The archetypical WD-repeat proteins are the G β-subunits. Coronins consist of one or two WD-domains each forming a 7 bladed β-propeller. The WD-domain has been shown to be involved in a number of important interactions: binding actin filaments, phosphorylation by protein kinase C and actin independent binding of membranes. More interactions are coming up slowly but definitely, like for example Golgi association, microtubule binding, Ca^{2+} release and many more.

The *D. discoideum* genome harbours two different genes coding for a short and long coronin-like protein. The small coronin has been the first to be described and has been extensively studied. We started to investigate the structural and biochemical functions of Crn7, a 105 kDa tandem WD-domain containing protein in *D. discoideum*. Crn7 binds directly to F-actin and shows actin dependence in its localisation. It is expressed throughout development of *D. discoideum* with marked elevation at vegetative and early aggregation state. Disruption of the *corB*$^-$ gene resulted in a stable cell line deficient for the Crn7 protein. The subsequent mutant analysis revealed Crn7 to be involved in receptor mediated establishment of adhesion and phagocytosis of large particles and pathogens like *Legionella pneumophila*. We postulate that Crn7 plays a role in establishing a level of immunity against invasive pathogens.

Disruption of the *corB*$^-$ gene in a *corA*$^-$ background resulted in a stable cell line deficient for both coronins. From double mutant analysis we conclude that both coronins do interact with each other in a compensatory way. Crn7 and coronin may have overlapping or redundant functions. During phagocytosis, Crn7 may act as an upstream or downstream regulator of coronin. There are many open questions surrounding Crn7 function that require future attention like how are these proteins regulated and what binding properties and binding partners do they have. Structural analysis especially of the long coronins may further reveal significant cues for presumable binding sites.