

Reassessment of the Reaction Mechanism for the Heme Dioxygenases

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Supporting information

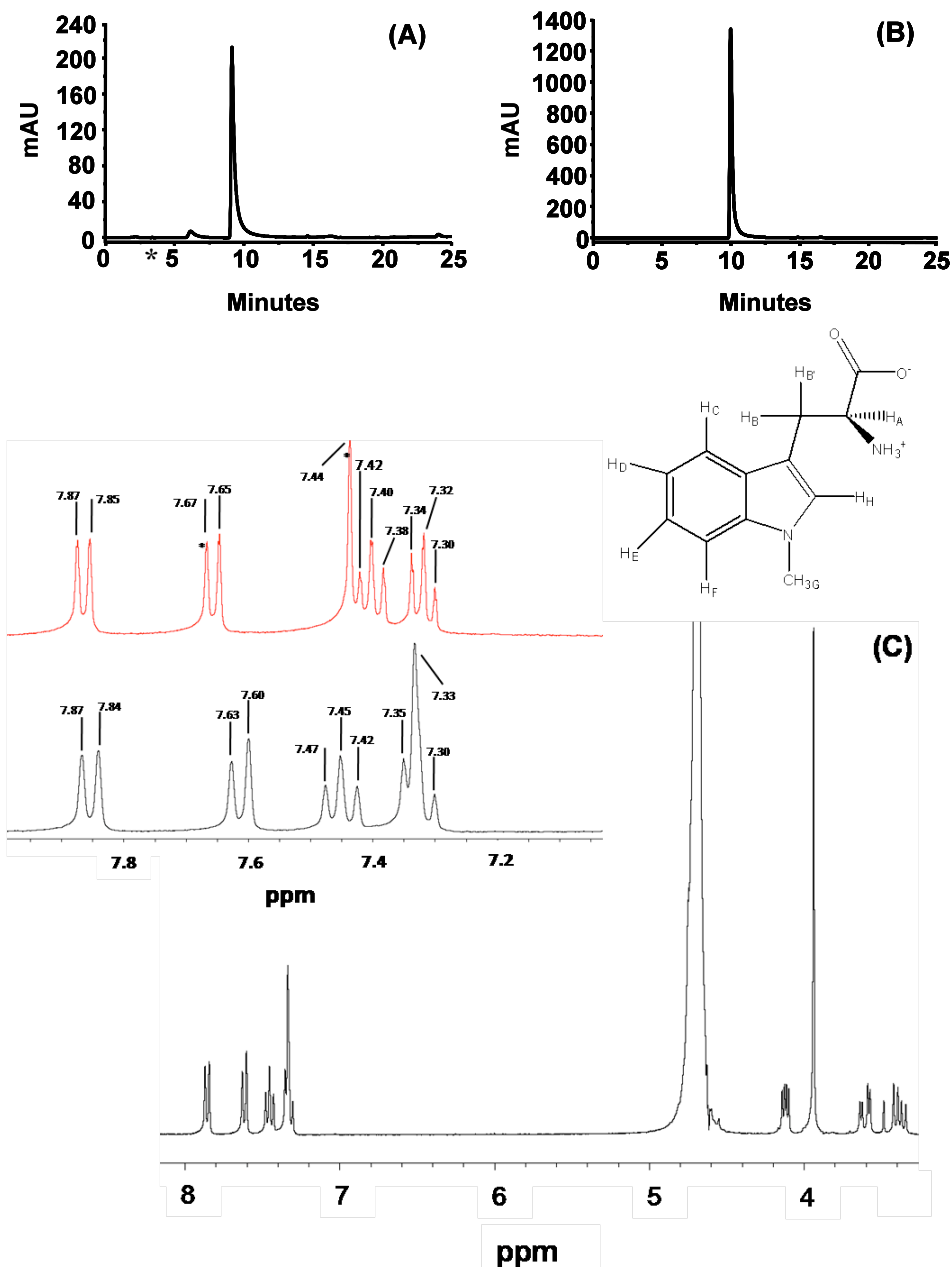


Figure S1. Chromatogram of commercially available 1-Me-L-Trp (A) before and (B) after purification by HPLC. The HPLC retention time for L-Trp (data not shown) was found to be identical to the contaminating species labeled * in (A). (C) NMR spectrum of purified 1-Me-L-Trp from (B). ¹H NMR (300 MHz, D₂O/CD₃CN) δ 3.33-3.65 (m, 2H, H_B + H_B'), 3.93 (s, 3H, H_G), 4.12 (dd, 1H, J = 8.2 Hz, 4.7 Hz, H_A), 7.33 (s + t, 2H, J = 7.5 Hz, H_H + H_{D/E}), 7.45 (t, 1H, J = 7.5 Hz, H_{D/E}), 7.61 (d, 1H, J = 8.5 Hz, H_{C/F}), 7.85 (d, 1H, J = 8.1 Hz, H_{C/F}). Inset: ¹H NMR spectra of commercially available L-Trp (red) and purified 1-Me-L-Trp (black) expanded between the 7-8 ppm region. * indicates the peaks that have shifted significantly in respect to the spectrum of 1-Me-L-Trp and therefore confirm the removal of L-Trp from purified 1-Me-L-Trp. HPLC conditions: wavelength - 280 nm; column - RP C18, 250 x 4.6 mm; eluant - H₂O:MeCN, 90:10 v/v; flow rate - 1 ml/min. NMR conditions: machine - Bruker DPX300; basic frequency - ¹H = 300.03 MHz; spectral width 16 ppm.

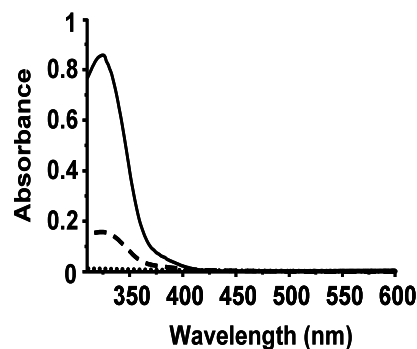


