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Size-dependent studies of macromolecular crowding on the thermodynamic stability, structure and functional activity of proteins: *in vitro* and *in silico* approaches

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Abbreviations

PEG, polyethylene glycol; FKBP, FK-506 binding protein; HSA, human serum albumin; GdmCl, guanidinium chloride; T_m , midpoint of denaturation; ΔH_m , enthalpy change at T_m ; Trp, tryptophan; bOBP, bovine odorant binding protein; BSA, bovine serum albumin; ANS, 1-anilinonaphthalene-8-sulfonate; FRET, fluorescence resonance energy transfer; Δr , change in inter domain distance; K_m , Michaelis constant; k_{cat} , catalytic constant; K_d , dissociation constant; AMPPNP, adenylyl imidodiphosphate; mi-CK, mitochondrial creatine kinase; HRP, horseradish peroxidase; LDH, L-lactate dehydrogenase; MDH, malate dehydrogenase; SPT, scaled particle theory; $\Delta\Delta G_N$, change in free energy change of folding; $\Delta\Delta G_{ND}$, the change in protein stability; CRABP I, cellular retinoic acid-binding protein I; GAPD, D-glyceraldehyde-3-phosphate dehydrogenase; PDI, protein disulfide isomerase.

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