EXPLORING FERRITIN PROTEIN PORES ON THE ATOMIC LEVEL WITH NMR

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Protein pores in ferritin provide a mechanism for the removal of iron from its concentrated form, a hydrated ferric mineral inside the protein nanocage. The metal becomes accessible to biological reductants when pore structure "melts" or unfolds. Evidence for this are available from crystallographic and biophysical studies of the wild type protein and various mutants, made using phylogenetic conservation of amino acids around the pore in 3D space, for which no other function had been assigned. Each mutation increased access of reductant and chelator to iron, with a 100% success rate. Pore structure is associated with a low temperature melting subdomain (CD spectroscopy) and sensitivity to physiological concentrations of urea, 1.0 mM, whereas global structure resists 7 M urea, at pH 7.

We now report our efforts towards studying the pores on an atomic level under biologically relevant conditions using NMR. The size of this molecule makes this feat a formidable one. However with the use of newly developed carbon detection pulse sequences or CRINEPT based proton detection we were able to follow the pore resonances under a variety of conditions including temperature and the presence of low concentrations (1 mM) urea. Part Support: NIH-DK- 20251).

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