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Letter to the Editor

Backbone resonance assignments of Ezrin C ERMAD in a non-covalent complex with Ezrin N FERM

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Ezrin belongs to the ERM family of proteins which are regulated membrane-cytoskeletal crosslinkers. Dormant Ezrin comprises an N-terminal 297-residue N FERM domain masked by its C-terminal 112-residue C ERMAD domain. Activation by PIP_2 binding to N FERM and/or phophorylation of T567 on C ERMAD leads to unmasking of the binding surfaces on both domains, allowing N FERM to bind to membrane associated proteins and C ERMAD to f-actin filaments (Bretscher et al., 2002). Recent implications of Ezrin in tumor progression and metastasis have increased the necessity to understand this regulatory switch (Hunter, 2004). We have used NMR to study the relative thermodynamic stability of individual regions of C ERMAD in this binding interface of human Ezrin and evaluate the effects of the above activating signals on their stability. Here, we report the backbone ^{1}H, ^{15}N and ^{13}C resonance assignments of C ERMAD in a non-covalent complex (49.5 kDa) with natural abundance N FERM. Backbone assignments are available for 101 out of 108 residues (excluding 4 Pro residues). The unassigned residues are H484, A501, S504, R509, N513, E515 and R529. BMRB deposit with Accession No. 7161.

References: Bretscher et al. (2002) *Nat. Rev. Mol. Cell Biol.*, **3**, 586–599; Hunter (2004) *Trends Mol. Med.*, **10**, 201–204.

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