**Hirano 2005**

PAR-6 and PKC-3 interact via their PB1 domains

**Beers 2006**

PAR-6/PKC-3 associate to the córtex in two ways: one mode via PAR-3 and one mode via CDC-42

Cdc-37 RNAi allows PAR-6 to bind to the cortex in the absence of PAR-3 and without PKC-3. This depends of CDC42. However, PKC-3 doesn’t bind without PAR-6.

Interestingly in cdc-37 RNAi PAR-6 shows ‘pericentriolar accumulation’ that looks a lot like PAR-2 GCN4

Reduction in pkc-3 levels in cdc37 RNAi

**Aceto 2006**

PAR-6 interacts with CDC42 via a semi-CRIB domain. This interaction is essential for normal PAR-6 localisation. Lower levels and more punctate in mutant. Seems to resemble PAR-3 distribution. Does this look the same as a cdc42 mutant?

**Li 2010a**

PAR-6 interacts with PAR-3 via the PDZ1 domain of PAR-3 and the PDZ domain of PAR-6. However, this interaction doesn’t appear to play an essential role in vivo, as mutations to this domain which disrupt the interaction in vitro have no effect on PAR-6 localisation in vivo (localises to puncta as normal)

**Li 2010b**

PAR-3 lacking PDZ2 retains weak ability to localise to the cortex, but cannot recruit PAR-6 and PKC-3, perhaps suggesting a concentration-dependent threshold for recruitment, or a direct role for PDZ2

Mutants lacking the c-terminal region have lower membrane affinity

**Soriano 2016**

PAR-3 has a consensus PKC-3 phosphorylation site in the CR3 domain (RXSpsi)

The phosphorylation site engages the pocket and provides a high affinity anchor point

PAR-3 binds to and strongly inhibits the catalytic activity of PKC-3

FxR motif binds to PKC but this doesn’t perturb the aPKC catalytic residues

Inhibitory arm of PAR-3 C-terminal of the phosphoacceptor site. Abbility of this arm to bind to PKC-3 influences whether Par3 can inhibit PKC-3 or act as a substrate. They predict that the inhibitory arm could be modulated by phosphorylation by ROCK kinase, or that changes at the level of PKC-3 which influence accessibility of the pocket.

AxA mutation massively enhances kcat in in vitro kinase assays. The authors suggest that this may indicate that this is due to weaker substrate binding and therefore weaker engagement of the inhibitory arm. However, this look remarkably similar for PAR-2, which doesn’t have the inhibitory arm.

Mutation of the inhibitory arm on top of this renders it not phosphorylated at all. Essentially, regardless of which sites are engaging with PKC, if the engagement is too tight then it’s an inhibitor. Intermediate then it’s a good substrate.

The phosphorylated product has a much lower affinity for PKC-3, indicating that this isn’t a failure to disengage with the product after phosphorylation.

A non-phosphorylatable form binds as normal to PAR-3 but is unable to be turned over and remains tightly associated

**Rodriguez 2017**

**Dickinson 2017**

**Wang 2017**

**Dong 2020**