

Capture Compound® Mass Spectrometry: Elucidating Off-Target Binding to Deconvolute Drug Toxicity

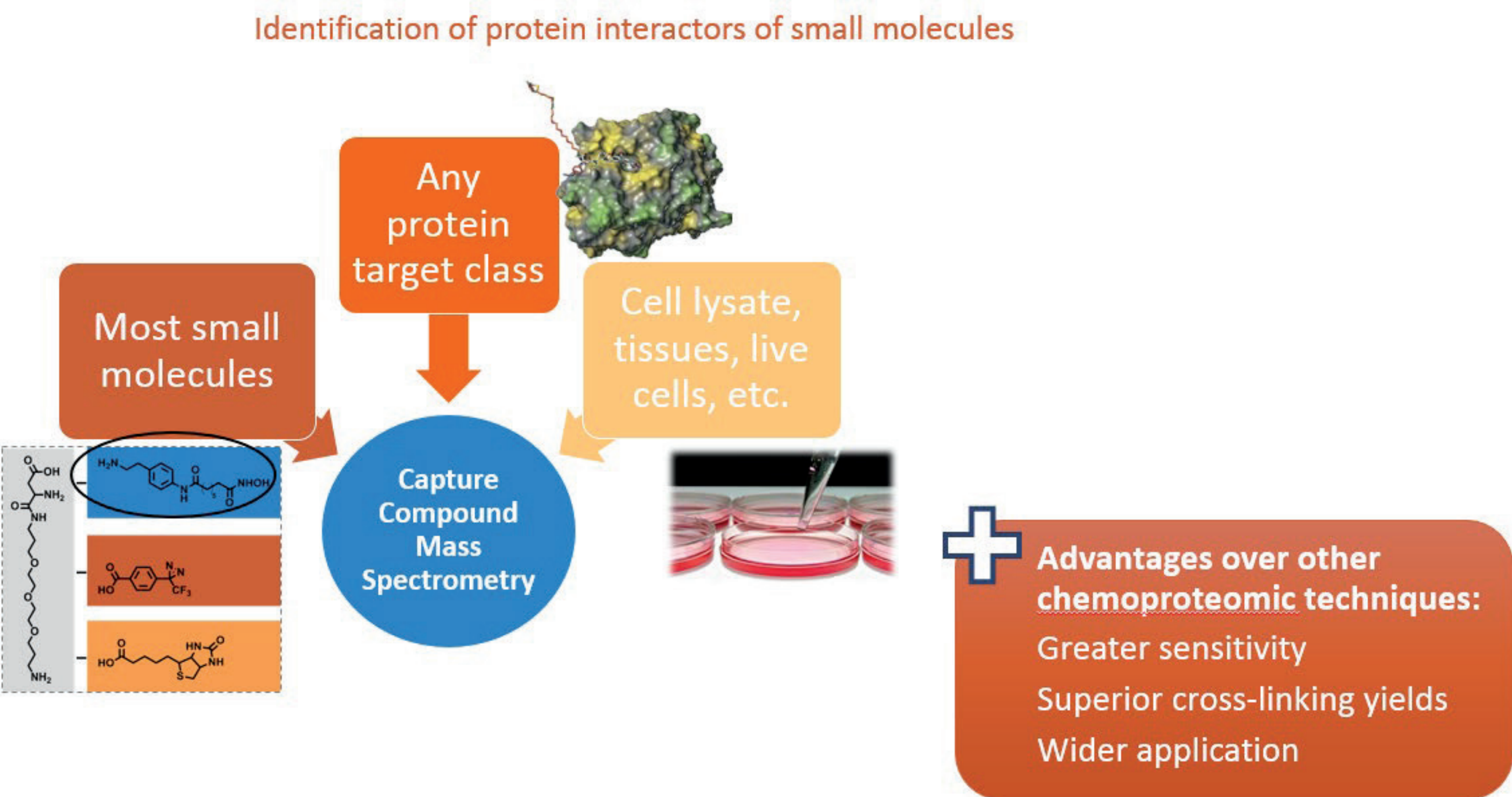
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1 CCMS INTRODUCTION

