

Protein intrinsic disorder in virus-host interactions

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Intrinsically disordered proteins do not have a rigid 3D structures in their native conformations and play an important role in diverse cellular processes such as regulation and signaling. It is known that eukarya possess significantly more protein intrinsic disorder than do bacteria and archaea. Surprisingly, we find that many viruses also have high disorder content, comparable to that of eukarya. Using herpesviral family as a representative of large DNA viruses, we investigated the source and potential function of the high viral disorder content in the context of virus-host interactions. In particular, we looked at the conservation of disorder across three major herpesviral subfamilies, the patterns of disorder-order interactions in viruses, in human, and in virus-host interactions. Our preliminary results show that protein intrinsic disorder does not clearly conserve along subfamily lines and that the amount of disorder in different types of viruses varies greatly. As protein intrinsic disorder is involved in many human diseases, it remains to be seen whether such disorder also mediates virus-host interactions and thus in part explains the high disorder content in viruses.