MOLECULAR BIOPHYSICS RESEARCH IN GRONINGEN

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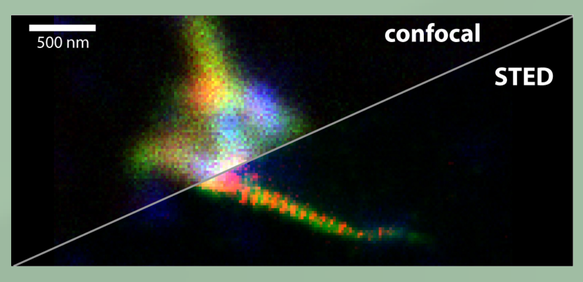
STED microscopy reveals the centrosome linker organization

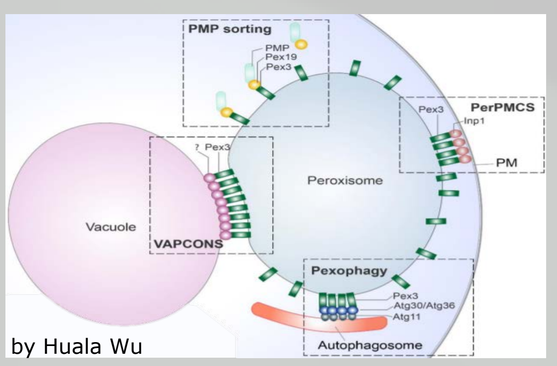
*Vlijm et al. PNAS 2018, **115(10)**.*

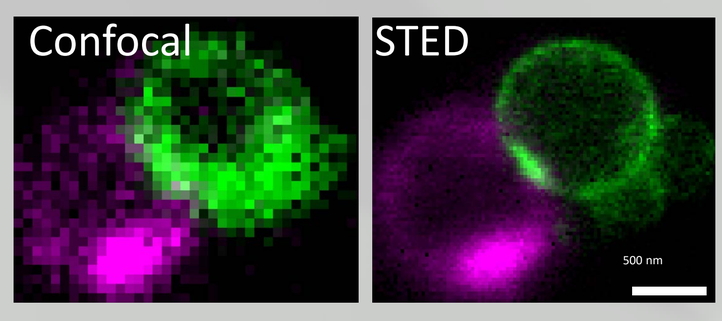


STED (STimulated Emission Depletion) microscopy is a fluorescent light microscopy technique which enables the visualization of cellular structures at a resolution well beyond the diffraction limit of light. This significantly improved resolution (~30nm instead of ~220nm using confocal microscopy) reveals how the centrosome linker is, unlike previously modelled, organized as a periodic rootletin and CEP68 network, anchored to a C-NAP ring at the centrioles.

Direct visualization of peroxisomal contact sites

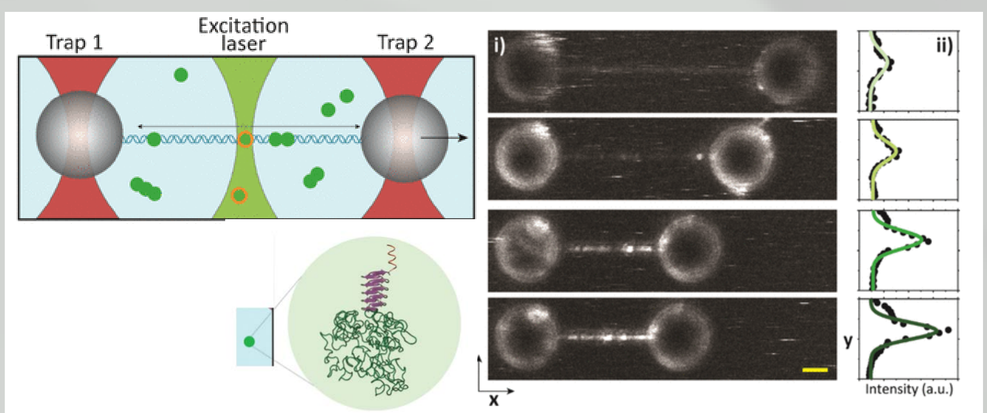
de Lange et al. accepted Meth. in Mol. Biol. 2022





Recent developments in STED nanoscopy, a super-resolution light microscopy technique, enable the direct visualization of (dynamic) structures in living cells at 40nm resolution. We use this technique to reveal how peroxisomes, crucial organelles that occur in almost all eukaryotic cells, are organized. Peroxisomes are known for their involvement in metabolic processes, but recent studies showed that they also have other functions, like in stress response, signalling and cellular ageing. Despite extensive studies no consensus has been reached on the functioning of the peroxisomal membrane. Multi-color STED however, can reveal the distribution membrane proteins in conjunction with contact sites to better understand peroxisome biogenesis.

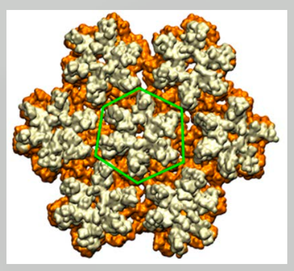
Real-Time Assembly of Viruses *Marchetti et al. Nano Letters 2019, **19**; Buzón et al. Science Advances 2021, **7***

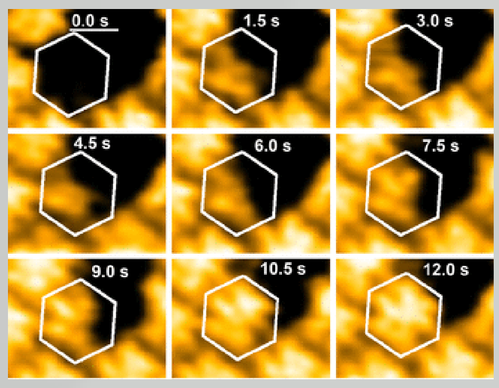


Optical tweezers combined with fluorescence confocal microscopy reveal protein binding and compaction into the virus capsid.