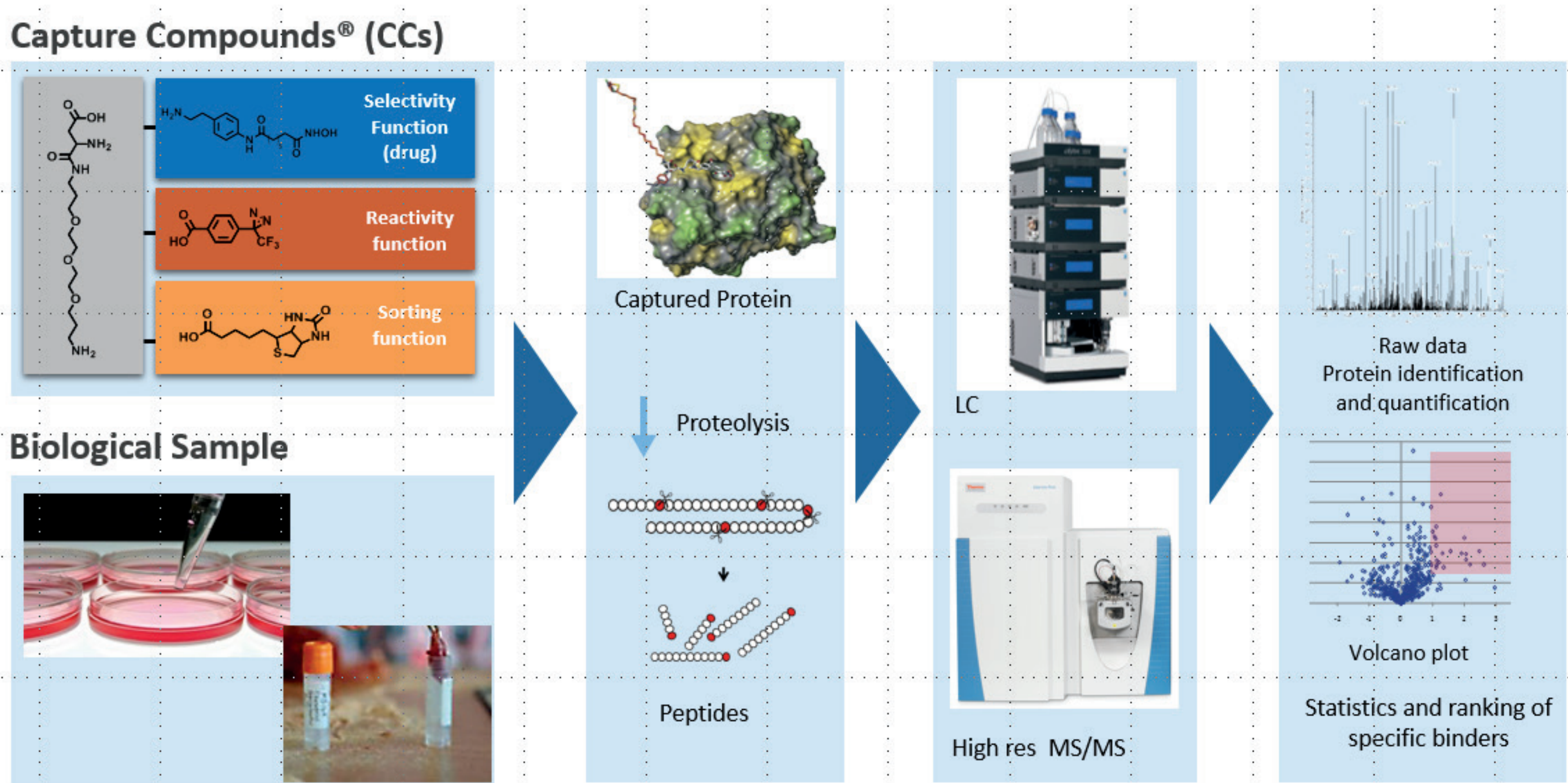
Capture Compound Mass Spectrometry (CCMS) is an unbiased, proteome-wide approach for the identification of specific on- and off-target binding protein targets for small molecules of interest.

