

Letters to the Editor

Backbone ^1H , ^{13}C , and ^{15}N assignments of a 56 kDa *E. coli* nickel binding protein NikA

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NikA (502 a.a., 56 kDa) is the periplasmic nickel-binding protein required for nickel transport and chemotactic response by *E. coli*. The recent X-ray crystallographic study on both liganded and unliganded NikA showed that the overall structure consists of two lobes connected by a hinge region (Heddle et al., 2003). To investigate the relationship between ligand-recognition and the dynamic properties, we assigned the NMR backbone resonances of unliganded NikA. 2D and 3D TROSY-based heteronuclear NMR experiments with uniformly $^2\text{H}/^{13}\text{C}/^{15}\text{N}$ -labelled NikA were used. Backbone resonances were assigned for 86% of residues. Missing residues are mainly localised around the nickel-binding site, suggesting conformational flexibility in the unliganded state. The BMRB accession number is BMRB-6416.

References: Heddle, J. et al. (2003) *J. Biol. Chem.*, **278**, 50322–50329Sundaresan Rajesh^{a,b,c}, Jonathan G. Heddle^{c,d}, Kaori Kurashima-Ito^{a,b,d}, Daniel Nietlispach^e, Masahiro Shirakawa^f, Jeremy R. H. Tame^c & Yutaka Ito^{a,b,d}^aCellular and Molecular Biology Laboratory, RIKEN, Saitama, 351-0198, Japan; ^bMolecular and Cellular Physiology; ^cProtein Design, Graduate School of Integrated Science, Yokohama City University, Yokohama, 230-0045, Japan; ^dCREST/JST; ^eDepartment of Biochemistry, University of Cambridge, CB2 1GA, UK;^fMolecular Biophysics Laboratories, Graduate School of Integrated Science, Yokohama City University, Yokohama, 230-0045, Japan

*To whom correspondence should be addressed. E-mail: ito@lousie.riken.go.jp

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A complete backbone assignment of the apolipoprotein E LDL receptor binding domain

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Human apolipoprotein E (apoE) is a 299-residue exchangeable apolipoprotein that plays critical roles in several major human diseases, including atherosclerosis and Alzheimer's disease. The crystal structure of the N-terminal domain of apoE is available (Wilson et al., 1991), but only contains residues 23–166. Recent studies have shown that regions beyond the X-ray crystal structure are also very important for the apoE's LDL receptor binding activity (Morrow et al. 2000). We carried out an NMR structure determination of apoE's LDL receptor binding domain (183-residues) and completely assigned backbone atoms (except backbone amide protons and nitrogens for residues Q41 and E168). Secondary structure prediction using NMR parameters indicates that apoE(1–183) consists of four rigid helical segments similar to the X-ray crystal structure. In addition, a new flexible helix is also observed between residues 171–180 in solution that is not found in the crystal structure. Thus, NMR structural studies of this apoE domain will provide new structural information about the LDL receptor binding activity of this protein. BMRB deposit with accession number: 6524.

References: Wilson, C., Wardell, M.R., Weisgraber, K.H., Mahley, R.W. and Agard, D.A. (1991) *Science*, **252**, 1817–1822; Morrow, J.A., Arnold, K.S., Dong, J., Balestra, M.E., Innerarity, T.L. and Weisgraber, K.H. (2000) *J. Biol. Chem.*, **275**, 2576–2580Chao Xu^a, Arun Sivashanmugam^a, David Hoyt^b, Jianjun Wang^{a,*}^aDepartment of Biochemistry and Molecular Biology, School of Medicine, Wayne State University, Detroit, MI 48201, U.S.A.; ^bHigh Field Magnetic Resonance Facility, EMSL, Pacific Northwest National Laboratory, Richland, WA, 99352, U.S.A.

*To whom correspondence should be addressed. E-mail: jjwang@med.wayne.edu

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