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Letters to the Editor

NMR resonance assignments of the NEAT (NEAr Transporter) domain from the *Staphylococcus aureus* IsdH protein

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In Gram positive bacteria Iron-responsive surface determinants (Isds) play an important role in acquiring heme-iron during infections (1). Through a process that remains to be elucidated, these proteins first bind to and remove heme from hemoproteins, before transporting the heme into the cytoplasm to ultimately release free iron. Four Isd proteins contain one or more NEAT domains (NEAr Transporter), a 125 residue motif whose name originates from its discovery in bacterial genes that are usually located in the vicinity of a putative Fe3+ siderophore transporter (2). Intriguingly, despite their relatedness, three of the NEAT containing Isd proteins have been shown to bind to different hemoproteins (IsdA-hemopexin, IsdB-hemoglobin, and IsdH with the haptoglobin–hemoglobin complex), while the fourth (IsdC) may act to relay heme to an integral membrane transporter. Knowledge of the three dimensional structure of a NEAT domain is an important first step towards elucidating their function in iron acquisition and may be useful in the design of new antimicrobial agents that target this process. We have applied 3D heteronuclear experiments to ^{15}N or ^{15}N and ^{13}C NEAT. Nearly all of the backbone ^{1}H, ^{15}N, $^{13}C_{\alpha}$, and CO atoms have been assigned using standard triple resonance methods (~95% complete). Assignments of the C_{β} and H_{β} atoms are ~92% complete. Assignments for the side chain atoms that extend beyond C_{β} are about ~85% complete, with the majority of unassigned resonances belonging to long chain aliphatic side chain atoms, which are generally difficult to assign unambiguously. The assignments have been deposited with BMRB accession code 6759.

References: Andrade et al. (2002) *Genome. Biol.* **3**, RESEARCH0047; Skaar and Schneewind (2004) *Microbes. Infect.*, **6**, 390–397.

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Backbone and side-chains ^{1}H, ^{13}C and ^{15}N NMR assignment of human β-parvalbumin

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β-parvalbumin, also known as oncomodulin, is a small Ca^{2+}-binding protein belonging to the so-called EF-hand family. At variance with the ubiquitary α-parvalbumin, the β-form is almost exclusively expressed in tumor cells. The solution structure of the recombinant human protein has been solved by us (Babini et al., 2004) mostly based on proton assignment. As this protein is a potential drug target, its full assignment may be of general interest *per se*. We present here its virtually complete assignment, obtained with the aid of ^{13}C-direct detection 2D experiments, including a novel pulse sequence designed for the assignment of aromatic C^{γ} nuclei (see Supplementary material). All backbone resonances are assigned except for the HN and N of M1. Still unassigned are the N terminal in Lys residues, the ring NH and N signals of H108, and the guanidine signals of R20 and R49. In summary, 93.7% ^{1}H, 99.4% ^{13}C and 89.8% ^{15}N of the total protein nuclei were assigned. BMRB deposit with accession number 6705.

Reference: Babini et al. (2004) *Biochemistry*, **43**, 16076–16085.

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