

Pressure-based mapping of protein functional landscape

Tejaswi Koduru, Philippe Barthe, Karyn De Guillen, Luke Fisher, Carleton Coffin, Noam Hantman, Pierce Leonardi, Jack Foland, Scott A. McCallum, Joel E. Morgan, Estella Yee, Christian Roumestand, Douglas H. Bartlett, Catherine A. Royer
(Rensselaer Polytechnic Institute, Troy, USA)

Abstract

Over 80% of the microbial biomass on Earth exists in high pressure environments. However, it is known that high pressure destabilizes the interactions and structure of proteins from mesophilic organisms. The question thus arises as to how microbes living at high pressure have adapted to their environments, which include very hot temperatures at hydrothermal vents or in the oceanic or continental crusts, as well as the low temperatures of the cold deep sea. Here we compare the enzymatic and structural properties of homologous exonucleases from the mesophilic *Staphylococcus aureus* and from *Carnobacterium* AT7 from the cold deep Aleutian trench under varying thermodynamic and chemical conditions. Results are discussed in light of recent work probing adaptive mutations in a strain of *E. coli* (AN62) which was evolved in the laboratory for growth under pressure.

[1] Qamar,
Mrovec,

M.,
M.,

Lysogorskiy, Y., Bochkarev, A., & Drautz, R. (2023). Atomic cluster expansion for quantum-accurate large-scale simulations of carbon. *Journal of chemical theory and computation*, 19(15), 5151-5167.

[2] Heimes, H., Turner, E. P., Salek, A. G., Wierbik, J., Huang, X., Dunstan, W. R., ... & Bradby, J. E. (2025). Mechanisms of nanodiamond and amorphous diamond-like carbon formation following room temperature compression of C60. *Diamond and Related Materials*, 112776.