Capture Compounds® (CCs) are unique tri-functional probes designed to interrogate proteins in their native environments. The distinct molecular architecture of the Capture Compounds® enables a three-stage process of binding, capture and isolation



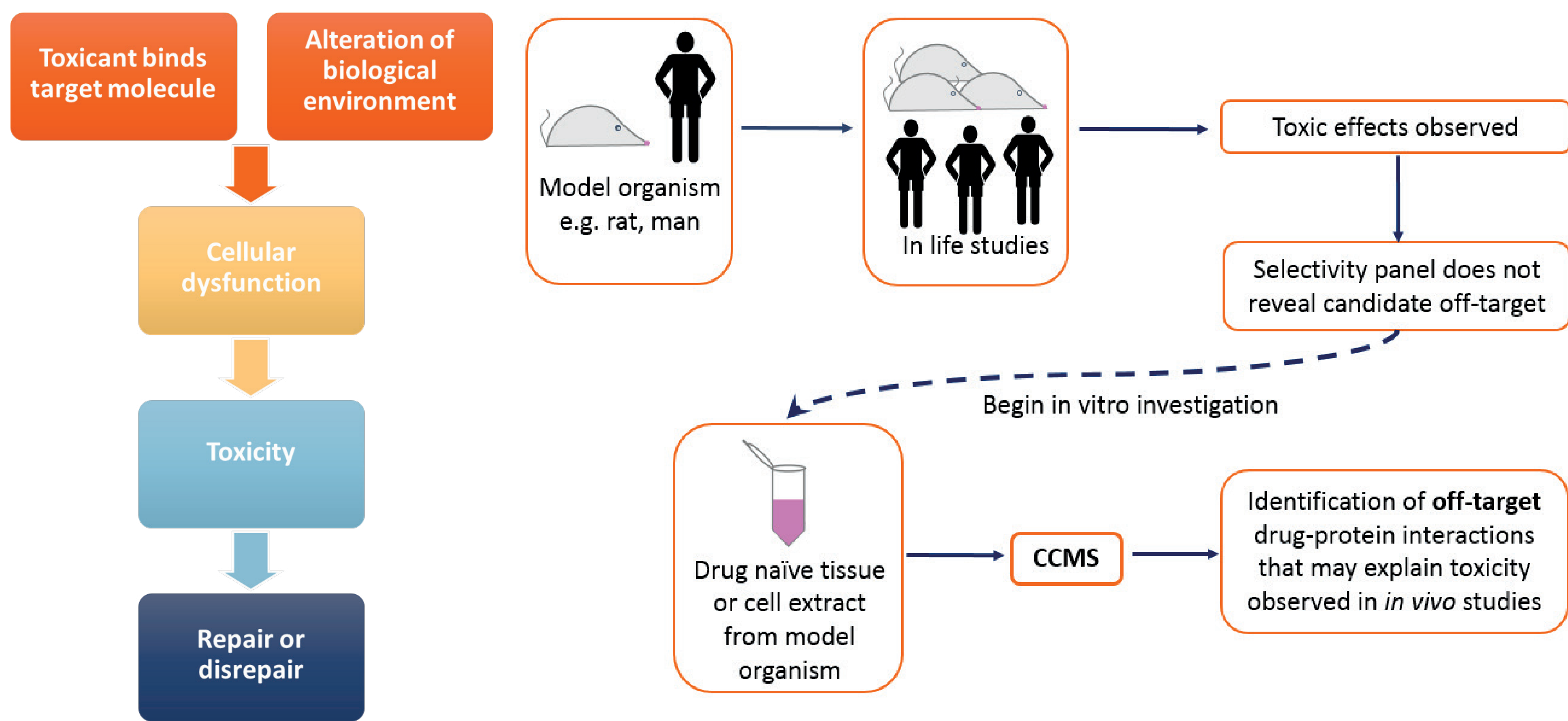
2 THE CCMS EXPERIMENT

A panel of CCs are synthesized with the selectivity function in a position compliant with on-target SAR and in alternative orientations to allow generation of a full interaction profile. CCs are incubated with a biological sample whereby binding of the selectivity function to interacting proteins occurs before covalent capture via photo-irradiation. Competition experiments include incubation of the sample with both the CC and an excess of the free ligand to allow specifically interacting proteins to be determined. Sample analysis by high-resolution LC-MS/MS reveals specific binding partners.



