*Supporting Information*

# Multicompartment Lipid Cubic Nanoparticles with High Protein Upload: Millisecond Dynamics of Formation

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## Additional results

**Figure S1. (a)** Cryo-TEM image of a tubular lipid nanoparticle characterized by an inverted hexagonal packing of aqueous nanochannels in the SAXS patterns.

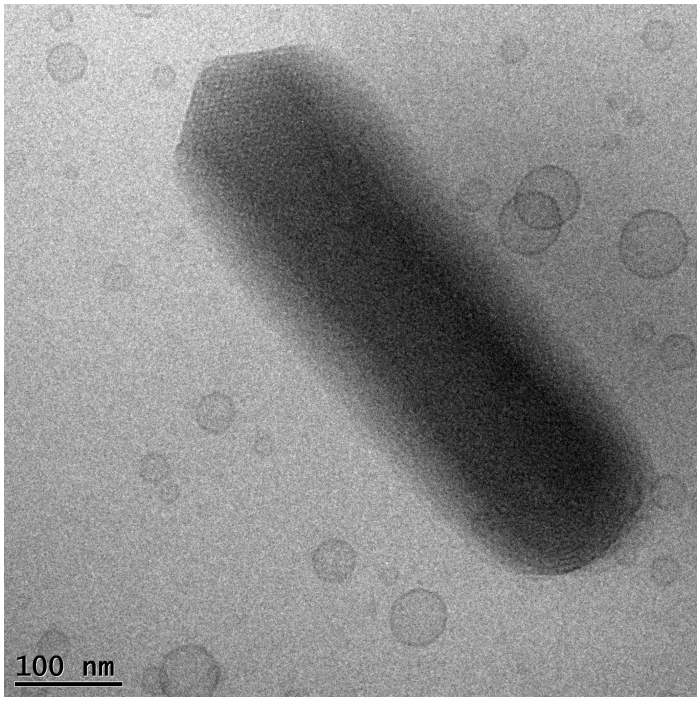


**Figure S1. (b)** Cryo-TEM image of a hexagonal cross-section (darker area revealing a periodic arrangement of nanochannels) of a tubular lipid nanostructure undergoing an initial stage of an inverted hexagonal – to – bilayer-membrane structural transition.

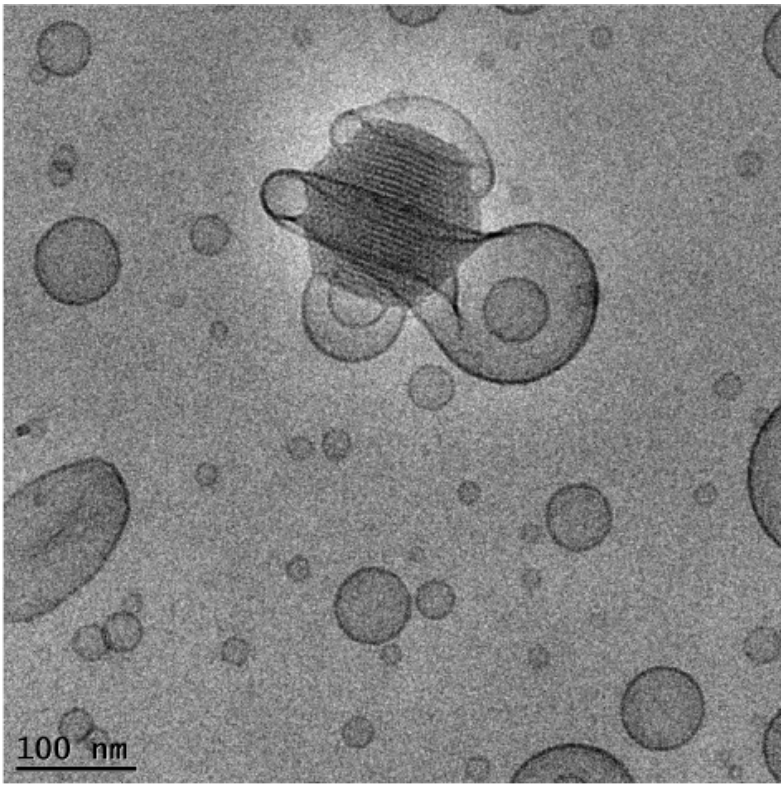


**Figure S2.** Sequence of time-resolved small-angle X-ray scattering (SAXS) patterns characterizing the initial lipid nanoparticulate system in the absence of protein molecules. This control experiment demonstrates that the SAXS patterns of the lipid nanocarriers are invariable with time. Therefore, all *in situ* observed structural changes in the present time-resolve SAXS investigation will be due to the protein coupling, assembly and loading in the lipid membranous and tubular nanoparticles.

