

P08.14.126*Acta Cryst.* (2008). A64, C457**Crystal structure and resonance Raman spectra of chloro[tetra(*p*-methoxyphenyl)porphyrinatoiron(III)]**Ratchadaporn Puntharod¹, Kenneth J. Haller¹, Don McNaughton², Bayden R. Wood²¹Science, Chemistry, 111 University Avenue Tambon Suranaree, Muang, Nakhon Ratchasima, 30000, Thailand, ²School of Chemistry, Monash University, Wellington Road, Victoria, 3800, Australia, E-mail : ratchada_aim@hotmail.com

Raman spectroscopy has been used to provide solution structural information on metalloporphyrins for many years. Recent solid state work [1] found that the totally symmetric ν_4 high spin iron(III) oxidation state marker band in malaria pigment is enhanced when using a 780-nm excitation line. Closely related 5 coordinate high spin Fe^{3+} heme compounds sometimes show the enhancement and sometimes do not. The single crystal X-ray structure of chloro[tetra(*p*-methoxyphenyl)porphyrinato iron(III)], $\text{Fe}(\text{TMPP})\text{Cl}$, recrystallized by vapor diffusion of diethyl ether into a dichloromethane solution was determined. The average Fe-N distance is 2.058(7) Å; and the geometry is entirely typical for a high-spin five coordinate iron(III) porphyrin. The corresponding resonance Raman spectrum shows enhancement of the ν_4 band with 780-nm excitation. The current work presents comparison of supramolecular features of closely related metalloporphyrin complexes that exhibit the ν_4 enhancement and those that do not in exhibit attempt to demonstrate correlation of structural features and then influences on ν_4 band. $[\text{FeCl}(\text{C}_{48}\text{H}_{36}\text{N}_4\text{O}_4)]$, Mr = 824.11, orthorhombic, *Pbca*, $a = 22.5275$ (7), $b = 15.0824$ (6), $c = 23.1602$ (9) Å, $V = 7869.1(5)$ Å³, $Z = 8$, $D_{\text{calc}} = 1.391$ Mg m⁻³, Mo $K\alpha$, $\mu = 0.503$ mm⁻¹, $F(000) = 3416$, $T = 123$ K, $R = 0.153$ for 6887 unique observed reflections.

Keywords: iron porphyrin, Raman spectrum, malaria pigment

P08.14.127*Acta Cryst.* (2008). A64, C457**Human monoamine oxidase A: Structure and control of opening the entry for substrates/inhibitors**Se-Young Son¹, Jichun Ma², Youhei Kondou³, Masato Yoshimura⁴, Eiki Yamashita⁵, Tomitake Tsukihara⁶¹Institute for Protein Research, Osaka University, Laboratory of Protein Crystallography, Yamadaoka 3-2, suite, osaka, 565-0871, Japan, ²Laboratory of Cell Biology, Center for Cancer Research, National Cancer Institute, NIH, 37 Convent Dr. Bethesda, MD 20892, USA, ³Department of Physiology and Cell Biology, Kobe University Graduate School of Medicine, 7-5-1 Kusunoki-cho, Chuo-ku, Kobe, 650-0017, Japan, ⁴Institute for Protein Research, Osaka University, Yamadaoka 3-2, suite, osaka, 565-0871, Japan, ⁵Institute for Protein Research, Osaka University, Yamadaoka 3-2, suite, osaka, 565-0871, Japan, ⁶Institute for Protein Research, Osaka University, Yamadaoka 3-2, suite, osaka, 565-0871, Japan, E-mail : sonseyoung@protein.osaka-u.ac.jp

Monoamine oxidase (MAO) is a mitochondrial outer-membrane anchored protein and a biochemically important flavor-enzyme that catalyzes the deamination of biogenic and xenobiotic amines, including neuroactive serotonin, norepinephrine, and dopamine. It has two subtypes, MAOA and MAOB. These are related to several psychiatric and neurological disorders like depression and Parkinson disease, respectively. MAOs are interesting targets for the drug design. To understand the relationship between structure and function of this enzyme as a membrane protein, we extended our previous low-resolution rat MAOA structure to the high-resolution

wild-type and G110A mutant human MAOA structures at 2.2Å and 2.17Å, respectively. New MAOA structures are similar to that of rat MAOA and human MAOB, but different from the known structure of human MAOA by De Colibus et al. (2005) in some important loops. The results confirm that the inhibitor selectivity of MAOA and MAOB is due to the structural differences arising from Ile335 in MAOA vs. Tyr326 in MAOB. The structures exhibit a C-terminal transmembrane helix with clear electron density. Mutations on one residue of loop 108-118, G110, which is far from the active center but close to the membrane surface, cause the solubilized enzyme to significantly decrease in activity, but have less effect when the enzyme is anchored in the membrane. These results suggest that the flexibility of loop 108-118, promoted by anchoring the enzyme into the membrane, is essential for controlling substrate access to the active site. We observed the structure-function relationship between a transmembrane helical anchor and an extra-membrane domain at the first.

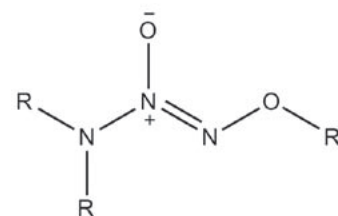
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Keywords: human monoamine oxidase A, C-terminal transmembrane helix, transmembrane helical anchor

P08.14.128*Acta Cryst.* (2008). A64, C457**Relationship between nitrogen conformation and spectral properties in nitric oxide prodrugs**Jeffrey R Deschamps¹, Harinath Chakrapani², Joseph E. Saavedra³, Larry K. Keefer²¹Naval Research Laboratory, Code 6030, 4555 Overlook Ave., Washington, DC, 20375, USA, ²Laboratory of Comparative Carcinogenesis, National Cancer Institute at Frederick, Frederick, MD, 21702, USA, ³SAIC-Frederick, National Cancer Institute at Frederick, MD, 21702, USA, E-mail : deschamps@nrl.navy.mil

In continuing the synthesis and characterization of nitric oxide prodrugs of structure $\text{R}_2\text{NN}(\text{O})=\text{NOR}'$ spectral differences with different R_2N groups have been noted. These differences are particularly pronounced when comparing pyrrolidiny derivatives and other $\text{R}_2\text{NN}(\text{O})=\text{NOR}'$ compounds. We postulate that differences in the absorbance maximum reflect an extension of the diazeniumdiolate chromophore through electronic interaction with the R_2N nitrogen in the case of the pyrrolidine derivatives that does not occur with the diethylamine, dimethylamine, or 6-membered heterocyclic analogues. This electronic overlap should be reflected in structural changes such as increasing planarity of the $\text{R}_2\text{N}-\text{N}$ system, decreasing $\text{N}-\text{OR}'$ bond length, and increasing single bond character of the $\text{R}_2\text{N}-\text{N}(\text{O})=\text{NOR}'$ molecule's $\text{N}=\text{N}$ linkage. In this study we provide evidence supporting this hypothesis by comparing structural parameters determined by x-ray crystallographic analysis of diazeniumdiolates.



Nitric Oxide Prodrugs

Keywords: structure analysis, UV effects, drug design