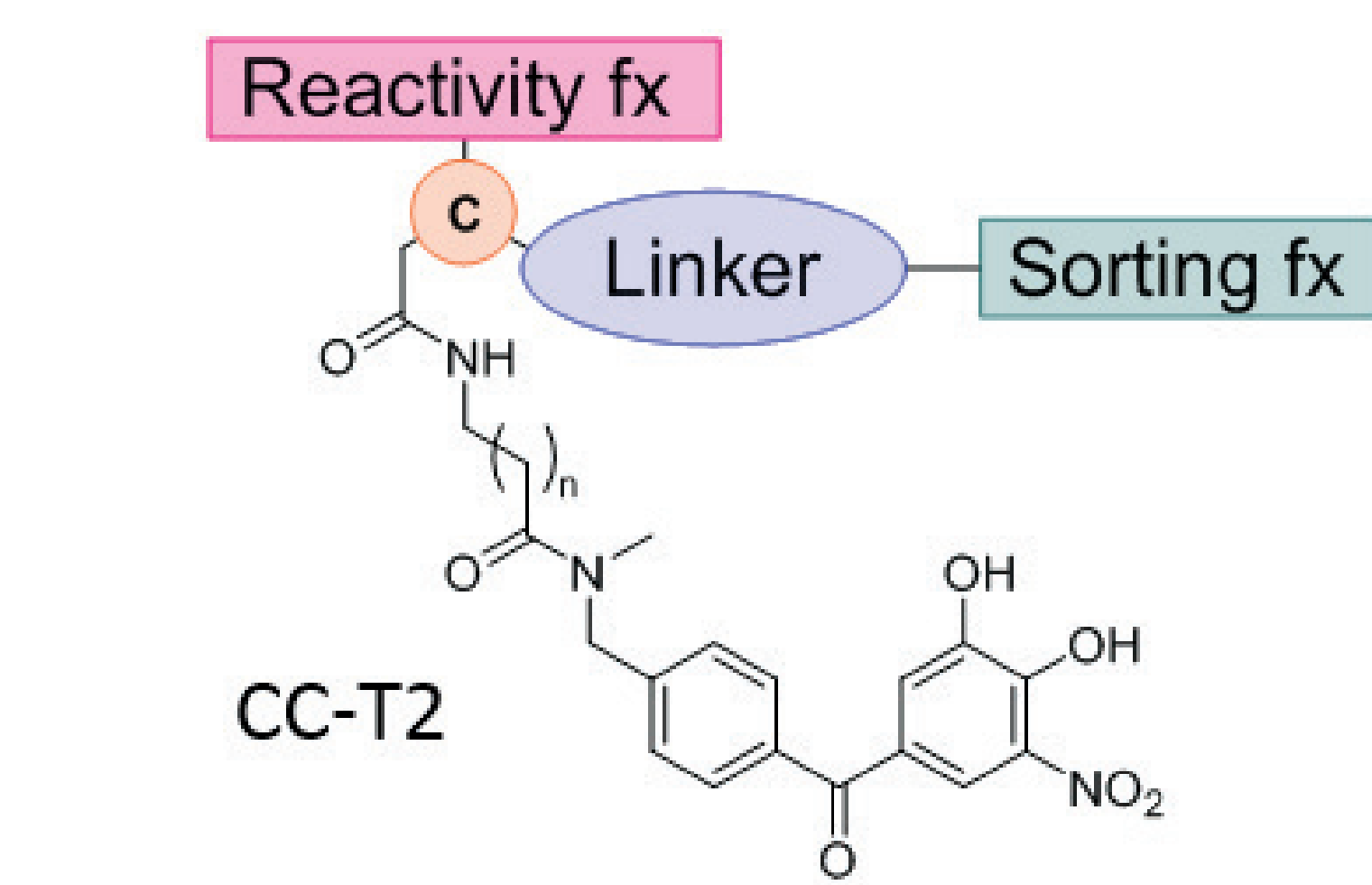
3 CCMS IN DRUG SAFETY

During Drug Discovery and Development, the timely assessment of the off-target liabilities of a lead molecule or the cause of an unexpected toxic event in vitro or in vivo can de-risk a molecule. With CCMS, both toxic pharmacological interactions and drug-protein adducts can be detected.