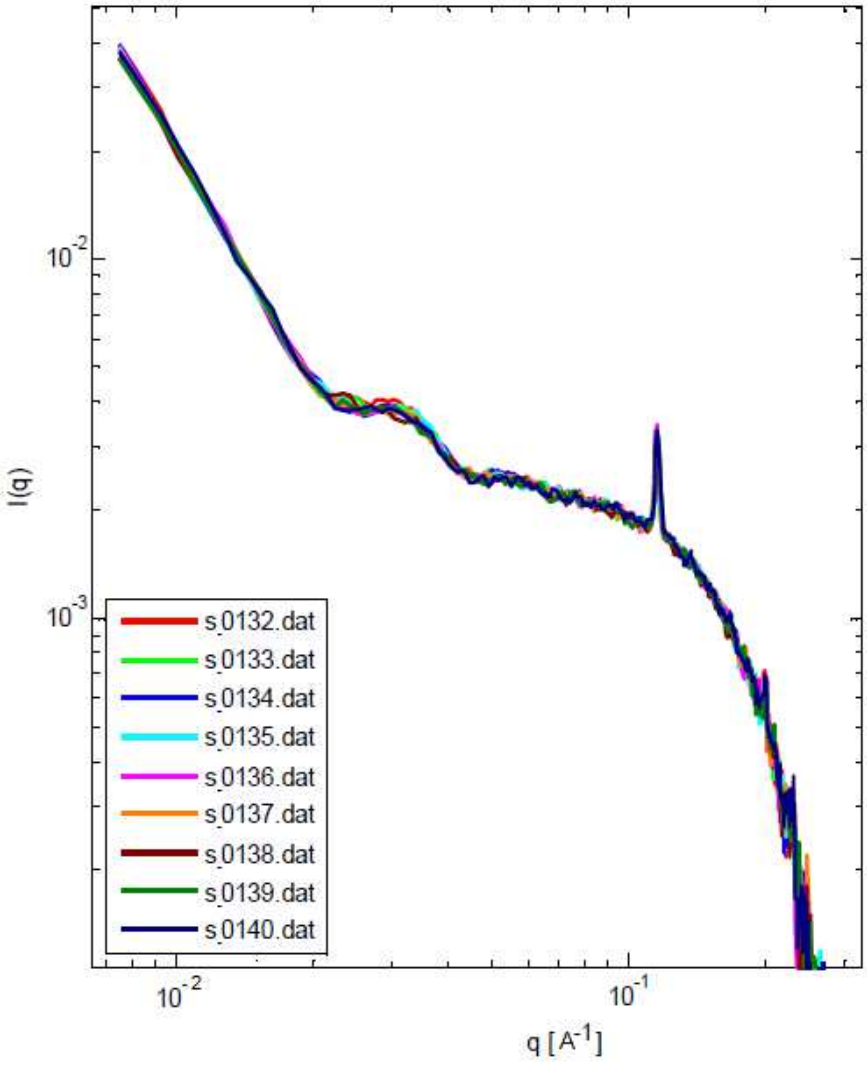


**Figure S3.** Volume weighted distribution of the average particle sizes of the studied self-assembled lipid nanocarriers determined by quasi-elastic light scattering (QELS). The error bars are shown in green.

