Bioprospecting the Arctic Ocean to investigate enzymatic cold-adaptation

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The ability of any organism to adjust to its surroundings is a crucial driving force of evolution, as it is essential for the survival of any organism. Psychrophiles are organisms that have inherently adapted to not only survive but thrive in conditions below 15 ℃. Life at such low temperatures is complicated by a range of exacerbating factors; as follows from the Arrhenius equation, temperature has a direct, exponential impact on enzyme catalysis. It is generally assumed that a 10 ℃ decrease in temperature leads to a 2-fold lower enzyme catalysis, yet enzymes of psychrophilic organisms, so-called psychrozymes, frequently retain relatively high activities at their habitual temperatures. Understanding mechanisms of cold-adaptation may generate fundamentally new principles for developing super-efficient enzymes in biotechnological applications.

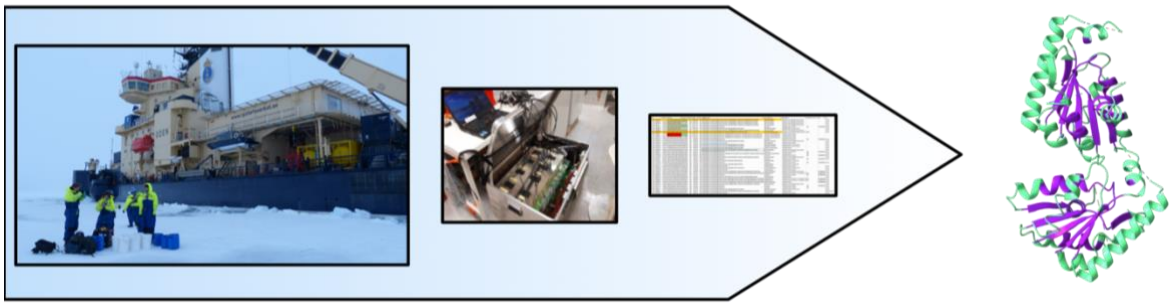

Figure 1: From the Arctic Ocean to atomic resolution. We used a bioprospecting strategy to investigate how an arctic Adenylate Kinase is optimized to function in cold environments.

We employed a bioprospecting approach to study structural principles of protein adaptation to cold temperatures by using Adenylate Kinase (AK) as a model system. Leveraging metatranscriptomics data from the Synoptic Arctic Survey 2021, we identified sequences of psychrophilic AKs. Subsequent experiments focused on AKarc, derived from an arctic archaeon, enabling direct comparison with a heat-adapted AK from hyperthermophilic Odinarchaeota[1].

AK_{arc} could be purified via bacterial expression in *E. coli* and subsequent affinity chromatography, suggesting a trimeric structure. Preliminary data indicates that, based on ITC and P-NMR experiments, AK_{arc} has a higher activity but lower substrate affinity than AK_{Odin}. Contrary to our expectations, DSC measurements revealed trimeric AK_{arc} to be remarkably thermostable, showing cooperative unfolding at a T_M of 81 ℃. Using a preliminary structure of AK_{arc} at 3.6 Å coupled with MEDUSA flexibility analysis, we hypothesize that these characteristics are achieved by increased flexibility in trimerization domains that destabilize monomeric conformations.

1 Verma, A. *et al.* Insights into the evolution of enzymatic specificity and catalysis: From Asgard archaea to human adenylate kinases. *Sci Adv* **8**, eabm4089 (2022). https://doi.org/10.1126/sciadv.abm4089