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Sommario/riassunto

Proteins suffer many conformational changes and interactions through their life, from their synthesis at ribosomes to their controlled degradation. Only folded and soluble proteins are functional. Thus, protein folding and solubility are controlled genetically, transcriptionally, and at the protein sequence level. In addition, a well-conserved cellular machinery assists the folding of polypeptides to avoid misfolding and ensure the attainment of soluble and functional structures. When these redundant protective strategies are overcome, misfolded proteins are recruited into aggregates. Recombinant protein production is an essential tool for the biotechnology industry and also supports expanding areas of basic and biomedical research, including structural genomics and proteomics. Although bacteria still represent a convenient production system, many recombinant polypeptides produced in prokaryotic hosts undergo irregular or incomplete folding processes that usually result in their accumulation as insoluble aggregates, narrowing thus the spectrum of protein-based drugs that are available in the biotechnology market. In fact, the solubility of bacterially produced proteins is of major concern in production processes, and many orthogonal strategies have been exploited to try to increase soluble protein yields. Importantly, contrary to the usual assumption that the bacterial aggregates formed during protein production are totally inactive, the presence of a fraction of molecules in a native-like structure in these assemblies endorse them with a

certain degree of biological activity, a property that is allowing the use of bacteria as factories to produce new functional materials and catalysts. The protein embedded in intracellular bacterial deposits might display different conformations, but they are usually enriched in beta-sheet-rich assemblies resembling the amyloid fibrils characteristic of several human neurodegenerative diseases. This makes bacterial cells simple, but biologically relevant model systems to address the mechanisms behind amyloid formation and the cellular impact of protein aggregates. Interestingly, bacteria also exploit the structural principles behind amyloid formation for functional purposes such as adhesion or cytotoxicity. In the present research topic we collect papers addressing all the issues mentioned above from both the experimental and computational point of view.