Supplementary Material

Extract2Chip—Bypassing Protein Purification in Drug Discovery Using Surface Plasmon Resonance

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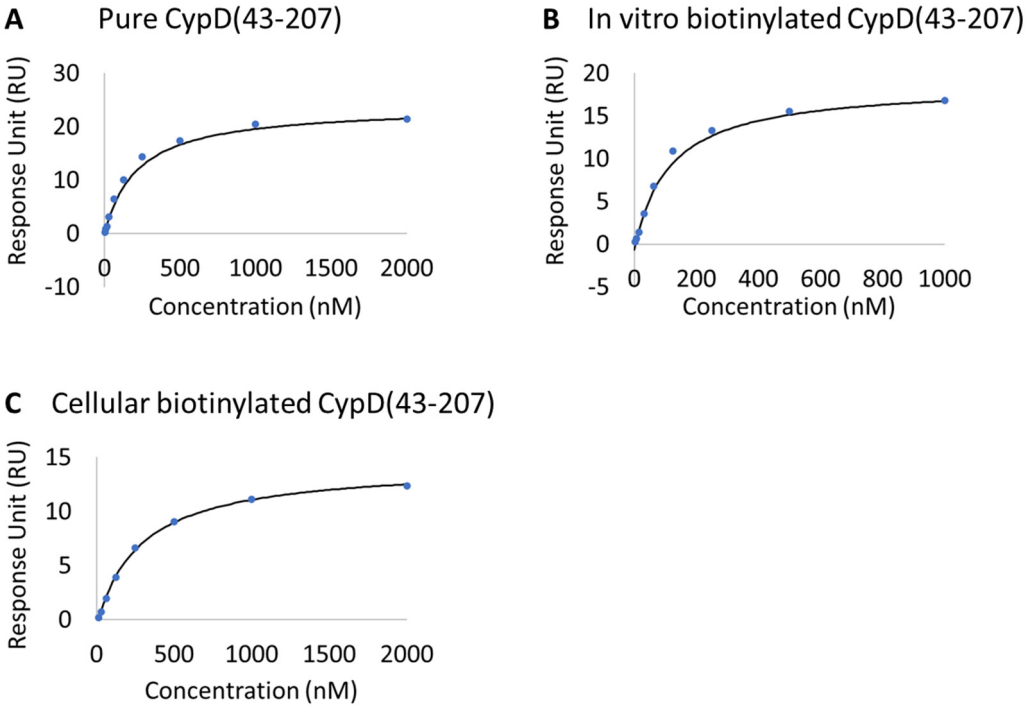

Figure S1. Steady-state affinity fit (KDss) for the interaction between pure (A), in vitro biotinylated (B) or cellular biotinylated (C) CypD(43-207) and a known inhibitor (CYPD-27). X-axis: concentration of CYPD-27 (nM); Y-axis: response unit (RU).

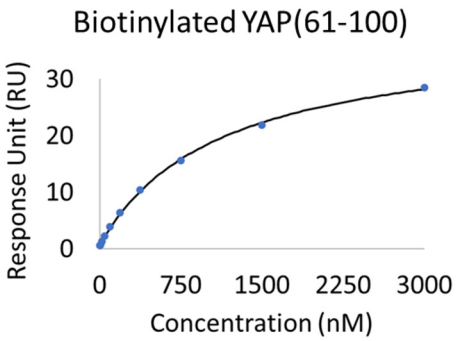

Figure S2. Steady-state affinity fit (KDss) for the interaction between biotinylated YAP(61-100) and TEAD1(209-436). X-axis: concentration of TEAD1 (nM); Y-axis: response unit (RU).

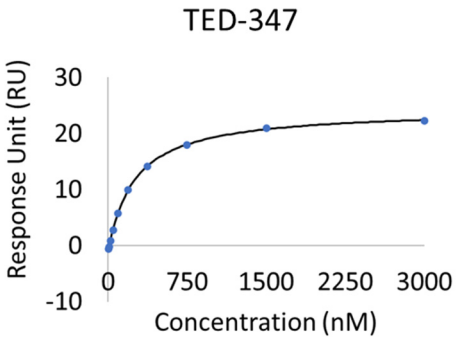

Figure S3. Steady-state affinity fit (KDss) for the interaction between biotinylated YAP(61-100) and TEAD1(209-436) in running buffer supplemented with 30 μM TED-347. X-axis: concentration of TEAD1 (nM); Y-axis: response unit (RU).