry, but the ab initio models are all D5-like: there is stuff at both ends of the procapsid. The "resolution" is sub-10 Å and the structure looks like that is reasonable for the parts of it away from the ends. But this is clearly an incorrect structure. Is there any way to fix this using cisTEM, or do I need to build an initial model using some other software?





timgrant

Hi,

Hi,

A new tutorial would probably accompany an official release, but I am not sure when that would be. IF you are getting 8A vs 3A it is likely your ab-initio is failing. I suggest to try again using class averages.

Tim







timgrant

David - it is pseudo D5? You

David - it is pseudo D5? You may find that if you run iterative auto-refine jobs starting at 20A it fixes this. Or 3D classification.

Tim

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