Figure S2. UV-visible spectrum of *N*-formyl-kynurenine (solid line) and *N*-formyl-methylkynurenine (dashed line) showing absorption bands at 321 nm. Spectra were obtained after isolation of the compounds from steady state assays with hIDO. Parallel experiments carried out with 1-Me-L-Trp in the absence of enzyme show no product formation at 321 nm (dotted line).

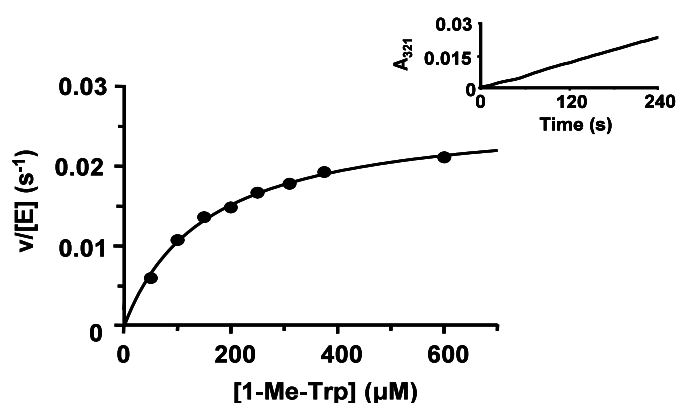


Figure S3. Steady state oxidation of 1-Me-L-Trp by hIDO. Solid line shows a fit of the data to the Michaelis-Menten equation. Inset: Time-dependence of absorbance changes at 321 nm, which report on *N*-formyl-methylkynurenine formation. Conditions: Tris/HCl buffer, pH 8.0, 25.0 °C. Reactions in the presence and absence of enzyme (Figure S2) confirm that product formation is due to enzymatic oxidation alone.

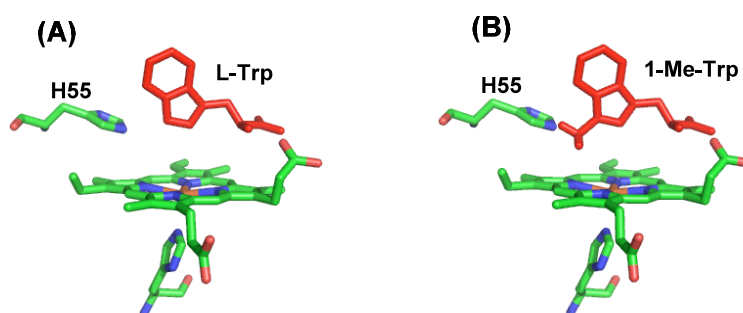


Figure S4. (A) Crystal structure of XcTDO in complex with (A) L-Trp⁸; (B) A model of 1-Me-L-Trp binding to XcTDO generated by overlay of 1-Me-L-Trp on the L-Trp coordinates in (A).

Table S1. Inhibition data (K_i) for inhibition of L-Trp oxidation by 1-Me-L-Trp (dash indicates no measurable activity).

^a The high K_M in this case meant that a reliable measure of K_i was not accessible.

	Variant	K_i (μ M)
hIDO	native	3.4 ± 0.4
	S167A	2.2 ± 0.2
hTDO	native	-
	H76S	^a
XcTDO	native	-
	H55A	150 ± 10
	H55S	400 ± 50