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Letters to the Editor

^{1}H, ^{13}C, and ^{15}N resonance assignments of SAP18

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SAP-18 (Sin3 associated polypeptide 18) is a factor associated with the Sin3 histone deacetylase corepressor complex (Zhang et al. 1997). While the functional role of SAP18 has not been defined clearly, SAP18 plays a key role in the recruitment of histone deacetylation machinery and repression of gene specific transcriptional activity (Cheng and Bishop, 2002). NMR-based structural studies are currently being pursued in order to provide insight into the functional role of SAP18 in the recruitment of the Sin3-HDAC complex. 2D and 3D NMR experiments were used to obtain near complete resonance assignments of uniformly ^{15}N and ^{13}C labeled recombinant hSAP18 (6-149, C26S). The backbone resonances were fully assigned with the exception of amide proton and nitrogen atoms of D95, R102, V103, and G130, and αCH atoms of P52, R102, P135, and P145. Approximately 90% of aliphatic sidechain resonances and aromatic proton resonances were assigned. The majority of resonances that could not be assigned unambiguously are associated with apparently unstructured polypeptide tail segments or the 11 proline residues. BMRB deposit has the accession number 6371.

References: Zhang et al. (1997) *Cell*, **89**, 357–364; Cheng and Bishop (2002) *PNAS*, **99**, 5442–5447.

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NMR assignment of the R-module from the *Azotobacter vinelandii* Mannuronan C5-epimerase AlgE4

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A family of seven mannuronan C5-epimerases has been identified in *Azotobacter vinelandii* (Ertesvag et al., 1999). They all consist of two types of structural modules, designated A and R, and a C-terminal signal peptide (Ertesvag et al., 1995). Here we report the assignment of the R-module of the smallest member of the C5-epimerase family, AlgE4. For NMR structure determination recombinant ^{13}C and ^{15}N-labelled R-module was produced and 2D/3D heteronuclear NMR experiments were recorded. The assignments of the backbone and the side-chain resonances are essentially complete (H^N, N, C, C^{α} > 98%; H and C side chains >95%). H^N and N of Gly 1, Gly 10, Gly 20, Ala 106 and Glu 117 could not be found, although the other atoms of these residues could be assigned. BMRB deposit: accession no. 6390.

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References: Ertesvag et al. (1995) *Mol. Microbiol.*, **16**, 719–731; Ertesvag et al. (1999) *Metab. Eng.*, **1**, 262–269

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NMR assignment of the *Xenopus laevis* prion protein fragment xlPrP(98-226)

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The polypeptide xlPrP has been identified as the homologue of the mammalian prion protein (PrP) in the African clawed frog *(Xenopus laevis)* (Strumbo et al., 2001). The prion protein in mammals is linked to the occurrence of transmissible spongiform encephalopathies (TSEs). In view of a better understanding of the so far enigmatic function of the prion protein in healthy organisms as well as its role in TSEs, we initiated a NMR structure determination of xlPrP(98–226), which corresponds to residues 93–230 of mammalian PrPs, with the C-terminal globular domain 125–230 (Riek et al., 1997). For the assignments we used 2D and 3D heteronuclear NMR experiments with ^{13}C,^{15}N-labeled xlPrP(98–226). The ^{1}H, ^{13}C, and ^{15}N chemical shift lists of xlPrP(98–226) are nearly complete. Missing assignments include the carbonyl carbons, some peripheral side chain $^{13}CH_n$ groups, and part of the labile side chain protons. BMRB deposition with the accession Nr. 6382.

References: Strumbo B. et al. (2001) *FEBS Lett.,* **508**, 170–174; Riek R. et al. (1997) *FEBS Lett.,* **413**, 282–288.

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^{1}H, ^{13}C, and ^{15}N assignments of MMP-12, a key protease implicated in lung tissue remodeling

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Matrix metalloprotease-12 (MMP-12, macrophage elastase) is involved in tissue remodeling and has been implicated in the progression of pulmonary diseases including emphysema (Hautamaki et al., 1997). We are interested in the structure of the catalytic domain bound to a novel inhibitor. We have undertaken NMR assignments for the complex with the ultimate goal of detailed information about how this inhibitor interacts with the catalytic domain. Assignments are based on 2D and 3D NMR spectra recorded on ^{15}N only and ^{15}N, ^{13}C labeled protein samples. Backbone ^{15}N assignments are 96% complete; C_α assignments are 99% complete. The largest stretch of residues with unassigned backbone amides includes H168–F171. Interestingly, assignments for these residues are also missing for MMP-13 (collagenase, Moy et al., 2000). Missing assignments are likely due to dynamics of a zinc-binding loop. Side chain assignments are complete for 121 of 165 residues (BMRB deposit with Accession Number 6391).

References: Hautamaki et al. (1997) *Science*, **277**, 2002–2004; Moy et al. (2000) *J. Biomol. NMR*, **17**, 269–270.

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