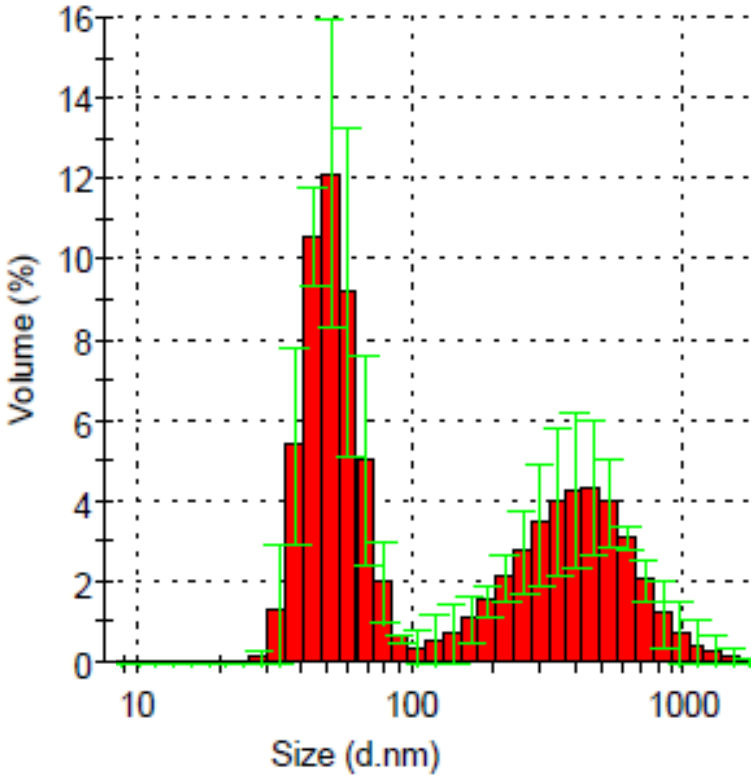
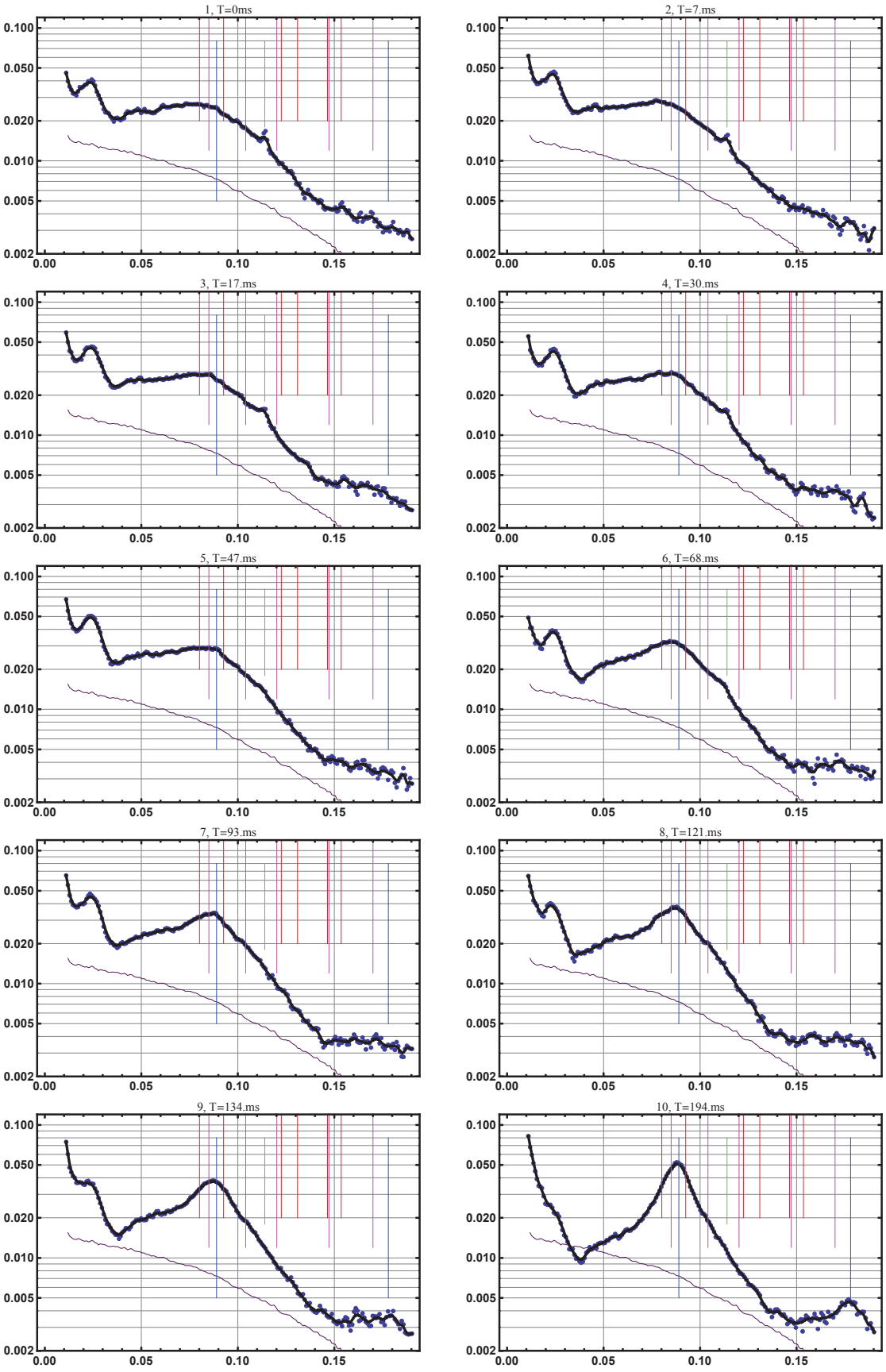



