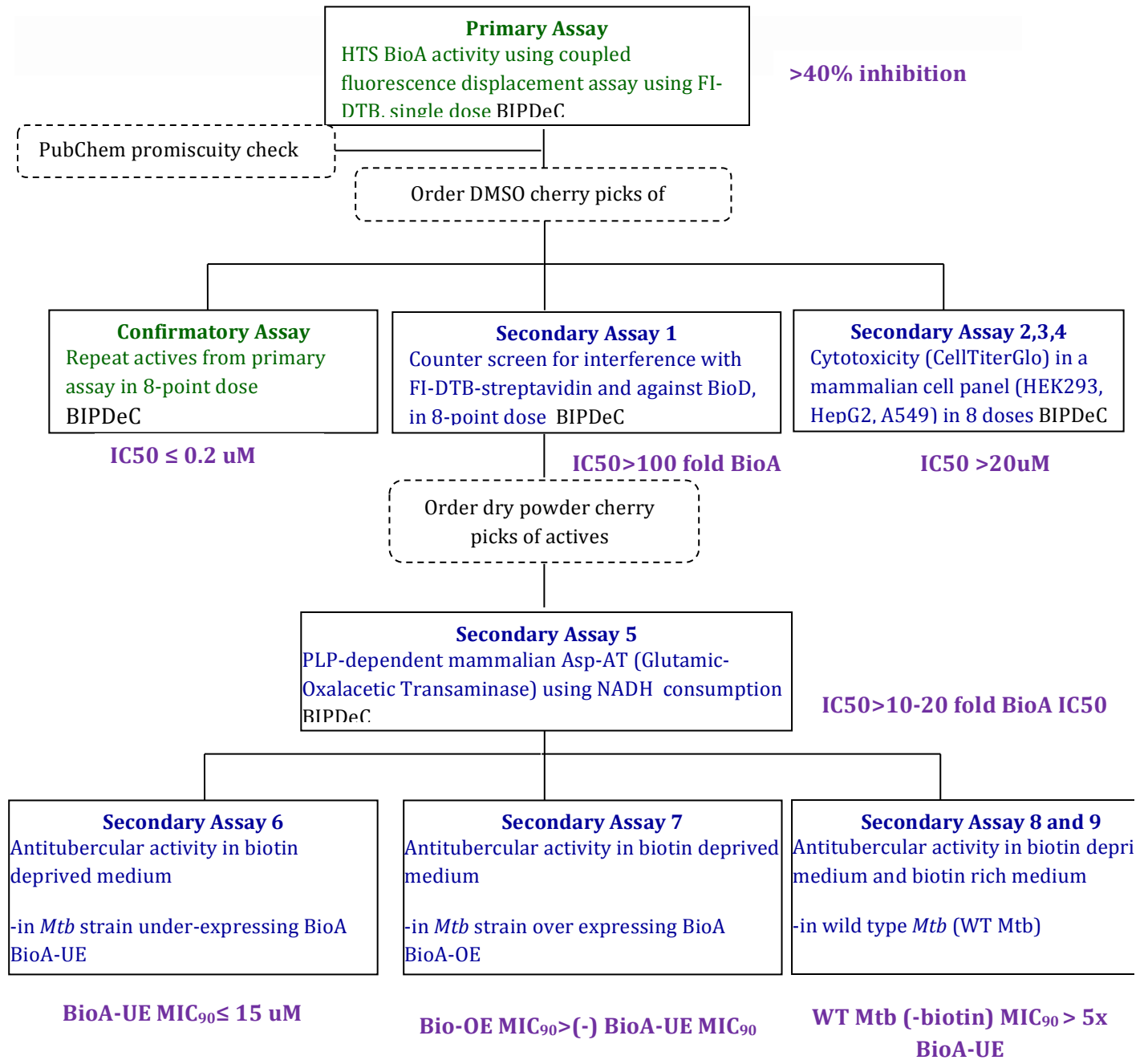


Figure S1. Assay Tree (Related to Figure 3).



