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Effects of pressure on the dynamics of a hyperthermophilic protein revealed by quasielastic neutron scattering[1]

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Inorganic pyrophosphatase (IPPase) from *Thermococcus thioreducens* is a large oligomeric protein derived from hyperthermophilic microorganism that is found near hydrothermal vents deep under the sea, where the pressure is nearly 100 MPa. Here we study the effects of pressure on the conformational flexibility and relaxation dynamics of IPPase over a wide temperature range using quasielastic neutron scattering (QENS) technique. Two spectrometers were used to investigate the β-relaxation dynamics of proteins in time ranges from 2 to 25 ps, and from 100 ps to 2 ns. Our results reveal that, under the pressure of 100 MPa, IPPase displays much faster relaxation dynamics than a mesophilic model protein, hen egg white lysozyme (HEWL) [1], opposite to what we observed previously under the ambient pressure [2]. These contradictory observations imply that high pressure affects the dynamical properties of proteins by distorting their energy landscapes. Accordingly, we derived a general schematic denaturation phase diagram that can be used as a general picture to understand the effects of pressure on protein dynamics and activities. [1] Shrestha et al. (2015), *Proc Natl Acad Sci USA*, doi: 10.1073/pnas.1514478112. [2] Chu et al. (2012), *J Phys Chem B* 116(33): 9917-9921.

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