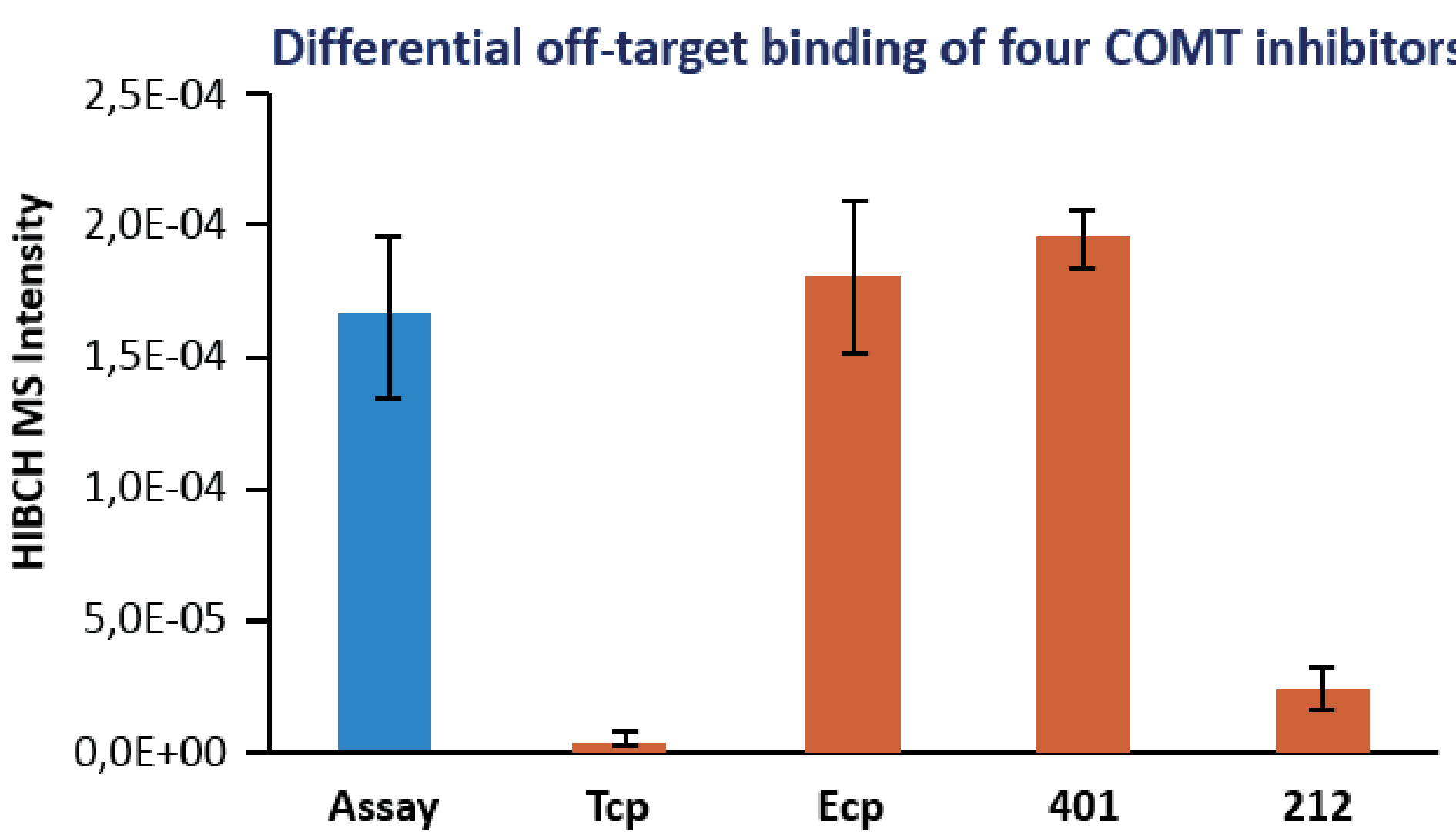