Legend

Primary assay protocol

Secondary assay

Assay cut-off

Supplemental Table S1 (Related to Table 1). Sheet 1: Complete List of BioA hits from Primary HTS. Sheet 2: Source of Compound and Smiles String. Sheet 3: Scaffold Analysis.

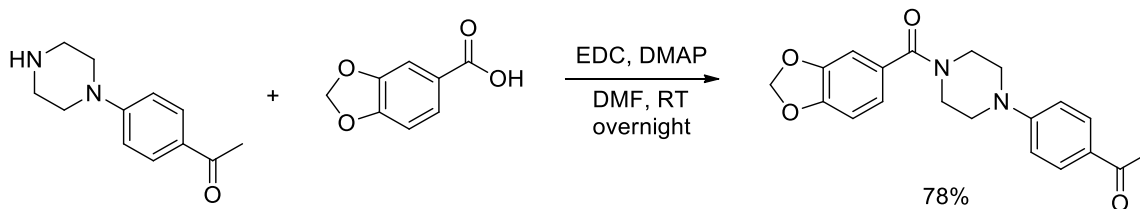
see Excel Spreadsheet

Supplemental Table S2 (Related to Figure 5). Summary of Crystallographic data and Refinement Statistics

| Inhibitor | 18 | 15 | 14-C1 |
|---|---|---|---|
| PDB Accession Code | 4W1V | 4W1W | 4W1X |
| <i>Cell dimensions</i> | | | |
| Space group | P2 ₁ 2 ₁ 2 ₁ | P2 ₁ 2 ₁ 2 ₁ | P2 ₁ 2 ₁ 2 ₁ |
| <i>a</i> , <i>b</i> , <i>c</i> (Å) | 63.04, 66.24, 204.24 | 63.08, 66.21, 204.44 | 63.13, 66.04, 203.56 |
| Molecules per ASU | 2 | 2 | 2 |
| <i>Data Summary</i> | | | |
| X-Ray source | Rigaku 007-MaxFlux | ALS | ALS |
| Detector | Saturn 944 ⁺ CCD | NOIR-1 CCD | NOIR-1 CCD |
| Wavelength (Å) | 1.541 | 1.000 | 1.000 |
| Resolution (Å) (highest shell) | 102.12-2.24 (2.14-2.24) | 63.08-1.80 (1.90-1.80) | 47.33-1.80 (1.86-1.80) |
| R _{merge} | 0.089 (0.471) | 0.076 (0.560) | 0.098 (0.529) |
| Mean I/σ ₁ | 10.2 (1.7) | 19.8 (2.6) | 9.2 (1.6) |
| Completeness | 96.1% (81.2%) | 90.5% (58.7%) | 96.8% (79.0%) |
| Multiplicity | 3.20 (1.90) | 6.6 (4.2) | 6.06 (2.89) |
| Observations | 133962 | 477296 | 468895 |
| Unique reflections | 41863 | 72681 | 77334 |
| Mosaicity | 0.14 | 0.12 | 0.4 |
| <i>Refinement</i> | | | |
| Resolution (Å) | 28.189-2.244 | 102.00-1.90 | 47.33-1.80 |
| R _{work} /R _{free} | 0.1768/0.2086 | 0.182/0.221 | 0.193/0.223 |
| Modeled atoms | 6938 | 7422 | 7138 |
| Modeled water | 383 | 738 | 481 |
| <i>Average B value (Å²)</i> | | | |
| Protein atoms | 20.48 | 22.85 | 21.11 |
| Ligand atoms | 21.29 | 22.50 | 20.14 |
| PLP atoms | 13.33 | 18.84 | 16.68 |
| Water O atoms | 23.95 | 33.71 | 27.71 |
| <i>Ramachandran plot</i> | | | |
| Favored | 96.63% | 96.63% | 96.42% |
| Allowed | 2.67% | 2.37% | 2.97% |
| Disallowed | 0.70% | 1.00% | 0.62% |
| <i>R.M.S deviations from ideal geometry</i> | | | |
| Bond lengths (Å) | 0.003 | 0.007 | 0.007 |
| Bond angles (°) | 0.948 | 1.264 | 1.190 |

