

SPECIFICITY AND SELECTIVITY IMPROVEMENT IN DOPING ANALYSIS USING COMPREHENSIVE TWO-DIMENSIONAL GAS CHROMATOGRAPHY COUPLED WITH TIME-OF-FLIGHT MASS SPECTROMETRY

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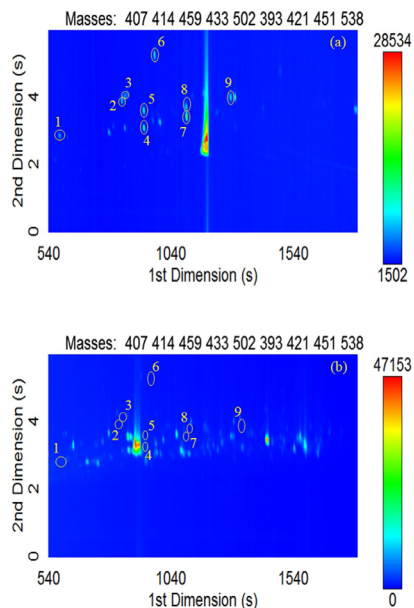


Figure 1S. Selected region of m/z 407, m/z 414, m/z 459, m/z 433, m/z 502, m/z 393, m/z 421, m/z 451 and m/z 538 mass chromatogram of brombuterol (1), hydromorphone (2), oxycodone (3), drostanolone metabolite (4), oxymorphone (5), hydroxybromantane (6), norethandrolone metabolite (7), clostebol metabolite (8), -zeranol (9): (a) spiked sample; (b) blank urine sample

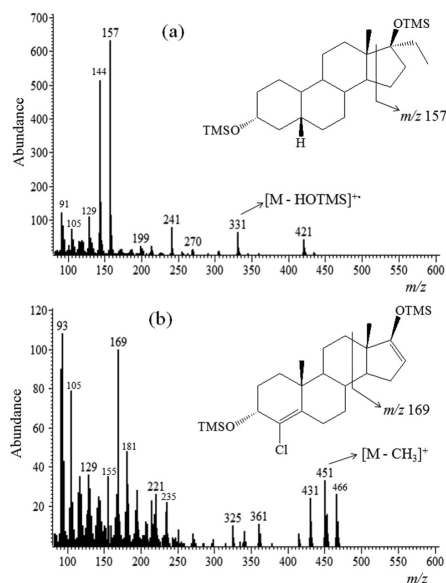


Figure 2S. Selected region of mass spectra of norethandrolone metabolite (molecular ion at m/z 450) (a) and clostebol metabolite (molecular ion at m/z 466) (b) as bis-OTMS ethers in the GC \times GC-TOFMS system. Lack of interference after chromatographic resolution

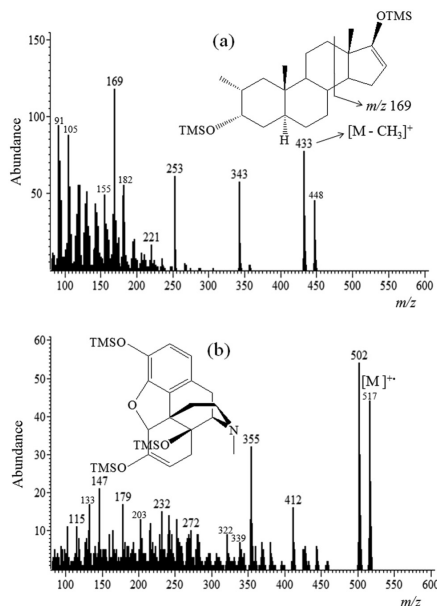


Figure 3S. Selected region of mass spectra of drostanolone metabolite (molecular ion at m/z 448) (a) and oxymorphone (molecular ion at m/z 517) (b), both as O-TMS ethers in the GC \times GC-TOFMS system. Lack of interference after chromatographic resolution

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