**Figure S4.** Sequence of selected TR-SAXS frames showing the complete structural pathway determined in real time. The data are presented as the scattering intensity in absolute units (dark blue curves) *versus* the wave vector $q$ ($Å^{-1}$). The colour bars indicate the positions of the Bragg peaks for an inverted hexagonal $H_{II}$ structure (green), a lamellar $L_\alpha$ structure (blue), a double diamond cubic (*Pn3m*) (purple) and a gyroid cubic (*Ia3d*) structure (red) formed by the protein-lipid membrane complexes. The scattering of the pure BDNF protein is presented by a violet plot (thin line).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0.05
0.10
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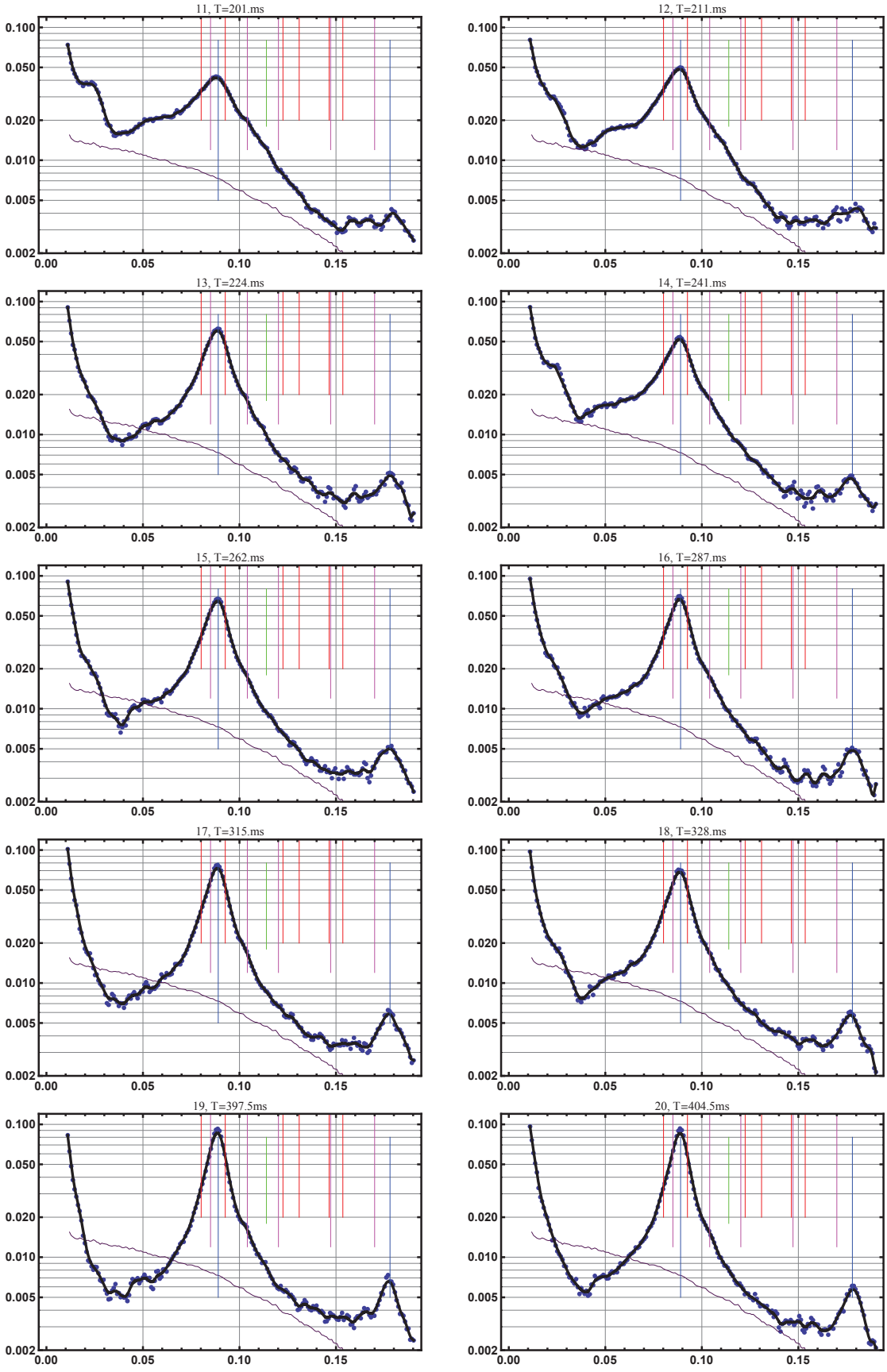
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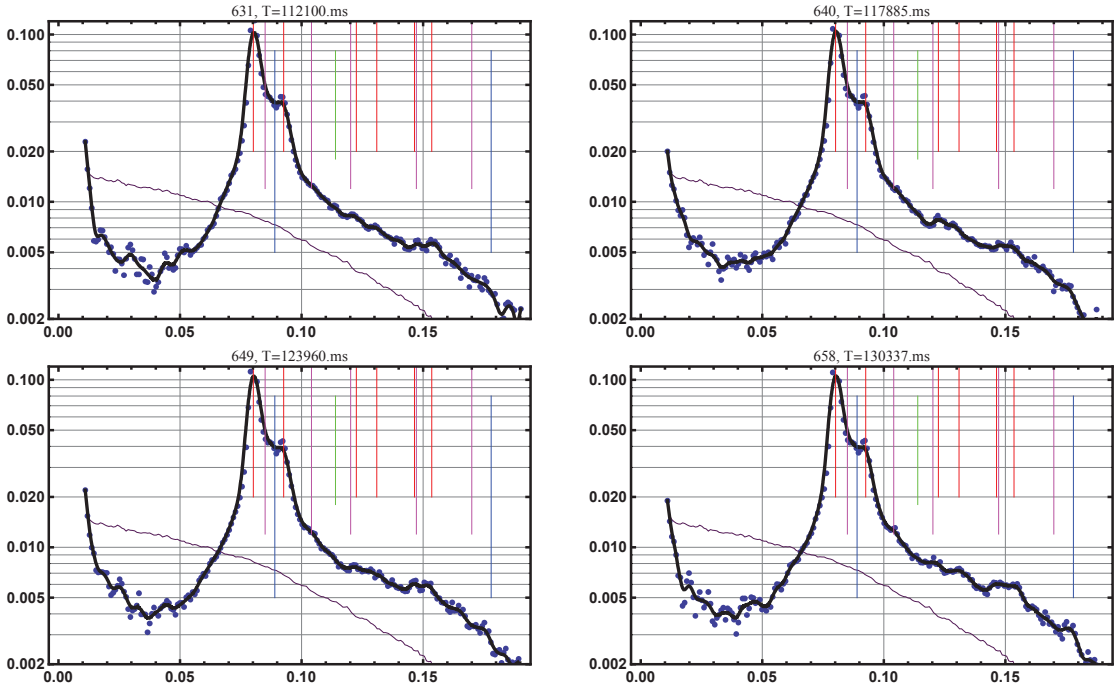
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