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Letter to the Editor

NMR assignment of the mTOR domain responsible for rapamycin binding

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The FKBP-12/rapamycin binding domain (FRB domain) of mTOR is an independently folded region that lies adjacent to the kinase domain (Chen et al., 1995) and binding of rapamycin is presumed to prevent the interaction of mTOR with its protein substrates (McMahon et al., 2002). Here, we report the assignments for the FRB domain and its secondary structure, which is a step towards the search for novel ligands. The limited solubility of the protein (≤150 μM) complicated NMR data interpretation, however, assignments were obtained for all backbone amide signals (except residues M1, E27, K78 and K107) and the non-exchangeable aliphatic side chain signals. ^{1}H assignments were obtained for the aromatic ring signals, but some signals could not be identified due to overlaps (W39: $H^{\varepsilon 3}$, $H^{\zeta 3}$; F82: H^{ε}, H^{ζ}; W113: $H^{\varepsilon 3}$; H118: $H^{\varepsilon 1}$, $H^{\delta 2}$). The FRB domain contains a flexible N-terminus followed by four helices (residues 35–52, 56–72, 77–102 and 106–124) joined by short loops. BMRB deposit with accession number 6760.

References: Chen et al. (1995) *Proc. Natl. Acad. Sci. USA*, **92**, 4947–4951: McMahon et al. (2002) *Mol. Cell. Biol.*, **22**, 7428–7438

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