and 0.1 M TRIS-HCl buffer, pH 8.5. Diffraction data was collected to 2.4 Å resolution at beamline BL6A of Photon Factory. ERK1 structure was solved by molecular replacement method using the ERK1 homology model as a probe. The structural refinement and model modification are currently in progress. A detailed structure of ERK1 and comparison with that of ERK2 will be reported.

Keywords: kinase, extracellular signal-regulated kinase, active-site structure

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Pheromone binding and realease by honey bee PBP is driven by a pH induced domain swapping

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The behavior and the perception of their surroundings by insects are in a large part driven by odorants and pheromones. This is especially true with social insects, such as honey bee, where the queen controls the development and the caste status of the other individuals. Pheromone perception is a complex phenomenon relying on a cascade of recognition events, initiated in antennae by pheromone recognition by a pheromone binding protein (PBP) and finishing with signal transduction at the axon membrane level. With an end to deciphering this initial step, we have determined the structures of the bee antennal PBP (ASP1) in the apo form or in complex with the main component of the queen mandibular pheromonal mixture, 9-keto-2(E)-decenoic acid (9-ODA) and with non pheromonal components. In the apo-protein the C-terminus obstructs the binding site. In contrast, ASP1 complexes have different open conformations, depending on the ligand shape, leading to different volumes of the binding cavity. The binding site integrity depends on the C-terminus (111-119) conformation, which involves the interplay of two factors: the presence of a ligand and a low pH. Ligand binding to ASP1 is favoured by low pH, opposite to what is observed with other PBPs such as those of Bombyx mori or Anopheles gambiae. At pH 7.0, ASP1 dimerizes forming a domain swapped structure, with loose affinity for pheromone. In contrast, Asp35Asn or Asn35Ala mutants are insensitive to pH and form the same monomer at pH 4.0 and pH 7.0. These results illustrate the influence of a unique residue in triggering ligand binding and protein fold, monomer or domain swapped dimer. We propose that this observation can be linked to the function of PBP when located in the lymph or in the vicinity of the SNMP co-receptor.

Keywords: insects behaviour, pheromone binding protein, domain swapping

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Structural basis of dynamic polymerization of DIX domains: A revised model of Wnt signaling

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The Wnt signaling pathway controls numerous cell fates in animal development, and is also a major cancer pathway. A key negative cytoplasmic effecter of this pathway is Axin, which promotes phosphorylation of β-catenin and its subsequent degradation. Another key cytoplasmic effector, Dishevelled (Dvl), a positive effector of this pathway, binds to the Wnt transmembrane receptors and interacts with Axin to transduce the Wnt signal. Both Dvl and Axin contain a DIX domain, a functionally important domain whose molecular properties and structure are unknown. We have determined the first crystal structure of the Axin-DIX domain at 2.9 Å resolution. DIX has a ubiquitin-like fold with five β-strands (β1-β5) and one α -helix. DIX interacts with neighboring molecules through a β-bridge between β2 and β4, forming filaments in the crystal by head-to-tail self-interaction through β-bridges. We also demonstrate that the DIX domain of Dvl2 mediates dynamic polymerization, which is essential for the signaling activity of Dvl2 in vivo. The purified DIX domain self-associates in vitro, and polymerizes gradually and reversibly in a concentration-dependent way, ultimately forming fibrils. Our studies point to a new mechanistic principle underlying Wnt signaling - namely signaling by reversible polymerization, whereby the DIX domain mediates the formation of a dynamic interaction platform with a high local concentration of binding sites for transient signaling partners.

Keywords: crystal structure, Wnt signaling, axin

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Structure of $CKI1_{RD}$, the receiver domain of the histidine kinase CKI1 from *Arabidopsis thaliana*

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Cytokinins (CKs) are essential phytohormones regulating proper growth and development of plants. CK signal is transduced to the nucleus by a phosphorelay signal transduction pathway via modified two-component system. In *A. thaliana*, signal transduction through cell membrane into the cell is carried out by a family of membrane-associated sensory histidine kinases. One of them, CYTOKININ INDEPENDENT1 (CKI1) constitutively activates the CK signaling pathway and is essential for the female gametophyte development. Here we present crystal structure (2.0 Å resolution) of the receiver domain ($CKI1_{RD}$, residues 979-1120) of CKI1. $CKI1_{RD}$ is a single domain