

Figure S1. Presteady-state binding of PAPS to SULT1A1. Reactions were initiated by rapidly mixing 1:1 (v/v) a solution containing SULT1A1 (30 nM, dimer), MgCl_2 (5.0 mM) and NaPO_4 (25 mM), pH 7.2, with an identical solution that lacked enzyme and contained PAPS (2.0 μM). Binding was monitored *via* nucleotide-induced change in SULT1A1 intrinsic fluorescence ($\lambda_{\text{ex}} = 290 \text{ nm}$, $\lambda_{\text{em}} \geq 330 \text{ nm}$). Fluorescence intensity is plotted relative to the protein fluorescence intensity at $t = 0$ (I/I_0). Solutions were equilibrated at $25 \pm 2 \text{ }^\circ\text{C}$ prior to mixing. The solid curve represents the best-fit behavior predicted by a single-exponential model.

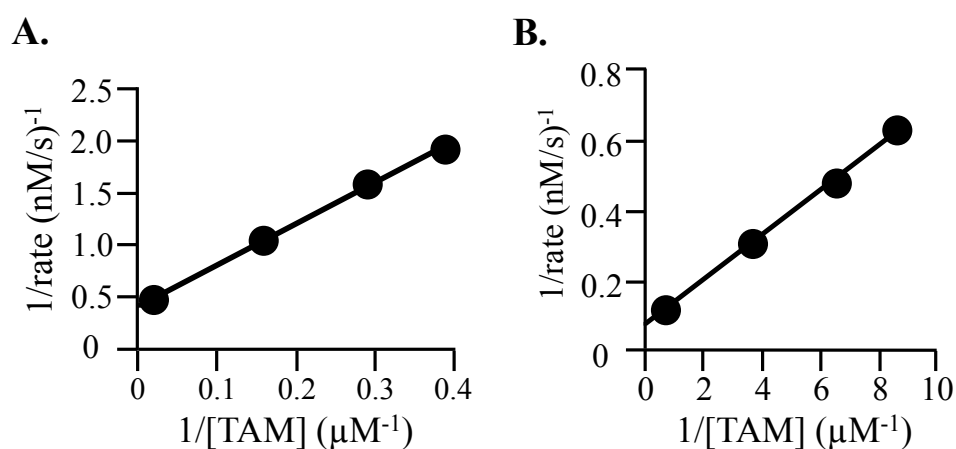


Figure S2. TAM initial-rate studies. A.) The turnover of $E\bullet PAPS$. The reaction conditions were SULT1A1 (3.0 nM, dimer), ^{35}S -PAPS (3.5 μM), MgCl_2 (5.0 mM), and NaPO_4 (50 mM), pH 7.2, $T = 25 \pm 2$ °C. **B.)** The turnover of $E\bullet(PAPS)_2$. Conditions were identical to A except that $[\text{PAPS}] = 300$ μM . Radiolabelled reactants were separated using reverse phase TLC and quantitated using storm imaging. Each point is the average of three independent determinations. K_m and k_{cat} values are compiled in Table 3. Further details are given in *Materials and Methods*.

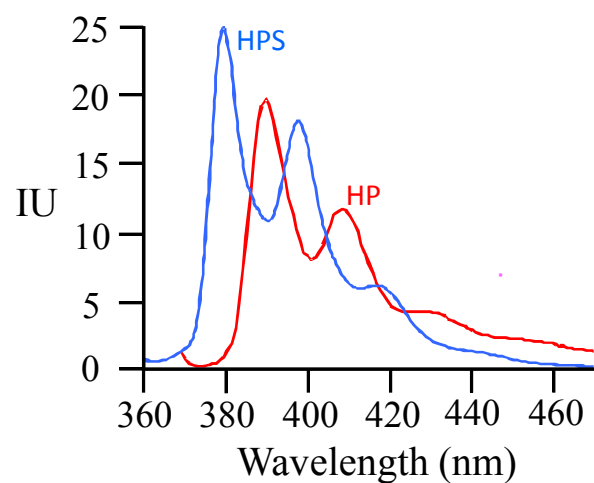


Figure S3. Fluorescence spectra of 1-HP & 1-HPS. Emission spectra of 1-HP (1-hydroxypyrene) and 1-HPS (1-hydroxypyrene sulfate) at $\lambda_{\text{ex}} = 320$ nm. Solutions contained 1-HP (1.0 μM) or 1-HPS (1.0 μM), MgCl_2 (5.0 mM), NaPO_4 (50 mM), pH 7.2, $T = 25 \pm 1$ °C.

