

**Determination of sedative-hypnotics in human hair by micropulverized extraction
and liquid chromatography/quadrupole-Orbitrap mass spectrometry.**

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Supplementary Information (SI)

Content:

- Table S1 Acquisition and calibration parameters
- Fig. S1 Extracted ion chromatograms (a) and mass spectra (b) of the standard sample (0.10 ng mL^{-1}) and spiked sample (1.0 pg mg^{-1}).

Table S1 Acquisition and calibration parameters

Analytes and internal standards	Molecular formula	Monoisotopic mass of protonated molecule	Time range (min)	Calibration parameters					
				Internal standard	Curve index	Weighting	Origin	Equation (y: peak area; x: concentration in pg mg ⁻¹)	R ²
alprazolam (ALP)	C ₁₇ H ₁₃ ClN ₄	309.090	22.0-24.5	ALP- <i>d</i> ₅	Linear	1/x ²	Ignore	y = -0.00129741 + 0.00255162x	0.9925
brotizolam (BROT)	C ₁₅ H ₁₀ BrClN ₄ S	392.957	27.0-30.0	TRI- <i>d</i> ₄	Linear	1/x ²	Ignore	y = -0.000356934 + 0.00097534x	0.9905
<i>N</i> -desmethyldiazepam (DMD)	C ₁₅ H ₁₁ ClN ₂ O	271.063	24.0-26.5	DMD- <i>d</i> ₅	Quadratic	Equal	Force	y = 0.00336914x + 1.38188 × 10 ⁻⁸ x ²	0.9999
<i>N</i> -desmethylfludiazepam (DMF)	C ₁₅ H ₁₀ ClFN ₂ O	289.054	26.0-28.5	DMF- <i>d</i> ₄	Linear	1/x ²	Ignore	y = -0.000924251 + 0.00286056x	0.9974
diazepam (DIA)	C ₁₆ H ₁₃ ClN ₂ O	285.079	30.0-35.0	DIA- <i>d</i> ₅	Quadratic	Equal	Force	y = 0.00290374x - 1.11029 × 10 ⁻⁷ x ²	0.9995
estazolam (EST)	C ₁₆ H ₁₁ ClN ₄	295.075	15.0-23.0	EST- <i>d</i> ₅	Linear	1/x ²	Ignore	y = 9.62685e-005 + 0.00274179x	0.9976
etizolam (ETI)	C ₁₇ H ₁₅ ClN ₄ S	343.078	27.0-30.0	TRI- <i>d</i> ₄	Linear	1/x ²	Ignore	y = -0.000797923 + 0.00368474x	0.9893
flunitrazepam (FLUN)	C ₁₆ H ₁₂ FN ₃ O ₃	314.094	27.0-30.0	FLUN- <i>d</i> ₇	Linear	1/x ²	Ignore	y = 0.000178267 + 0.00276029x	0.9973
nitrazepam (NIT)	C ₁₅ H ₁₁ N ₃ O ₃	282.087	15.0-23.0	NIT- <i>d</i> ₅	Linear	1/x ²	Ignore	y = 0.000464354 + 0.00245904x	0.9892
ramelteon (RAM)	C ₁₆ H ₂₁ NO ₂	260.165	25.0-28.0	DMF- <i>d</i> ₄	Linear	1/x ²	Ignore	y = 0.000804807 + 0.00385956x	0.9929
triazolam (TRI)	C ₁₇ H ₁₂ Cl ₂ N ₄	343.051	23.0-26.5	TRI- <i>d</i> ₄	Linear	1/x ²	Ignore	y = 0.000289182 + 0.00241819x	0.9871
zolpidem (ZOL)	C ₁₉ H ₂₁ N ₃ O	308.176	12.5-20.0	ZOL- <i>d</i> ₆	Linear	1/x ²	Ignore	y = 0.00019509 + 0.00163075x	0.9972
zopiclone (ZOP)	C ₁₇ H ₁₇ ClN ₆ O ₃	389.112	8.0-13.5	ZOP- <i>d</i> ₄	Linear	1/x ²	Ignore	y = -0.00115316 + 0.0028835x	0.9967
ALP- <i>d</i> ₅	C ₁₇ H ₈ D ₅ ClN ₄	314.122	22.0-24.5						
DMD- <i>d</i> ₅	C ₁₅ H ₆ D ₅ ClN ₂ O	276.095	24.0-26.5						
DMF- <i>d</i> ₄	C ₁₅ H ₆ D ₄ ClFN ₂ O	293.079	26.0-28.5						
DIA- <i>d</i> ₅	C ₁₆ H ₈ D ₅ ClN ₂ O	290.110	30.0-35.0						
EST- <i>d</i> ₅	C ₁₆ H ₆ D ₅ ClN ₄	300.106	15.0-23.0						
FLUN- <i>d</i> ₇	C ₁₆ H ₅ D ₇ FN ₃ O ₃	321.137	27.0-30.0						
NIT- <i>d</i> ₅	C ₁₅ H ₆ D ₅ N ₃ O ₃	287.119	15.0-23.0						
TRI- <i>d</i> ₄	C ₁₇ H ₈ D ₄ Cl ₂ N ₄	347.076	25.0-28.0						
ZOL- <i>d</i> ₆	C ₁₉ H ₁₆ D ₆ N ₃ O	314.213	23.0-26.5						
ZOP- <i>d</i> ₄	C ₁₇ H ₁₃ D ₄ ClN ₆ O ₃	393.137	12.5-20.0						