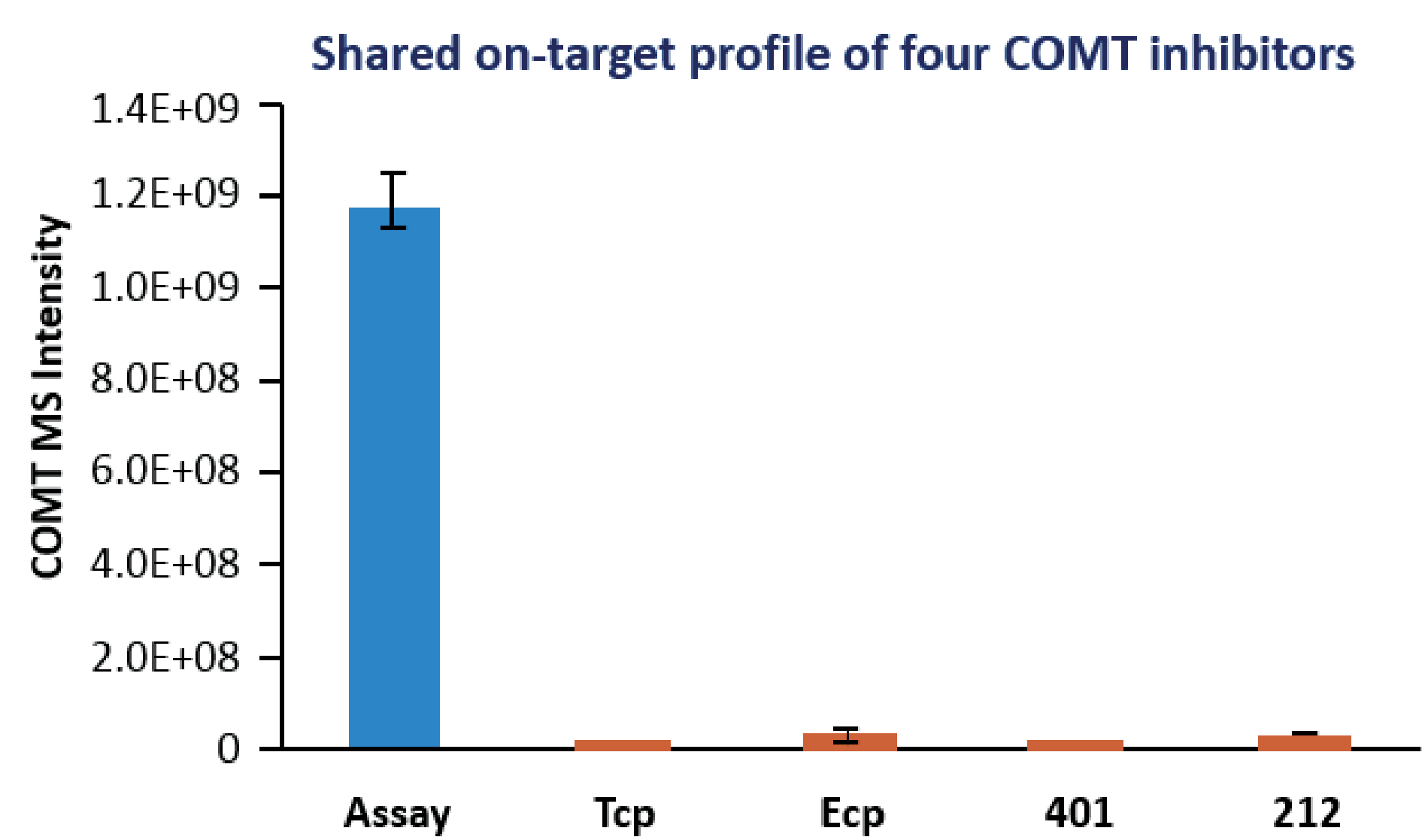


