

S001 Evolution and assembly of protein complexes

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There is an abundance of data on protein interactions and protein complexes, both from conventional small-scale experiments collected over the decades, including three-dimensional structures, and more recently by large-scale functional genomics experiments. We can now draw on the information available about protein interactions in order to study the evolution of interactions. We have shown that interactions, just like individual proteins, frequently emerge by duplication and divergence. The duplication of a protein that engages in protein-protein interactions raises issues about the stoichiometry and equilibrium of protein complexes when the quantity of one component increases. Nevertheless, our results indicate that most interactions and complexes have evolved by step-wise duplications of individual proteins engaged in interactions. We show that duplicated-complexes retain the same overall function, but have different binding specificities and regulation, revealing that duplication is associated with functional specialization.

From analysis of crystal structures of proteins as well as the domain architectures of multi-domain proteins, it is clear that physical interactions between identical or homologous domains and protein chains are extremely common. How have this particular class of interactions evolved, and how do they fold and assemble? These questions will be addressed during the talk.