Report

Project MX-1234: Analysis of isoforms of phospholipase C using SAXS

 We analyzed protein constructs derived from one of phosphoinositide-specific phospholipase C (PLC) enzymes, PLCγ1. As all other PLC enzymes, PLCγ1 has a conserved core architecture containing an N-terminal PH domain followed by a series of EF hands, a catalytic TIM barrel and a C-terminal C2 domain. This common core unit is further elaborated by the insertion of a highly structured region (PLCγ-specific array, γSA) between the two halves of the catalytic TIM-barrel. The γSA comprises a split PH (spPH) domain flanking two tandem SH2 domains and a SH3 domain. We analyzed wt PLCγ1 in its phosphorylated and non-phosphorylated states, wt PLCγ1 high affinity complex with FGF-receptor and γSA in its phosphorylated and non-phosphorylated states. Comparison of the data obtained indicates a conformational change upon phosphorylation. However, we need further experimental support. In particular, we need to repeat the experiments on phosphorylated γSA.