Summary report for project MX-1100 - 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 γSA from human PLCγ1, without or with SUMO-tag, high affinity complex of γSA with FGF-receptor and γSA construct lacking the SH3 domain. Comparison of the data obtained indicates possible positions of the added tag, SH3 domain and relative arrangement in the complex. These data, however, need further experimental support. In particular, we need to exclude that under the conditions used (low salt) there is no dimerisation of γSA.