ESRF	**Experiment title:** BAG Barcelona- The C2 domain of PKCε in complex with acidic phospholipids	**Experiment number:** LS1666
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Report:

PKCε is a member of the novel protein kinase Cs which are activated by acidic phospholipids, diacylglycerol (DAG) and phorbol esters but lack the Ca^{2+}-dependence of the classical PKC isotypes.

We have solved the crystal structure of the C2 domain of PKCε crystallized in the presence of two acidic phospholipids: 1,2-dicaproyl-*sn*-phosphatidyl-L-serine (DCPS) and 1,2-dicaproyl-*sn*-phosphatidic acid (DCPA). Two complete data sets were measured at the beam line ID14.3 at 1.7 and 2.8 A resolution respectively (Table1). The structure of the isolated PKCε-C2 domain was determined previously using phase information from mercury and aurate derivatives. (The X-ray data was collected at the beam line ID14.2. See the report: The C2 domain of PKCe; Hg and Au derivatives).

The central feature of the PKCε–C2 domain structure is an eight stranded, antiparal.lel β-barrel with a molecular topology closely related to that found in the C2 domain of phospholipases C-δ1 and A2 (Figure 1). The PKCε–C2 domain determined presents major differences with respect the structure of the PKCδ–C2 domain, the only other novel PKC–C2 domain available. Despite the phospholipid ligands were found to be disordered in the crystals of the two complexes, differences with the uncomplexed C2 domain structure allowed to define the phospholipid binding sites as mainly involving the protein loops β1-β2 and β5-β6. The information provided by these results suggest that C2-domains, either Ca^{2+} dependent or independent, can have similar membrane binding mechanisms though with different regulatory switches.

Table 1. Data collection statistics

	PKCe-C2_DCPS	PKCe-C2_DCPA
Cell parameters(A)	40.3, 56.5, 58.7	34.3, 47.1, 45.2
Space group	$P2_12_12_1$	$P2_1$
Resolution (A)	1.7	2.8
Completeness (%)	100	98
R-merge (%)	6	8.8
Average I/σI	23.1	6.7

Figure 1. Overall structure of the C2 domain of PKCε. β-strands are depicted as arrows. The Mg^{2+} ion located near the β5-β6 loop is also shown as an orange sphere

References

W.F.Ochoa, S. Corbalan-Garcia, I.Fita, J.C. Gomez-Fernandez, N. Verdaguer "Structure of the C2 domain of Protein Kinase Cε: a membrane binding model for C^{2+} independent PKCs." (2000, submited).