4 CASE STUDY: CCMS IDENTIFIES OFF-TARGET MECHANISM OF TOLCAPONE TOXICITY

CCMS was used to determine on- and off-target interactions of the catechol-O-methyl transferase (COMT) inhibitor tolcapone in a human liver cancer cell line (HepG2).

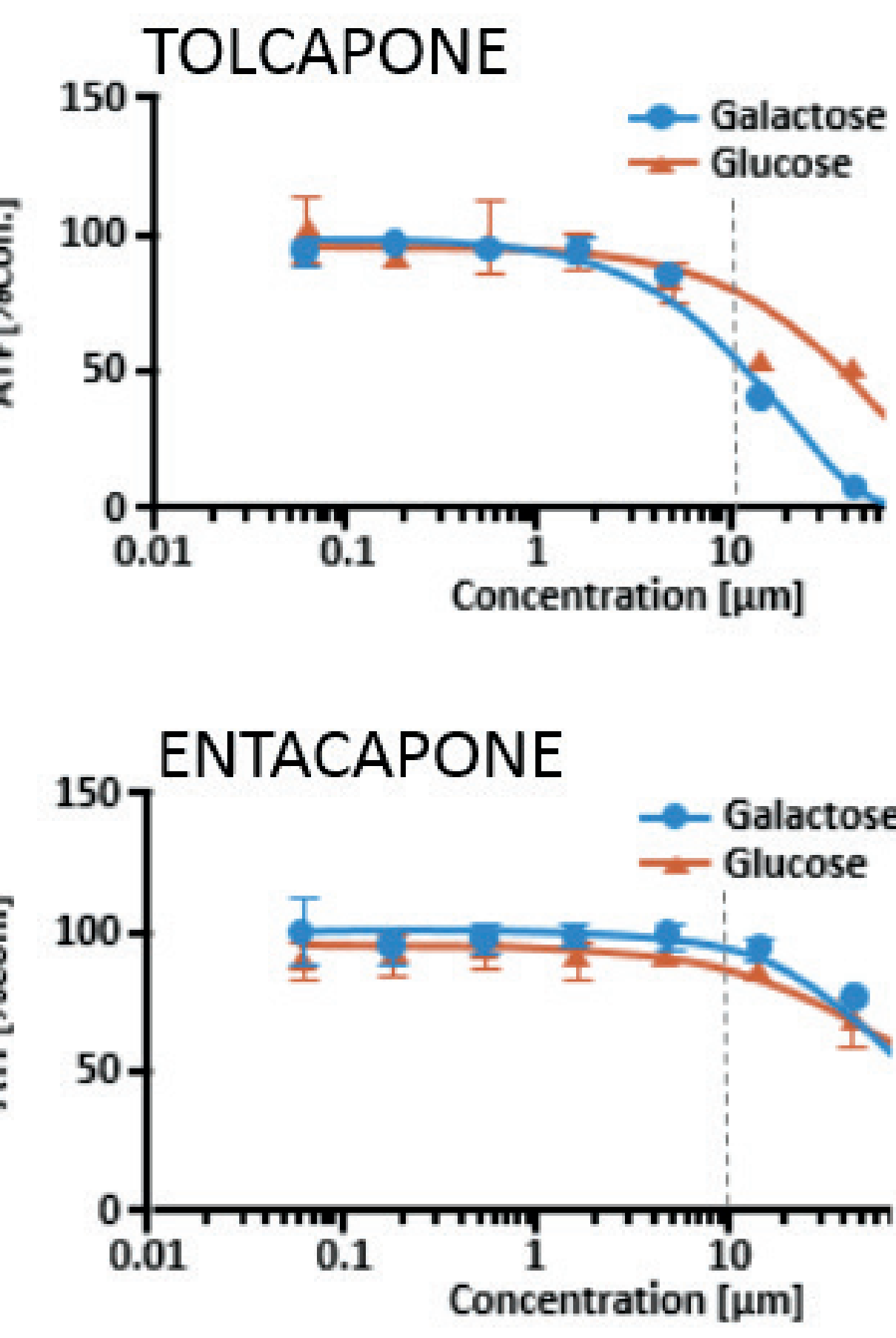


Inhibitors and CCs	IC ₅₀ [nM], rec. human COMT
Tolcapone	127
Tolcapone CC - T1	>6,000
Tolcapone CC - T2	448
Entacapone	386
Cmpd 212	179
Cmpd 401	54

