Solid-state NMR and oriented CD of a receptor tyrosine kinase transmembrane segment and its interactions with a viral oncoprotein

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Membrane proteins and polypeptides are key players in many biological processes, as they control the flow of information and material between cells and their environment, and they are prime drug targets. The focus of our group lies on the structure-function analysis of membrane-active peptides and transmembrane protein segments of cell surface receptors. We are especially interested to find out how they insert into the membrane, how they fold and align within the hydrophobic core of the bilayer, and how they find and bind to their corresponding interaction partners. Complementary solid-state NMR and oriented CD measurements on macroscopically aligned samples are used to determine the conformation, alignment and dynamics of membrane-bound peptides and proteins in the quasi-native environment of a lipid bilayer. Here, we will present two interacting proteins: the PDGF-receptor β (PDGFR), a receptor tyrosine kinase, that gets activated by the oncogenic E5 protein via transmembrane helix-helix interactions [1,2]. A complementary PISEMA-NMR and OCD analysis of the PDGFR transmembrane domain and the E5 protein was used to resolve the structures and orientations of both proteins in their native environment [3,4,5].

References:
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