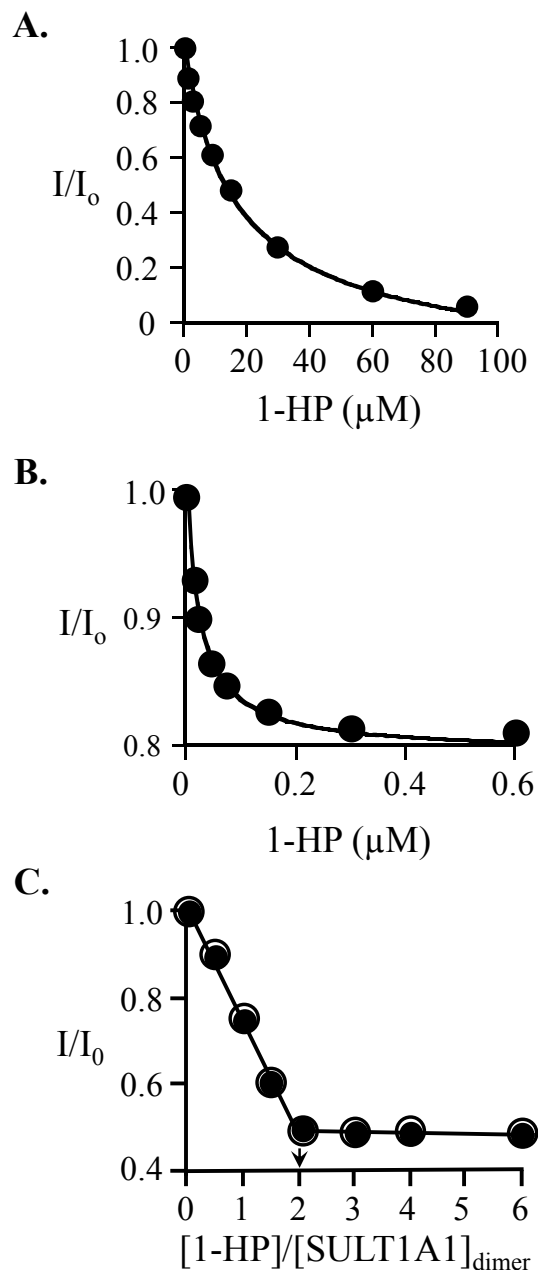


Figure S4. I-HP binding to the E and E·(PAP)₂ forms of SULT1A1. **A.)** I-HP binding to E. Ligand binding was monitored *via* changes in SULT1A1 intrinsic fluorescence ($\lambda_{\text{ex}} = 280 \text{ nm}$, $\lambda_{\text{em}} = 335 \text{ nm}$). The conditions were as follows: SULT1A1 (8.0 μM , dimer), MgCl₂ (5.0 mM), NaPO₄ (50 mM), pH 7.2, T = 25 \pm 2°C. Each point is the average of three independent determinations. The line through the points is the behavior predicted by a best-fit of the data assuming a single binding site *per* subunit. **B.)** I-HP binding to E·(PAP)₂. The conditions were identical to A except SULT1A1 = 50nM (dimer) and [PAP] = 2.0 μM . **C.)** The stoichiometry of I-HP binding to E and E·(PAP)₂. Conditions were identical to A except that [SULT1A1] = 120 μM (dimer, \circ), or [SULT1A1] = 1.0 μM (dimer), [PAP] = 1.5 μM (\bullet). I-HP binds to E and E·(PAP)₂ with a stoichiometry of 1.0 *per* subunit.