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Letter to the Editor

Backbone resonance assignment of human adult hemoglobin in the deoxy form

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Hemoglobin (Hb A) is a heterotetrameric protein with molecular weight of 65 kDa, that transports O_2 from the lungs to tissues, and has served as an excellent model for investigating the structure–function relationship in allosteric proteins. Hb A is paramagnetic ($S = 2$) in the deoxy (or ligand-free) form, becomes diamagnetic upon binding with O_2 or CO, and undergoes a reversible quaternary structural transition in going from the deoxy (or T) state to the ligated (or R) state (Perutz, 1970). By measuring the ^{1}H–^{15}N residual dipolar couplings (RDCs), we have found that the quaternary structure of HbCO A in solution is a dynamic intermediate between the R and R2 crystal structures (Lukin et al., 2003). The solution structure of Hb A in the T-state in solution is lacking. TROSY-based 2D and 3D experiments on uniformly and chain-specifically (^{2}H,^{15}N)- and/or (^{2}H,^{15}N,^{13}C)-labeled Hb A in deoxy form have been carried out for sequential resonance assignments. In (^{1}H,^{15}N)-TROSY and HSQC spectra, a number of peaks are missing because of line broadening due to paramagnetic relaxation, solvent exchange, and/or conformational exchange exhibited by the Hb molecule on the ms–μs time scale. We have unambiguously assigned all of the 106 and 114 out of the 115 observed backbone resonances for the α-chain and β-chain, respectively. BMRB accession number 6683.

References: Perutz (1970) *Nature*, **228**, 726–739; Lukin et al. (2003) *Natl. Acad. Sci. USA*, **100**, 517–520.

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