Structure of a Cell Polarity Regulator, an aPKC and Par6 PB1 Domain Complex

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A complex of atypical PKC and Par6 is a common regulator for cell-polarity related processes, which is an essential clue to evolutionary conserved cell-polarity regulation. Here, we determined the crystal structure of the aPKC and Par6 PB1 domain complex to a resolution of 1.5 Å. Both PB1 adopt a ubiquitin fold. aPKC PB1 presents an OPCA motif, 28 amino acid residues with acidic and hydrophobic residues, which interacts with the conserved lysine residue of Par6 PB1 in a front-and-back manner. Structural comparison of the aPKC and Par6 PB1 complex with the p40^{phcx} and p67^{phcx} PB1 complex, subunits of neutrophil NADPH oxidase, reveals that the specific interaction is achieved by tilting the interface so that the insertion or extension in the sequence is engaged in the specificity determinant. The PB1 domain develops the interaction surface on the ubiquitin fold to increase the versatility of molecular interaction.

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