Matrix Solid-Phase Dispersion Procedure for Determination of Antibiotics and Metabolites in Mussels: Application in Exposure Bioassays

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Table S1. Box–Behnken design matrix for the optimisation of clean-up sorbent amount.

Experiment	C18 amount (g)	PSA amount (g)	Florisil® amount (g)
1	0.8	0.4	0.8
2	0.8	0	0.4
3	0.4	0.4	0.4
4	0.4	0.8	0
5	0	0.8	0.4
6	0	0.4	0
7	0.8	0.8	0.4
8	0.4	0	0
9	0	0	0.4
10	0.4	0.4	0.4
11	0.4	0	0.8
12	0.4	0.8	0.8
13	0.4	0.4	0.4
14	0	0.4	0.8
15	0.8	0.4	0

Table S2. Method application to mussels (expressed as ng g^{-1} dm).

Compound	Mussels			
	S_F	S_0	S_{14}	S_{28}
TMP	-	-	62.3	77.5
4-OH-TMP	-	-	-	-
DM-TMP	-	-	-	-
SMX	-	-	1.17	1.26
AcSMX	-	-	-	-
SMX-GL	-	-	-	-
SDZ	-	-	-	-
AcSDZ	-	-	-	-
SMZ	-	-	-	-
AcSMZ	-	-	-	-

-: lower than MDL; Parent compounds are marked in bold; S_F: field sample; S_0: sample at time 0 (after acclimatisation period, before spiking); S_{14}: sample at time 14 days of exposure to SMX and TMP (1 µg L^{-1}); S_{28}: sample at time 28 days of exposure to SMX and TMP (1 µg L^{-1}).
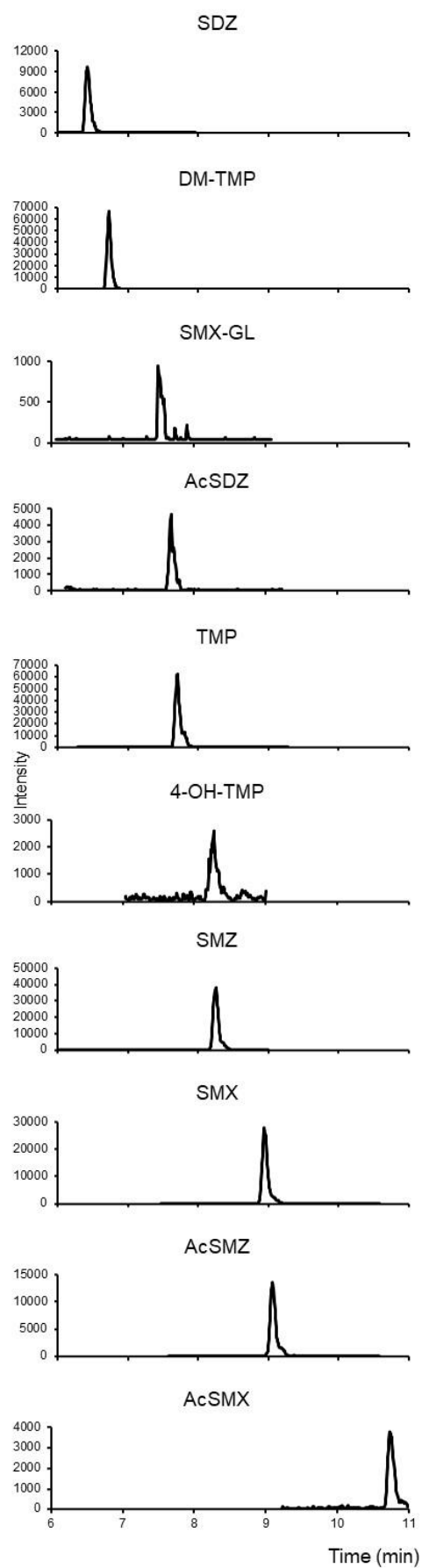
Figure S1. LC-MS/MS chromatogram of a 10 ng g^{-1} d.m. spiked mussel sample.