

# RECRYSTALLIZATION KINETICS AND INHIBITION CAUSED BY ICE-BINDING AGENTS

Carsten Budke<sup>1</sup>, Carolin Plattner<sup>2\*</sup>, Anna S. Norgren<sup>2#</sup>, Arthur L. DeVries<sup>3</sup>,  
Kerstin Hartkamp<sup>1</sup>, Thomas Berkemeier<sup>1</sup>, Lilly Nagel<sup>2</sup>,  
Norbert Sewald<sup>2</sup>, Thomas Koop<sup>1</sup>

<sup>1</sup>Department of Chemistry, Physical Chemistry, Bielefeld University, Bielefeld, Germany

<sup>2</sup>Department of Chemistry, Organic and Bioorganic Chemistry, Bielefeld University, Bielefeld, Germany

<sup>3</sup>Department of Animal Biology, University of Illinois at Urbana-Champaign, Urbana, USA

\* currently at ChemCon GmbH, Freiburg, Germany

# currently at Syntagon AB, Södertälje, Sweden

The recrystallization of polycrystalline ice in aqueous solutions is a diffusion-limited Ostwald ripening process, which can be described by the theory of Lifshitz, Slyozov, and Wagner (LSW). This theory provides a recrystallization rate constant for ice volume fractions near zero. Because in real systems with non-zero volume fractions larger recrystallization rates occur, experiments were performed to quantify the effect.

The resulting modified LSW rate equation allows for investigating the effect of ice binding additives on ice recrystallization. The recrystallization inhibition efficiency of several synthetic polymers (e.g. PEG, PVA) as well as that of natural antifreeze glycoproteins (AFGP) and their synthetic analogues was determined and described by the modified LSW rate equation. It was found that efficient antifreeze proteins are able to inhibit ice recrystallization down to concentrations of only  $0.02 \mu\text{g mL}^{-1}$ , implying a molar concentration of  $0.001 \mu\text{mol L}^{-1}$  for a mixture of natural AFGP 1-5 with a mean molecular mass of 22.1 kDa. In contrast, poly(ethylene glycol) with a mean molecular mass of 3.0 kDa did not show any inhibition effect at concentrations up to  $2700 \mu\text{g mL}^{-1}$ . In total, we have analyzed 26 different substances such that we can classify them according to their inhibition efficiency in a quantitative manner.

The authors gratefully acknowledge support from Deutsche Forschungsgemeinschaft (SFB 613), the NRW International Graduate School in Bioinformatics and Genome Research, and Fonds der Chemischen Industrie. L. N. was funded by a PhD fellowship of Bielefeld University.