Supporting Information

A Method for Rapid Screening of Photosensitizers by Scanning Electrochemical

Microscopy (SECM) and the Synthesis and Testing of a Porphyrin Sensitizer

Fen Zhang,^b Vladimir Roznyatovskiy,^a Fu-Ren F. Fan,^{a,b} Vincent Lynch,^a Jonathan L.

Sessler,^{*a,c**} Allen J. Bard^{*a,b**}

^a Department of Chemistry and Biochemistry, The University of Texas at Austin, Texas 78712, USA

^b Center for Electrochemistry and Department of Chemistry and Biochemistry, The University of Texas at Austin, Texas 78712

^c Department of Chemistry, Yonsei University, Seoul 120-749, South Korea

*Corresponding authors: sessler@mail.utexas.edu, ajbard@mail.utexas.edu, ajbard@mail.utexas.edu, ajbard@mail.utexas.edu)

HPLC analysis of 2a.

HPLC analysis of **2a** was carried out on Shimadzu HPLC system: SIL-20AC auto sampler, DGU-20A5 degasser, SPD-M20A diode array detector and LC-6AD liquid chromatograph, equipped with an Agilent eclipse XDB-C18 column (3.5 μ m, 2.1 × 150 mm) and water-acetonitrile mixture used as a mobile phase.



Crystallographic analysis of 1.

X-ray experimental for $C_{50}H_{46}N_4O_4S_4$: Crystals grew as red plates by slow diffusion of methanol into the dichloromethane solution. The crystal had the following approximate dimensions: 0.52 mm × 0.40 mm × 0.10 mm. The data was collected using a Nonius Kappa CCD diffractometer coupled with a graphite monochromator with MoK α radiation ($\lambda = 0.71073$ Å). A total of 477 frames of data were collected using ω -scans

with a scan range of 1.4° and a counting time of 163 s per frame. The data was collected at 153 K using an Oxford Cryostream low temperature device. Details of crystal data, data collection and structure refinement are listed in Table S1. Data reduction was performed using a DENZO-SMN.¹ The structure was solved by direct methods using SIR97² and refined by full-matrix least-squares on F² with anisotropic displacement parameters for the non-H atoms using SHELXL-97.³ The hydrogen atoms were calculated in ideal positions with isotropic displacement parameters set to 1.2xUeq of the attached atom (1.5xUeq for methyl hydrogen atoms).

One of the ethyl methyl ester groups and two of the thiophene rings were disordered. The disorder was modeled in the same manner for each group. The variable x was assigned to the site occupancy factor for one component of the disordered group, while (1-x) was assigned to the alternate component. A common isotropic displacement parameter was refined while refining x. Geometric restraints were applied throughout the refinement process. Bond length and angle constraints were applied to the ethyl methyl ester groups. All non-H atoms were refined anisotropically but were restrained to be approximately isotropic. All H atoms were calculated in idealized positions.

The function, $\Sigma w(|F_0|^2 - |F_c|^2)^2$, was minimized, where $w = 1/[(\sigma(F_0))^2 + (0.1*P)^2]$ and $P = (|F_0|^2 + 2|F_c|^2)/3$. $R_w(F^2)$ refined to 0.318, with R(F) equal to 0.104 and a goodness of fit, S, = 2.38. Definitions used for calculating R(F), $R_w(F^2)$ and the goodness of fit, S, are given below.⁴ Neutral atom scattering factors and values used to calculate the linear absorption coefficient are from the International Tables for X-ray Crystallography (1992).⁵ All figures were generated using SHELXTL/PC.⁶ Tables of positional and thermal parameters, bond lengths and angles, torsion angles and figures are found elsewhere. Further details of the crystallography may be obtained from the Cambridge Crystallographic Data Centre by quoting reference no. 795817.

Empirical formula	C50 H46 N4 O4 S4	
Formula weight	895.15	
Temperature	153(2) K	
Wavelength	0.71069 Å	
Crystal system	Monoclinic	
Space group	P21/c	
Unit cell dimensions	a = 17.7560(10) Å	α= 90°.
	b = 21.9782(12) Å	β= 100.667(4)°.
	c = 11.5593(7) Å	$\gamma = 90^{\circ}$.
Volume	4433.0(4) Å ³	
Ζ	4	
Density (calculated)	1.341 Mg/m ³	
Absorption coefficient	0.265 mm ⁻¹	
F(000)	1880	
Crystal size	0.52 x 0.40 x 0.10 mm	
Theta range for data collection	2.96 to 25.00°.	
Index ranges	-21<=h<=21, -26<=k<=25, -13<=l<=13	
Reflections collected	15074	
Independent reflections	7778 [R(int) = 0.0265]	
Completeness to theta = 25.00°	99.8 %	
Absorption correction	Semi-empirical from equivalents	
Max. and min. transmission	1.00 and 0.85	
Refinement method	Full-matrix least-squares on F ²	
Data / restraints / parameters	7778 / 917 / 722	
Goodness-of-fit on F ²	2.192	
Final R indices [I>2sigma(I)]	R1 = 0.1037, wR2 = 0.2969	
R indices (all data)	R1 = 0.1420, wR2 = 0.3177	
Largest diff. peak and hole	1.344 and -0.895 e.Å ⁻³	

 Table S1. Crystal data and structure refinement for 1.













References

- DENZO-SMN. (1997). Otwinowski Z. and Minor W., Methods in Enzymology, 276: Macromolecular Crystallography, part A, 307 – 326, C. Carter Jr. W. and Sweets R. M., Editors, Academic Press.
- SIR97. Altomare A., Burla M. C., Camalli M., Cascarano G. L., Giacovazzo C., Guagliardi A., Moliterni A. G. G., Polidori G., Spagna R., A program for crystal structure solution. *J. Appl. Cryst.* 1999, *32*, 115-119.
- 3) Sheldrick, G. M. (1994). SHELXL97. Program for the Refinement of Crystal Structures. University of Gottingen, Germany.
- 4) $\begin{aligned} R_w(F^2) &= \{ \Sigma w(|F_o|^2 |F_c|^2)^2 / \Sigma w(|F_o|)^4 \}^{1/2} \text{ where } w \text{ is the weight given} \\ &= \operatorname{each reflection.} \\ R(F) &= \Sigma (|F_o| |F_c|) / \Sigma |F_o| \} \text{ for reflections with } F_o > 4(\sigma(F_o)). \\ S &= [\Sigma w(|F_o|^2 |F_c|^2)^2 / (n p)]^{1/2}, \text{ where } n \text{ is the number of reflections and } p \text{ is the} \\ &= \operatorname{number of refined parameters.} \end{aligned}$
- 5) International Tables for X-ray Crystallography (1992). Vol. C, Tables 4.2.6.8 and 6.1.1.4, Wilson A. J. C. Editor, Boston: Kluwer Academic Press.
- 6) Sheldrick G. M. (1994). SHELXTL/PC (Version 5.03). Siemens Analytical X-ray Instruments, Inc., Madison, Wisconsin, USA.