# SEMINAR Department of Biological Sciences



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## Hosted by Professor Hew Choy Leong

News about antifreeze and other ice-binding proteins (IBPs)

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Come and see the amazing diversity of protein structures that have independently evolved to bind to ice. They include alpha-, beta- and polyproline type II helices, as well as globular proteins. Many of these proteins are specially adapted to fold and function well at freezing temperatures. Some of the simpler repetitive IBPs have evolved on several occasions and have converged to look alike. Other more complicated IBPs have been spread by lateral gene transfer - even between fish species. Often there is evidence of intense selective pressure on the organism to adapt to climate change and survive in contact with ice. Some of the IBPs are true antifreezes that protect fish and insects from freezing; others help cold-hardy plants and microorganisms tolerate freezing; a third newly discovered function is that of binding its host to ice - hence the catch-all name IBP. All these IBPs are freely soluble in liquid water but will irreversibly adsorb to water in the frozen state. How do they do that? After arguing for decades about the role of hydrogen bonding vs the hydrophobic effect in the binding mechanism, it seems that the modellers are right. Both forces are in play. The hydrophobicity of the ice-binding site on an antifreeze protein organizes and anchors water into an ice-like pattern that merges with the ice-like water in the "quasi liquid layer" next to the ice. With cooling, this layer readily turns into ice and freezes the IBP onto it. In effect, the protein forms the ligand to which it binds. Ice nucleation proteins (found on plant pathogenic bacteria) are the antithesis of antifreeze proteins: they promote freezing at high sub-zero temperatures. Now, modeling suggests that they look and function like IBPs, but are many orders of magnitude larger. By organizing ice-like waters over a large surface area they can nucleate freezing.

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Artwork by Ann Nee, DBS, NUS