

Probing the transmembrane structure and dynamics of microsomal cytochrome P450 reductase by solid-state NMR

Rui Huang*, Kazutoshi Yamamoto*, Meng Zhang*, Nataliya Popovych*, Ivan Hung[†], Sang-choul Im[†], Zhehong Gan[‡], Lucy Waskell[†] and Ayyalusamy Ramamoorthy*

*Biophysics and Department of Chemistry, University of Michigan, Ann Arbor, MI, 48109-1055; [†]Department of Anesthesiology, University of Michigan, and VA Medical Center, Ann Arbor, MI 48105; [‡]National High Magnetic Field Lab, Tallahassee, FL, 32310-3708.

Supporting Material

Amino acid sequence of membrane-bound FMN binding domain (MFBD) of rat CPR. The transmembrane domain is underlined according to TMHMM prediction (1).

10	20	30	40	50	60
MGDSHEDTSA	TMPEAVAEV	<u>SLFSTDMVL</u>	<u>FSLIVGLTY</u>	<u>WFIFRKKKEE</u>	IPEFSKIQTT
70	80	90	100	110	120
APPVKESFV	EKMKKTGRNI	IVFYGSQTGT	AEEFANRLSK	DAHRYGMRGM	SADPEEYDLA
130	140	150	160	170	180
DLSSLPEIDK	SLVVFCMATY	GEGDPTDNAQ	DFYDWLQETD	VDLTGVKFAV	FGLGNKTYEH
190	200	210	220	230	
FNAMGKYVDQ	RLEQLGAQRI	FELGLGDDD	NLEEDFITWR	EQFWPAVCEF	FGVEATGEE

References

1. Krogh, A., B. Larsson, G. von Heijne, and E. L. Sonnhammer. 2001. Predicting transmembrane protein topology with a hidden Markov model: application to complete genomes. *J Mol Biol* 305:567-580.