Mammalian Cell Cytotoxicity Assays. HepG2, HEK293, and NIH3T3 cells (ATCC) were cultured in Dulbecco's modified Eagle's medium with 10% FBS, 100 units/mL penicillin, 100 $\mu\text{g}/\text{mL}$ streptomycin, and 2 mM L-glutamine. Confluent cells were trypsinized, and seeded in 40 μL in 384-well plates at 5000 cells/well and incubated at 37 °C (5% CO₂, 95% humidity) for 24 h. Next, 100 nL of each compound in DMSO was pin transferred to afford final concentrations ranging from 20.0-0.156 μM . The proteasome inhibitor MG132 (Tocris) was used as a positive control for HEK293 and NIH3T3 cells while mitoxantrone dihydrochloride was used for HepG2 cells. After 3 days at 37 °C, the plate was removed from the incubator to cool for 15 min, then 20 μL of 50% Promega CellTiterGlo reagent (diluted 1:1 with PBS, pH 7.4) was added and the plate was incubated at rt for 5 min. Luminescence was read on a Perkin-Elmer EnVision with US LUM settings for 0.1 sec per well.

Aspartate aminotransferase counter-screen. Inhibition of aspartate transaminase (AST) was determined using the EnzyChrom™ Aspartate Transaminase Assay Kit (EnzyChrom) according to the manufacturers instructions. Briefly, 5 μL of each compound (10 mM DMSO stock solution) was transferred to a 384 well assay plate. Next, 50 μL of assay solution was dispensed to each well (250 nL EnzyChrom™ AST assay kit cofactor, 250 nL EnzyChrom™ assay kit enzyme mix, and 1 uL EnzyChrom™ assay kit NADH Solution in 50 uL EnzyChrom™ assay kit assay buffer) followed by 5 μL of plasma (5 μL of water to the standard and blank wells) and the plate was tapped to mix the compounds and reagents. Blank (negative control) and standard control wells contain 5 μL of DMSO only. The plate was read at 340 nm on a spectrophotometer at 0 and 10 min. For each sample the rate of NADH consumption was calculated by subtracting the OD₃₄₀ at 10 min from the OD₃₄₀ at time 0 (ΔOD).



1-{4-[4-(Benzo[*d*][1,3]dioxole-5-carbonyl)piperazin-1-yl]phenyl}ethanone (14). To a solution of piperonylic acid (66 mg, 0.4 mmol, 1.0 equiv) and 4'-piperazinoacetophenone (98 mg, 0.48 mmol, 1.2 equiv) in DMF (3 mL) was added EDC (77 mg, 0.4 mmol, 1.0 equiv) followed by DMAP (49 mg, 0.4 mmol, 1.0 equiv) at room temperature. The mixture was stirred at room temperature overnight then partitioned between H₂O (10 mL) and EtOAc (10 mL). The organic layer was washed with H₂O (2 × 10 mL), saturated aqueous NaCl (10 mL), and dried over anhydrous Na₂SO₄. The solvent was removed *in vacuo* and the residue was purified by flash chromatography (1:1 hexane–EtOAc) to afford the title compound (110 mg, 78% yield) as white solid: *R_f* = 0.23 (1:1 hexane–EtOAc), ¹H NMR (400 MHz, CDCl₃) δ 2.48 (s, 3H), 3.34 (br s, 4H), 3.73 (br s, 4H), 5.97 (s, 2H), 6.79–6.85 (m, 3H), 6.91–6.94 (m, 2H), 7.84 (d, *J* = 8 Hz, 2H); ¹³C NMR (100 MHz, CDCl₃) δ 26.0, 47.6*, 47.7*, 101.4, 107.9, 108.1, 113.8, 121.6, 128.2, 128.7, 130.2, 147.6, 148.9, 153.6, 169.8, 196.3 (*C signals not observed in 1-D ¹³C NMR, but through an HMQC experiment due to nitrogen quadrupole broadening); LRMS (ESI+) 353.17 [M + H]⁺.