Journal of Biomolecular NMR (2006) 36:2

Letter to the Editor

NMR assignment of region 655–775 of human MAN1

DOI 10.1007/s10858-005-2628-9

MAN1 is a 911 residue vertebrate protein anchored at the inner nuclear membrane. Heterozygous loss-of-function mutations in MAN1 cause syndromes characterized by increased bone density in humans. We here focus on the C-terminal nucleoplasmic region of MAN1, which binds to BAF, to the transcription regulators GCL and Btf, and is responsible for the inhibition of the Smad signalling pathway by interacting with R-Smad proteins (Lin et al., 2005). This region comprises a first domain of unknown fold that we have assigned using heteronuclear NMR on ^{13}C, ^{15}N-labeled MAN1 (655–775), and a second domain (776–911) predicted to be an UHM (RRM-like protein domain). On the basis of the assignment of the first domain, we aim at solving the 3D structure of this domain, and map the interaction site with the second domain, in order to model the 3D structure of the whole C-terminal nucleoplasmic region.

Residues corresponding to region 655–761 of MAN1 were almost all identified: 91% of the backbone chemicals shifts and for the side chains, 82% of the aliphatic and 62% of the aromatic ^{1}H–^{13}C nuclei were assigned. BMRB deposits with Accession No. 6919.

Reference: Lin et al. (2005) *Hum. Mol. Genet.*, **14**, 437–445.

Sandrine Caputo[a], Feng Lin[b], Bernard Gilquin[a], Howard J. Worman[b], Sophie Zinn-Justin[a] & Joël Couprie[a,*]

[a]*Département d'Ingénierie et d'Etudes des Protéines, CEA Saclay, 91191, Gif-sur-Yvette, France*

[b]*Departments of Medicine and of Anatomy and Cell Biology, College of Physicians and Surgeons, Columbia University, New York, NY 10032, U.S.A.*

*To whom correspondence should be addressed. E-mail: jcouprie@cea.fr

Supplementary material is available in electronic format at http://dx.doi.org/10.1007/s10858-005-2628-9.