

Local curvature analysis of ice recrystallisation inhibition

Agata M. Malinowska¹, Thomas Reus¹, Roderick Tas², Roma Suris Valls², Ilja K. Voets², Iddo Heller¹

¹Physics and Astronomy, VU Amsterdam, Amsterdam, Netherlands, ²Chemical Engineering and Chemistry, TU Eindhoven, Eindhoven, Netherlands.

Ice-binding proteins (IBPs) have the ability to protect cells and tissues from frost-damage by controlling the nucleation and growth of ice crystals. Our goal is to elucidate how IBPs can modulate the water-ice phase transition and function as such remarkable cryo-protectants by quantifying the organization of the IBPs at the solid-liquid interface and the dynamics of advancing ice-crystal planes. To this end, we have developed a new experimental approach that is suited for high-resolution imaging of ice crystals and for fluorescence microscopy for localization of single proteins, and developed analysis to assess dynamic reshaping of the interface - both on a local scale and in the context of the entire system.