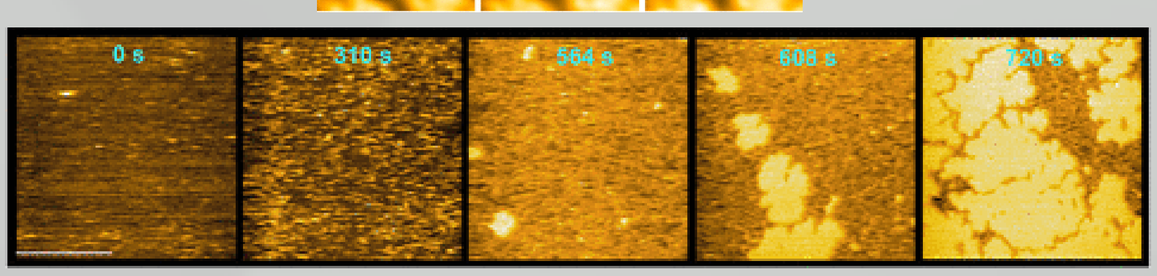
Two focused leaser beams trap two microspheres attached to a DNA molecule. Proteins bind to the DNA and their fluorescent tag lights up when the scanning laser illuminates them. Fluorescence intensity is then directly proportional to the number of bound proteins to the DNA.

Single molecules build a viral capsid *Valbuena et al. ACS Nano 2020, **14**.*



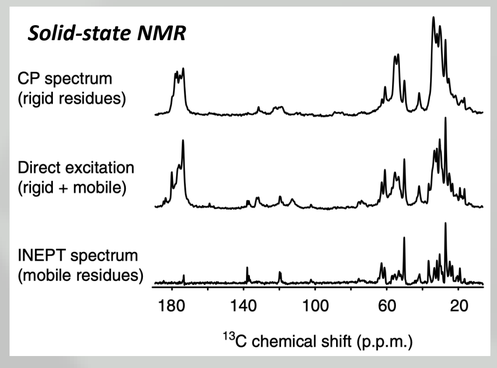


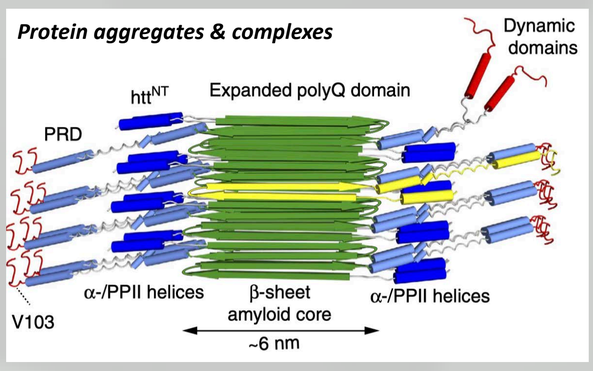
Monomers of mature HIV proteins arrange into a lattice, which then forms the full capsid.



High Speed Atomic Force Microscopy reveals the step by step formation of the HIV capsid protein lattice. These steps were identified as nucleation, diffusion, growth, and fusion.

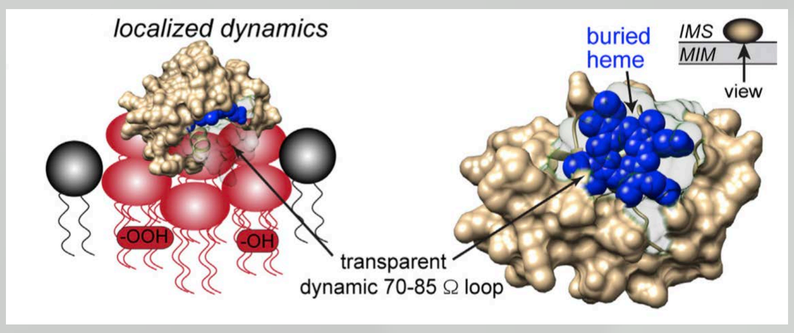
Molecular (domain) motion in aggregated proteins *Lin et al. Nature Commun. 2017, **8**. 15462*

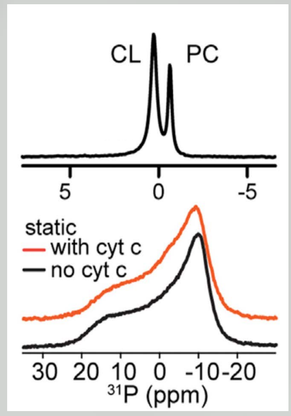




Solid-state NMR reveals changes in dynamics (and structure) of aggregating or self-assembling proteins, even in cases where the resulting aggregates are amorphous, heterogeneous or fibrillar. Comparative analysis of polymorphic states of aggregated, self-assembled or sedimented proteins allows for structural and dynamic fingerprinting. Unique information on dynamically disordered protein segments, as well as rigid domains is accessible by dynamically sensitive techniques.

Lipid studies: phases & Protein interactions *Li et al. Structure 2019, **27**. 806*





Solid-state NMR is a classic and powerful tool to probe and understand (lipid) phase transitions, non-bilayer phases, and protein-lipid interactions in biological membranes. Our ssNMR capabilities include studies of lipid-bound proteins (especially peripherally bound), as well as order parameter measurements (of lipids or protein) by various means (including ^{2}H, ^{31}P, ^{1}H-^{13}C static and magic angle spinning (MAS) ssNMR).