

Letters to the Editor

^{1}H, ^{13}C, and ^{15}N sequence-specific resonance assignment and secondary structure of *Plasmodium falciparum* thioredoxin*

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The malaria parasite *Plasmodium falciparum* spends part of its life cycle in human erythrocytes, where it is challenged with enhanced oxidative stress, and where it needs efficient anti-oxidants to maintain its reducing milieu and to protect itself against damage (Rahlfs et al., 2002). Thioredoxin (*Pf*Trx) is one of the major redox-regulatory molecules which, because of its dithiol/disulfide exchange activity, determines the oxidation state of protein cysteines, being therefore a potential target in research towards anti-malarial drugs (Kanzok et al., 2000). We initiated the structure determination of the recombinant 104-amino acid polypeptide, using multidimensional NMR spectroscopy. Sequential backbone resonance assignments were carried out on the basis of HNCA, CBCA(CO)NH, CBCANH, HNCO, $^{1}H-^{15}N$-HSQC and $^{1}H-^{15}N$-NOESY-HSQC experiments. Side-chain assignments were done using the HCCH-TOCSY experiment with the sample in $^{2}H_2O$. The chemical shifts for 99% of the backbone $^{1}H^{N}$, $^{13}C^{\alpha}$ $^{15}N^{H}$ (without considering the proline residues), for 89% of the $^{13}C'$, 99% of the $^{1}H^{\alpha}$, and 88% of all side-chain atoms (except the ^{13}C shifts of the aromatic rings) of the *Pf*Trx were assigned. Data were deposited in the BioMagResBank under accession number 6442.

References: Kanzok et al. (2000) *J. Biol. Chem.*, **275**, 40181–40186; Rahlfs et al. (2002) *Cell. Mol. Life Sci.*, **59**, 1024–1041.

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NMR assignment of human ubiquitin conjugating enzyme Ubc7

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Human Ubc7, which is involved in the targeting of ER-associated proteins for degradation by the 26S proteasome, is unique among class I enzymes in that it can catalyze the linkage of ubiquitin to ubiquitin in the absence of other substrates and ubiquitin protein ligases (Kikkert et al., 2004). The presence of this activity indicates that Ubc7 contains a specific binding site for ubiquitin and has catalytic features that are distinct from other E2 enzymes. In order to gain an understanding of this activity at molecular detail, we have initiated NMR structural studies of Ubc7. 2D and 3D heteronuclear NMR experiments were carried out with uniformly ^{13}C, ^{15}N-labeled Ubc7, either fully protonated or ~70% perdeuterated. The ^{1}H, ^{13}C, and ^{15}N chemical shift assignments of Ubc7 are nearly complete, with exception of residues M1, A2, P20, P68 and aromatic carbon resonances. BMRB deposit with accession number 6711.

Reference: Kikkert et al. (2004) *J. Biol. Chem.*, **279**, 3525–3534.

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