

Structure of the PB1 domain of NBR1 and complex formation with the PB1 domain of p62

S. Müller, I. Kursula and M. Wilmanns

EMBL, Notkestr. 85, 22603 Hamburg, Germany

Keywords: NBR1; PB1 domain; protein-protein interaction

Specific protein-protein interactions are pivotal in regulation of signal transduction. Various interaction domains like SH2, SH3, PX, WW and PDZ domains have been investigated intensively. The PB1 domain (Phox and Bem1p) is a recently discovered interaction domain [1]. The OPCA motif (according to the QPR, PC and AID motif) within a PB1 domain interacts with its acidic hairpin to the basic back of another PB1 domain [2]. The PB1 domains are accordingly classified into 3 types: A-type (with OPCA motif), B-type (basic back with Lysine) and AB-type (with both OPCA motif and basic back Lysine to form front-to-back interactions) [2]. We have determined the 1.55 Å resolution crystal structure of the OPCA-motif containing PB1 domain of NBR1 (next to breast cancer 1). It shows the typical ubiquitin-like β grasp fold as shown for PB1 domains of Bem1p [3], Cdc24 [4], p40phox and p67phox [5], similar to that found in several Ras-GTP-binding domain families. The scaffold protein p62 is a ligand of NBR1, also presenting a multidomain protein with a similar domain architecture as NBR1. Their N-terminal PB1 domains are responsible for interaction [6]. The complex formation of the PB1 domains of NBR1 with p62 has been investigated and a high affinity in the nM range is proposed. At present, we are in the process to crystallise the PB1 heterodimer of NBR1/p62.

- [1] Ito et al. *EMBO J.* 20, 3938 (2001)
- [2] Noda et al. *JBC* 278, 43516 (2003)
- [3] Terasawa et al. *EMBO J.* 20, 3947 (2001)
- [4] Yoshinaga et al. *EMBO J.* 22, 4888 (2003)
- [5] Wilson et al. *Mol. Cell* 12, 39 (2003)
- [6] Lamarck et al. *JBC* 278, 34568 (2003)