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Assembly of plant storage proteins: role of intrinsic disorder and charge anisotropy

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Increasing plant protein content in human diet constitutes a world challenge to meet protein needs of the growing world population. However, the assembly properties of such proteins are poorly understood as compared to their dietary animal counterparts. This limits their use as ingredients in food matrices. Most of plant proteins are storage proteins which are synthesized in seed and have to be efficiently stored and dehydrated during seed development. The overall objective of our research activities is to investigate the driving force of plant storage proteins assembly and the influence of their primary role of storage on their structure and functionality. Through this talk, we will first show using computational predictors that amino-acid sequences of plant proteins are predicted to be more disordered than globular animal proteins such as whey or egg proteins. Looking in more details in plant protein sequences reveals that most of them contain low complexity regions comprising polar and/or charged amino acids which are mostly predicted disordered. Then, we will discuss how protein flexibility as well as charge anisotropy can affect the assembly of protein-polysaccharide and protein-protein. We will compare two globular proteins: lysozyme, an egg-white protein, and napin, a rapeseed protein. Lysozyme and napin are very similar in terms of molecular weight and charge density but differ in their surface charge distribution as well as in their intrinsic flexibility. Finally, we will discuss how the use of model polypeptides can help to unravel the role of intrinsic disorder in plant protein self-assembly.