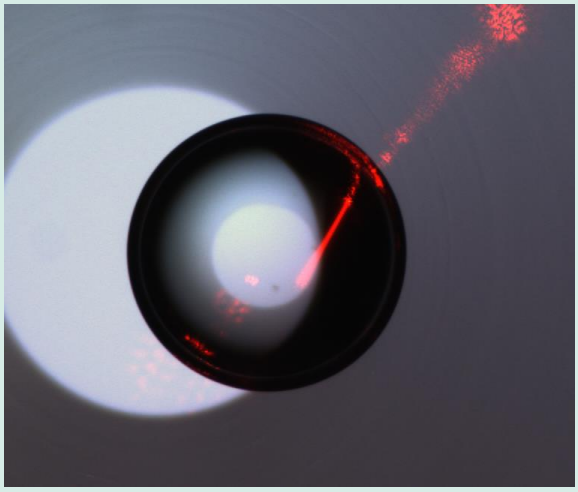
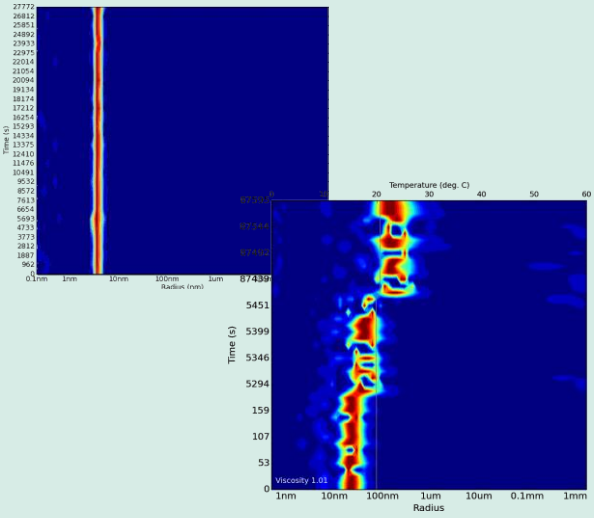
Long Term Stability Analysis

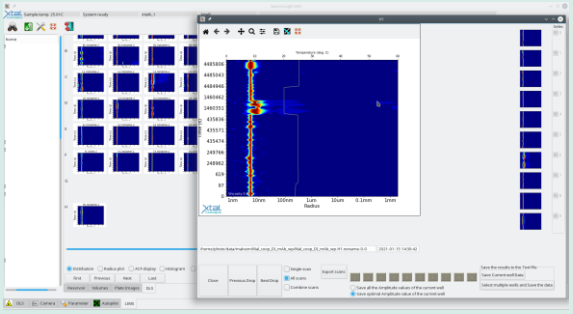
Protein stability is essential when it comes for structural characterization. Even when applying state of the art biophysical methods, predictability for gradually aggregation is limited. A reliable method is to examine stability in an empirical approach, which is enabled by the announced dynamic light scattering set-up. Key feature is the enclosing of the sample in an inert medium in our case paraffin oil. The oil cover prevents a sample for evaporation, oxidization and for getting dusty. It is the optimal set-up for long term stability analysis even for months.

An encased droplet is prevented for evaporation. This allows to analyze the sample stability even in aliquots as small as 100 nl. Other advantages are also provided by this setup like protection refractive index matching and protection from oxidization. Since DLS is one of the rare non-invasive methods, it can be applied for an infinite amount of time without influencing the sample by itself.

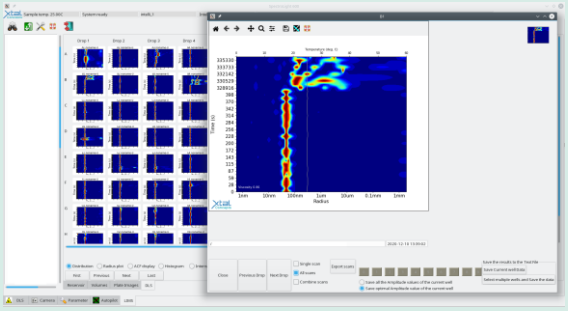


Stability and Instability Signatures can be identified at a glance by size vs time plots. Scattered light intensities can be allocated to particle sizes. That allows to plot the output of a series of DLS-measurements in highly useful plots like those are shown here. Many samples can be scored in terms of their stability immediately. This is also supported by the fact that DLS is a so called direct method. The output is a particle size distribution which can be detected with remarkable reliability.





High Stability: An optimal formulated sample can be stable for months, in some cases even when stored at room temperature. This of course depends on the sample itself but its long term stability can be detected highly reliable without any pipetting efforts and highly sample and cost efficient.



Spontaneous Aggregation may also occur even when the sample was stored under stable ambient conditions. Since this is a property of the sample in a given buffer, it is important to know the time frame in which the sample can be used. This is relevant for many protein applications and by far not limited to structural characterization alone.