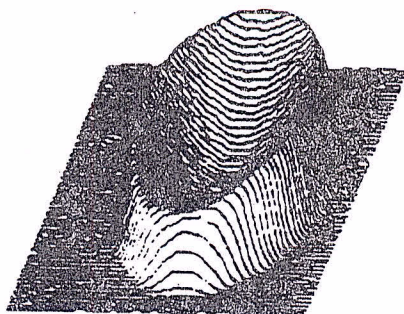


**2º ENCONTRO  
DA  
ASSOCIAÇÃO PORTUGUESA  
DE  
RESSONÂNCIA MAGNÉTICA**



**LIVRO DE RESUMOS**

**Curia, 17 e 18 de Outubro de 1993**

**Hotel Palace da Curia**

**Curia**

ASSIGNMENT OF HEME REDOX POTENTIALS OF  
CYTOCHROME  $c_3$  FROM *Desulfovibrio gigas* BY 2D NMR

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Several aromatic amino acid residues and haem resonances in the fully reduced form of *Desulfovibrio gigas* cytochrome  $c_3$ , are assigned, using two-dimensional  $^1\text{H}$  NMR, on the basis of the interactions between the protons of the aromatic amino acids and the haem protons as well as the intrahaem distances known from the X-ray structure [Kissinger (1989) p.H.D. Thesis, Washington State University]. The interhaem interactions observed in the NMR spectra are in full agreement with the *D. gigas* X-ray structure and also with the NMR data from *Desulfovibrio vulgaris* (Hildenborough) [Turner, Salgueiro, LeGall and Xavier (1992) Eur. J. Biochem., **210**, 931-936]. The good correlation between the calculated ring-current shifts and the observed chemical shifts strongly supports the present assignments. Observation of the two-dimensional nuclear-Overhauser-enhancement spectra of the protein in the reduced, intermediate and fully oxidized stages led to the ordering of the haems in terms of their midpoint redox potentials and their identification in the X-ray structure. The first haem to oxidize is haem I, followed by haems II, III and IV, numbered according to Cys ligand positions in the amino acids sequences [Mathews (1985) Prog. Biophys. Mol. Biol. 54, 1-56]. Although the haem core architecture is the same for the different *Desulfovibrio* cytochromes  $c_3$ , the order of redox potentials is different.