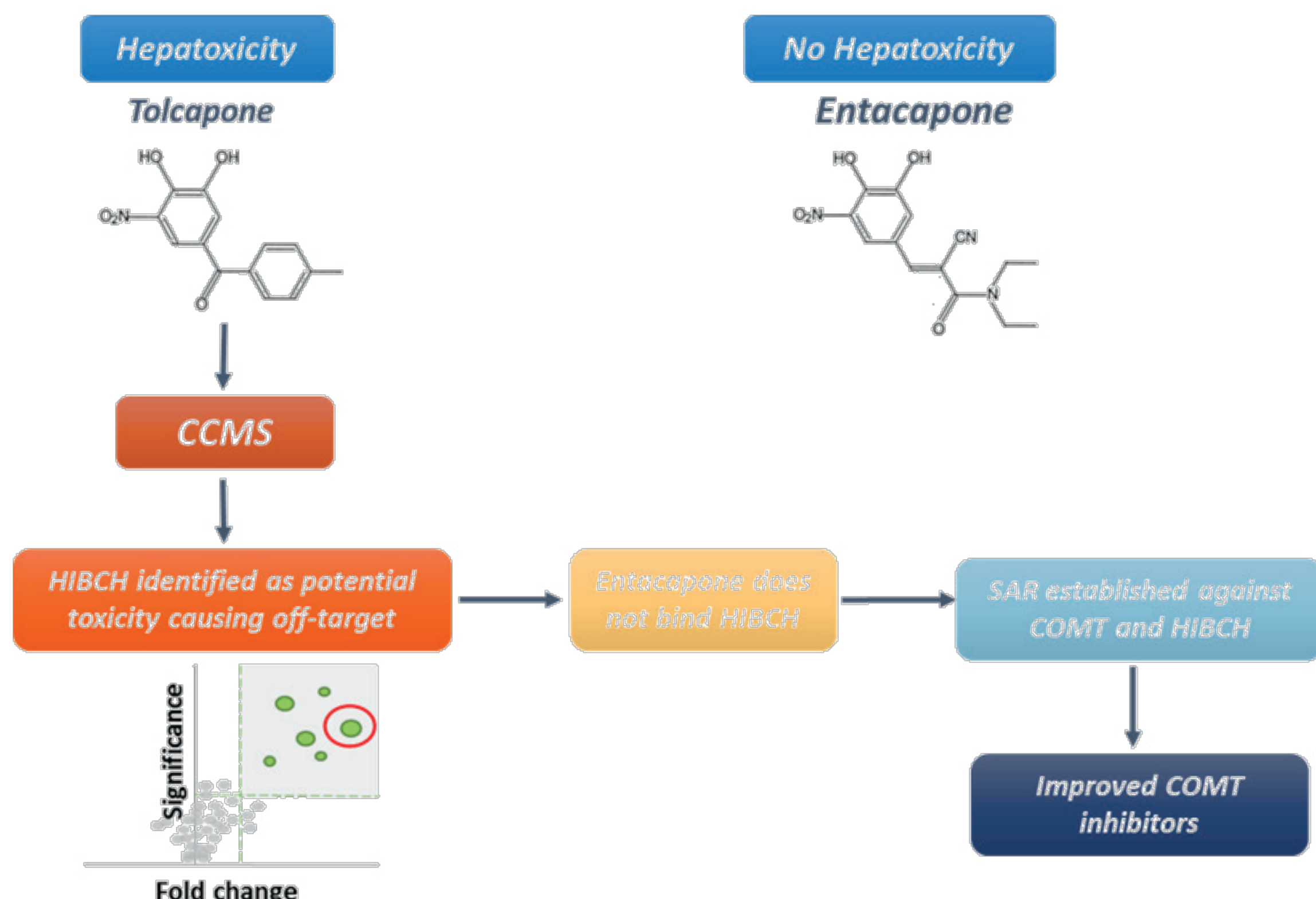


Differential binding profiles were seen against on- and off target proteins. These binding profiles correlated with cellular hepatotoxicity.

ATP levels in HepG2 cells following 24 hour treatment with COMT inhibitors (ToxGlo)



Compound	COMT Affinity	HIBCH Affinity	Cellular Hepatotoxicity
Tolcapone	✓	✓	✓
Entacapone	✓	✗	✗
Cpd 212	✓	✓	✓
Cpd 401	✓	✗	✗



CCMS is a powerful chemoproteomic tool for profiling protein interactions of small molecules

- Unbiased screening of the entire proteome versus traditional selectivity screening
- Can be used to probe the potential mechanisms causing toxicity by identifying specific binding off-targets
- CCMS can support projects at a variety of stages throughout drug discovery and development.

