Insights revealed by the co-crystal structure of the Saccharomyces cerevisiae histidine phosphotransfer protein Ypd1 and the receiver domain of its downstream response regulator Ssk1
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A key feature of the yeast Sln1 pathway is the ability of the histidine phosphotransfer protein, Ypd1, to bind to multiple structurally similar partners possessing different physiological roles. We present the co-crystal structure of Ypd1 with a near wild-type variant of its downstream binding partner, Ssk1. For the first time, this has allowed for a structural analysis of the upstream and downstream interactions within the yeast osmoregulatory system. The variant Ypd1/Ssk1-R2-W638A complex exhibits distinctive electrostatic properties, providing insight into the pathway’s regulation as a function of osmolyte concentration.
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The Urfold: Structural Similarity Just above the Superfold Level?
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How can we compare complicated curves that look similar, while allowing for various degrees of variability? Given a way to do that, what does classifying the curves teach us about the nature of protein shapes? (Imagine comparing and classifying children’s bead mazes.) Decades of research have illuminated these and related questions, yet our picture of the protein structural universe remains far from clear. Here, we suggest a level of structural granularity intermediate between the classical levels of ‘architecture’ and ‘topology’, as reflected in such phenomena as structural similarity above the level of superfolds. We articulate this notion of “architectural identity despite topological variability” as a concept we call the ‘Urfold’.
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