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Critical radius in the organisation of synuclein-alpha interacting protein in living cells ARJUN NARAYANAN, Massachusetts Inst of Tech, ANATOLI MERIIN, MICHAEL SHERMAN, Boston University Medical school, IBRAHIM CISSE, Massachusetts Inst of Tech — We report a super-resolution imaging study of protein aggregation in the living cell. Focusing on the aggregation of the Parkinsons's disease linked Synuclein-alpha interacting protein, we found and characterized sub-diffraction aggregates in healthy cells and studied the progression of these aggregates in stressed cells. Our results allowed us to establish the aggregation process as amenable to a simple physical description - the well-established thermodynamics of condensation phenomena. This description turned out to be both robust and useful. Not only did the distribution of aggregate sizes fit exceedingly well to the thermodynamic predictions in all tested conditions, but its evolving shape under pharmacological and genetic perturbations correlated intuitively with predictions from cell biology. The picture emerging from measurements in different genetic and pharmacological states is a view of protein aggregate size distribution as resulting from a non-equilibrium steady state maintained - even in healthy cells - with continuous and concurrent aggregate production and clearance.

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