Dehydrins are intrinsically disordered plant proteins (IDPs) that improve plant desiccation tolerance. By definition, dehydrins contain at least one lysine-rich, semi-conserved sequence motif known as the K-segment. In vitro evidence suggests that dehydrins are involved in several protective mechanisms, one of which is protein stabilization. However, there is no definitive explanation for how dehydrins accomplish this. Dehydrins preserve structure in the cold-labile protein, yeast frataxin homolog 1 (Yfh1), in a manner that may be partly sequence-based. Yfh1 acquires more α-helicity in the presence of dehydrins whose K-segments are left intact, and less when the positive charge within the K-segments is spread evenly throughout the sequence or locally neutralized. As IDPs, dehydrins may form specific but reversible interactions with many proteins, however little is known about the interaction network that dehydrins are a part of.

The aim of this project is to identify the binding partners of a YSK2-type dehydrin from *Vitis riparia* within *E. coli* and plant cells using an in vivo cross-linking assay followed by analysis with mass spectroscopy. This will also be performed with a dehydrin construct with the same amino acid composition but where the lysine residues will be evenly distributed throughout the sequence. In-cell NMR will follow this to determine whether or not the disordered protein acquires structure in a crowded environment while also providing information on which residues are most often involved in intracellular interactions. Finally, desiccation survival assays will be conducted to assess whether the changes in sequence result in decreased cell survival.