Disorder in proteins: abundance and functional characterization in 1000 proteomes across the three domains of life and viruses

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Numerous proteins were shown to lack a unique tertiary structure as a whole or in part [1]. These intrinsically disordered proteins and intrinsically disordered protein regions have highly flexible structures and exist as dynamic conformational ensembles. Biological functions of the disordered proteins/regions, which include regulation, signaling, and control pathways, complement the functional repertoire of ordered/structured proteins [2-4]. They are also commonly involved in the pathogenesis of various human diseases [5].

We will present first-of-its-kind in-silico investigation of the abundance and functional roles of the disorder on the proteomic scale. In contrast to prior attempts that looked into a limited set of proteomes [6,7] or performed a much simpler analysis [8], we comprehensively analyze disorder in nearly 1000 complete proteomes and 6.4+ million proteins, including 59 species in archaea, 471 in bacteria, 110 in eukaryota, and 325 viral proteomes. We will discuss generic disorder characteristics, such as abundance and distribution, relation to evolution, and provide in-depth functional analysis including enrichment in biological processes, cellular compartment, and post-translational modifications. We will wrap up with a brief case study that involves our recent analysis of functional roles of disorder in the nucleosome complex [9].

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