

m07a.o01**Bacterial tubulin BtubA/B: A folding mystery**Daniel Schlieper^{a,b}, Jan Löwe^a^aMRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH, UK. ^bMarie Curie Research Institute, The Chart, Oxted RH8 0TL, UK. *E-mail: d.schlieper@mcri.ac.uk**Keywords: bacteria, cytoskeleton, protein structure and folding**

$\alpha\beta$ -Tubulin heterodimers, from which the microtubules of the cytoskeleton are built, have a complex chaperone-dependent folding pathway. They are thought to be unique to eukaryotes, whereas the homologue FtsZ can be found in bacteria. The exceptions are BtubA and BtubB from *Prostheco-bacter*, which have higher sequence homology to eukaryotic tubulin than to FtsZ. Some of their properties are different from tubulin, such as weak dimerization and chaperone-independent folding. However, their structure is strikingly similar to tubulin including surface loops, and BtubA/B form tubulin-like protofilaments. Also, the protein packing of the crystallized heterodimer resembles protofilaments due to the P6₅22 space group (see figure). Presumably, BtubA/B were transferred from a eukaryotic cell by horizontal gene transfer because their high degree of similarity to eukaryotic genes is unique within the *Prostheco-bacter* genome. The results indicate that eukaryotic tubulin's dependence on chaperones lies in the amino acid sequence and not in the overall fold. The chaperones might have a regulatory function [1].



[1] Schlieper D, Oliva M.A., Andreu J.M., Löwe J., *Proc. Natl. Acad. Sci. USA*. 2005, 102, 9175.

m07a.o02**Molecular mechanism of a signal transduction in cells**V.I. Gordeliy^{a,c,d}, R. Moukhametzianov^{a,c}, J. Klare^d, R. Efremov^{a,c}, J. Labahn^a, S. Grudinin^{a,c}, M. Engelhard^b, G. Bueldt^a^aIBI-2, FZ-Juelich, 52425 Juelich, Germany; ^bMPI of Molecular Physiology, 44227 Dortmund, Germany; ^cCBPCSS of MIPT, Dolgoprudny, 141700 Moscow District; ^dFLNPh, JINR, Dubna, 141980 Moscow District, Russia**Keywords: signal, transduction, proteins**

About 30% of our genome encodes membrane proteins which are responsible for crucial functions of the cells. Importance of these proteins can be illustrated by the fact that 70% of pharmaceuticals drugs have as their targets membrane proteins. However, there are just a few dozens of membrane proteins of known structure. Broadening of our knowledge of membrane protein structures is considered as one of main challenges in biology.

Communication (signaling) between organelles within a cell as well as between a cell and its surrounding environment including the other cells is transmitted by so called membrane receptors. Recently we have solved the first structure of such transmembrane signaling complex - receptor NpSRII with its transducer NpHtrII - which is responsible for repellent phototaxis in *Natronobacterium pharaonis* [1]. In addition, very recently we have determined structural changes of the receptor in course of its function [2]. All this together with computer modelling of the receptor properties provide a detailed insight into a molecular mechanism of early steps in transmembrane signalling.

[1] Gordeliy et al. (2002) *Nature* 419:484-487.

[2] Mukhametzianov et al. (2006) *Nature* 440:115-119.