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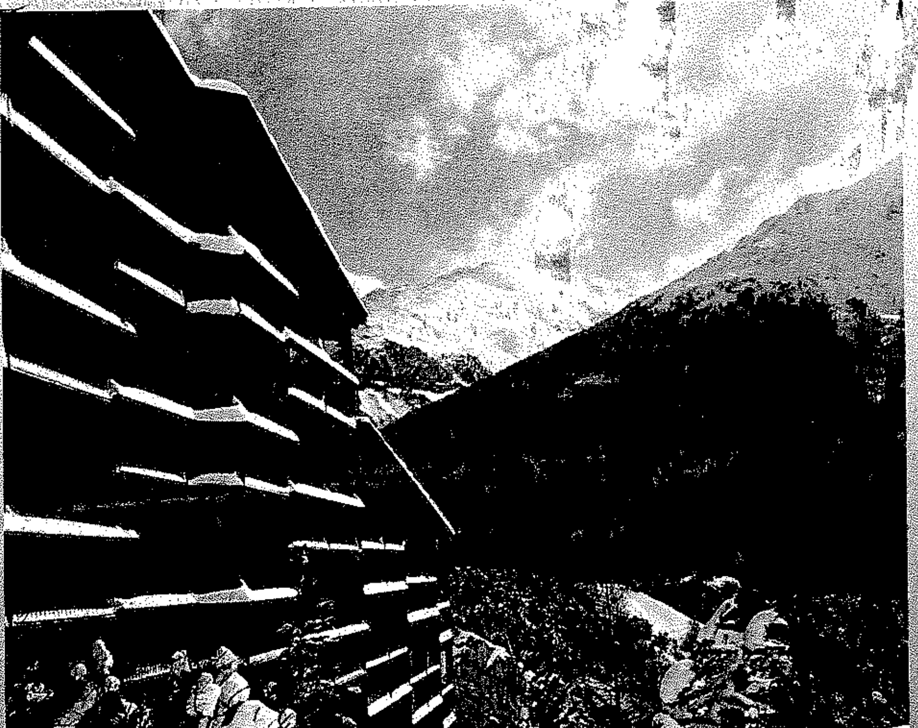

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7- VPgs (Viral Proteins Genome-Linked) from phytoviruses display intrinsically disordered features

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VPgs are viral proteins linked at the 5' end of the genome of many plant and animal viruses. Although sharing this common feature, VPgs are highly diverse in size, sequence and function. They are involved in key steps of the viral cycle such as genome replication, protein translation and viral movement in plant hosts. According to *in silico* predictions, many VPgs of non-related viruses share intrinsic disorder properties. These predictions were experimentally validated for several potyviral and sobemoviral VPgs. In this study, we show that the monomeric LMV and RYMV VPgs display structural features inducing an hydrodynamic behavior in-between a native premolten globule and a molten globule. Secondary structure elements are predicted *in silico* and detected by Far UV-circular dichroism. Transitions from disorder to order were observed using low percentages of TFE.

Intrinsically disordered domains of phytovirus VPgs generally comprised the functional sites involved in plant resistance-breaking. For instance, the central domain of the LMV VPg predicted as intrinsically disordered is involved in VPg association with the natively folded plant resistance factor eIF4E. One may expect that during the complex formation VPg undergoes a disorder-to-order transition. Fast kinetic measurements of the association between eIF4E and the VPg central domain are consistent with a two steps association compatible with the "fly-casting" model.