

Abstract Submitted
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Why are hyperactive ice-binding-proteins so active?¹ IDO BRASLAVSKY, YELIZ CELIK, NATALYA PERTAYA, YOUNG EUN CHOI, Physics Department, Ohio University, Athens, OH, MAYA BAR, Structural Biology, Weizmann Institute of Science, Rehovot, Israel, PETER L. DAVIES, Department of Biochemistry, Queen's University, Kingston, Ontario, Canada — Ice binding proteins (IBPs), also called 'antifreeze proteins' or 'ice structuring proteins', are a class of proteins that protect organisms from freezing injury. These proteins have many applications in medicine and agriculture, and as a platform for future biotechnology applications. One of the interesting questions in this field focuses on the hyperactivity of some IBPs. Ice binding proteins can be classified in two groups: moderate ones that can depress the freezing point up to ~ 1.0 °C and hyperactive ones that can depress the freezing point several-fold further even at lower concentrations. It has been suggested that the hyperactivity of IBPs stem from the fact that they block growth out of specific ice surfaces, more specifically the basal planes of ice. Here we show experimental results based on fluorescence microscopy, highlighting the differences between moderate IBPs and hyperactive IBPs. These include direct evidence for basal plane affinity of hyperactive IBPs, the effects of IBPs on growth-melt behavior of ice and the dynamics of their interaction with ice.

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