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Letter to the Editor

NMR assignment of the L27 heterodimer from LIN-2 and LIN-7 scaffold proteins

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LIN-2/7 (L27) domains are protein interaction modules that preferentially hetero-oligomerize, a property critical for their function in directing specific assembly of supramolecular signaling complexes at synapses and other polarized cell–cell junctions. L27 domains, which are ~60 residues (Doerks et al., 2000), are largely unfolded in isolation but fold to form a helical heterodimer upon interaction with the proper heterotypic partner (Harris et al., 2002). Interestingly, the cross-species interaction between the L27 domain from the *C. elegans* LIN-7 and the *H. sapiens* C-terminal L27 domain from LIN-2 bind at 150-fold higher affinity than the native same-species heterodimers. We report here the backbone and side-chain ^{1}H, ^{13}C, and ^{15}N resonance assignments of the artificially linked L27 heterodimer from the cross-species pair. 94% of the LIN-7 L27 and 84% of the C-terminal L27 domain from LIN-2 backbone resonances were assigned, and respectively 90 and 77% of the aliphatic side chains were assigned. The majority of resonances that could not be assigned are found near the unstructured linker. BMRB deposit with accession number 6837.
References: Doerks et al. (2000) *Trends Biochem. Sci.*, **25**, 317–318; Harris et al. (2002) *J. Biol. Chem.*, **277**, 34902–34908.

Keiko Y. Petrosky[a], Frank Löhr[b] & Volker Dötsch[b,*]
[a]*Biophysics Graduate Program, University of California, San Francisco, 600-16th Street, San Francisco, CA, 94143, Germany;* [b]*Institute for Biophysical Chemistry, University of Frankfurt, Frankfurt am Main, 60439, Germany*

*To whom correspondence should be addressed. E-mail: vdoetsch@em.uni-frankfurt.de