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Shifts: 1.5	Local contact(s): Dr. Michel PIROCCHI	<i>Received at ESRF:</i>
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Report:

L. Renault: Structural studies of actin self-assembly regulation by multi-domain proteins containing intrinsically disordered WH2 repeats

We study the regulation of actin cytoskeleton remodeling by multi-domain protein organizations with WH2 domains. WH2 domains are widespread, intrinsically disordered actin-binding peptides (25 to 50 residues) that display significant sequence variability. They are found in many proteins of different organisms as single or repeated (from 2 to 4 repeats) domains. They regulate alone or in synergy with other adjacent domains and other actin-binding proteins different key activities in actin assembly such as actin monomer sequestration, nucleation, or/and unidirectional assembly, and filament barbed end regulation or severing. We study their structure-function relationship in these multi-domain proteins.

Pathogen bacteria *Vibrio cholerae* induce cholera, a diarrheal disease. The bacterial multidomain protein VopF from *Vibrio cholerae* contributes to remodel actin cytoskeleton of the host cell and to the disruption of epithelial integrity and the diarrheal response. It contains an N-terminal localizing domain, a Proline-Rich domain, 3 consecutive WH2 domains which have been recently identified to nucleate pure G-actin (Tam et al., (2007) Cell Host Microbe 1, 95-107), and an unknown C-terminal domain. We isolated the C-terminal domain and showed that it displays a weak nucleating activity on its own with G-actin-ATP and forms stable dimers. We obtained two crystal forms (small needle-like and cubic crystals) of the C-terminal domain of VopF. The best diffraction we could obtain from these two forms on BM30A on July 2011 was 8 Å. The crystal structure of the new dimeric domain from a close homologous protein has been now published by two other groups (Namgoong et al. (2011) Nat Struct Mol Biol. 18, 1060-7; Yu et al. (2011) Nat Struct Mol Biol. 18, 1068-74).