Journal of Biomolecular NMR (2005) 32: 257

Letters to the Editor

Resonance assignments for Mouse S100A13

DOI 10.1007/s10858-005-6730-9

S100A13 is a ~12 kDa protein that is selectively expressed in heart, kidney, spleen and small intestine. S100A13 shares only about 50% amino acid sequence homology with other members of the S100 family (Heizmann and Cox, 1998). Interestingly, polyclonal antibodies raised against S100A13 fail to cross react with other S100 proteins. S100A13 is the only member of the S100 family that is shown to be involved in the non-classical export of signal-peptide less proteins such as fibroblast growth factors, interleukin 1 α and synaptotagmins (Prudovsky et al., 2003). No NMR structure of S100A13 is available and, to our knowledge this is the first report of the resonance assignment of the protein (S100A13). ^{1}H–^{15}N HSQC spectrum of S100A13 is reasonably well-dispersed with uniform signal intensities. About 97% of the ^{1}H–^{15}N cross peaks in the HSQC spectrum (excluding 1 proline residue) were assigned. The backbone ^{1}H–^{15}N resonances of Lys30, Leu56 and Lys91 could not be assigned. Regions near these sites exhibit weakened and broadened signal in all spectra acquired. About 97% of the C^{α}, 95% of the C^{β}, 97% of the $C^{\alpha}H$ and 95% of the $C^{\beta}H$ resonances in the protein have been unambiguously assigned. Secondary structure prediction using CSI method and TALOS revealed that S100A13 consists of 4 helices [helixI (residues 8–24), helixII (residues 35–47), helixIII (residues 54–69) and helixIV (residues, 75–93)] and 2 antiparallel beta strands (strandI (residues, 31–34) and strandII (residues, 70–73)] (BMRB accession number 6484).

References: Heizmann and Cox (1998) *Biometals*., **11**, 383–397; Prudovsky et al. (2003) *J. Cell Sci.* **116**, 4871–4881.

Vaithiyalingam Sivaraja[a], Thallapuranam Krishnaswamy Suresh Kumar[a] & Chin Yu[a,b,*]
[a]*Department of Chemistry and Biochemistry, University of Arkansas, Fayetteville, 72701, Arkansas, USA;* [b]*Department of Chemistry, National Tsing Hua University, Hsinchu, 30043, Taiwan*
*To whom correspondence should be addressed. E-mail: cyu@uark.edu

Supplementary material to this paper is available in electronic format at http://dx.dio.org/10.1007/s10858-005-6730-9

NMR assignment of the barnacle cement protein *Mr*cp-20k

DOI 10.1007/s10858-005-7029-6

A barnacle, *Megabalanus rosa*, secretes underwater adhesive, mainly composed of 10 cement proteins, to hold itself to the liquid–solid interface. One of them, *Mr*cp-20k, is a highly hydrophilic, cystein-rich protein of a monomeric form (Kamino, 2001). The cystein residues are assembled in regular repetitive positions in the primary structure, leading to the prediction of six repeated sequences while amino acids other than the cystein residues and one proline residue in the module are less conserved. To gain insight into *Mr*cp-20k function in the barnacle settlement, we initiated a NMR structure determination of the recombinant polypeptide. Using multidimensional heteronuclear NMR experiments with ^{13}C, ^{15}N-labeled *Mr*cp-20k, essentially complete ^{1}H, ^{13}C and ^{15}N assignments were obtained for 149 out of the 186 residues. Unassigned resonances in the remaining residues, most of which reside in the third and fourth repeats, may be largely shifted or severely broadened due to the paramagnetic effect. The observed periodical pattern of the reduced cystein $^{13}C\beta$ chemical shifts indicates that the six repeats of *Mr*cp-20k assume similar folds. BMRB deposit with accession number 6565.

References: Kamino (2001) *Biochem. J.* **356**, 503–507.

Rintaro Suzuki[a], Youichi Mori[b], Kei Kamino[b] & Toshimasa Yamazaki[a,*]
[a]*National Institute of Agrobiological Sciences, Tsukuba, Ibaraki, 305-8602, Japan;* [b]*Marine Biotechnology Institute, Kamaishi, 026-0001, Japan*
*To whom correspondence should be addressed. E-mail: tyamazak@nias.affrc.go.jp

Supplementary material to this paper is available in electronic format at http://dx.dio.org/10.1007/s10858-005-7029-6