R², Coefficient of determination

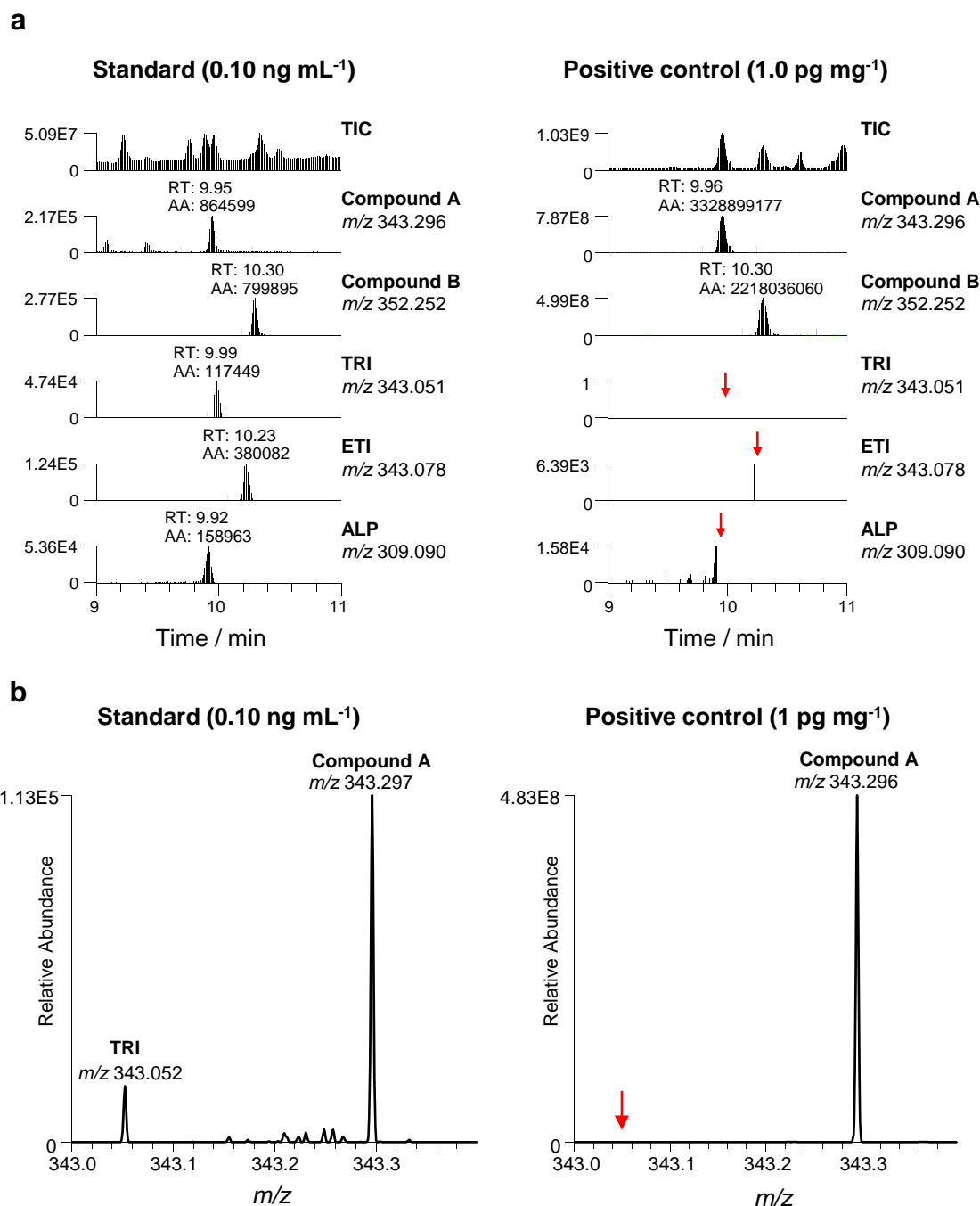


Fig. S1 Extracted ion chromatograms (a) and mass spectra (b) of the standard sample (0.10 ng mL⁻¹) and spiked sample (1.0 pg mg⁻¹).

Losses of small peaks of the analytes because of the limitations of the intra-scan dynamic range are indicated by arrows. The following conditions differed from the final protocol: mobile phase, 10 mol L⁻¹ ammonium formate (A, pH 3.5)–acetonitrile (B) (0.3 mL/min); and gradient program, 0–2 min 10 % B, 2–8 min 10–90 % B, 8–15 min 90 % B, 15–20 min 10 % B.