

Molecular Insights into the Interactions between Antifreeze Proteins and Ice

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Fishes, insects and other organisms are able to survive in frigid polar environments with the help of antifreeze proteins (AFPs), which suppress freezing by preferentially binding ice crystals and passivating them. The ability of AFPs to perform one of the most challenging molecular recognition tasks in all of biology – distinguishing between two different phases of water – has long been a source of amazement and intrigue; not only are there no chemical differences to leverage, the structural differences between water and ice are also subtle. In addition to binding ice, AFPs must also resist engulfment by ice, and their ability to do so can influence their thermal hysteresis activity. Thus, AFPs must have certain regions that preferentially interact with ice and facilitate binding as well as other regions that interact unfavorably with ice (relative to water) and resist engulfment. Which AFP regions facilitate their binding to ice and which molecular characteristics enable them to subsequently resist engulfment? Moreover, how do these characteristics influence the AFP thermal hysteresis activity? To answer these questions, we combine molecular simulations with enhanced sampling techniques. We find that larger AFPs are better able to resist engulfment than smaller ones and that naturally occurring AFPs have evolved to optimally resist engulfment. By uncovering the molecular basis for AFP activity, we hope that our work will facilitate the engineering of novel AFPs with superior function.