Automated Enrichment of Sulfanilamide in Milk Matrices by Utilization of

Aptamer-Linked Magnetic Particles

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Apt 2.1

Apt 3.1





Apt 4.1





Figure S1: Predicted secondary structures for generated sulfanilamide aptamers using mfold V4.6.

Sulf Apt 1	CATCCGTCAC	ACCTGCTCCA	CCCGTCACAC	TCATCCGTCA	CACTGCTCTC	CCACTGGGGGG	TGTTCGGTCC	CGTATC
Sulf Apt 2			ACT		CTGCTC.	C.ACT		
Sulf Apt 3		C	AGGCGT.	GGGGGGG.A.C	.CTGT.AGC.	CTC.C		
Sulf Apt 4		C	AGGGGT.	GACC.G.A.C	.CTGT.AGC.	CGG.C		
Identität	******	******	* *	* *	* *	** ***	*****	*****

Figure S2: Alignment of aptamer sequences with an affinity towards sulfanilamide. Primer regions are marked in grey.



Figure S3: Resulting LC-ESI-MS/MS calibration curves for quantitation of particle coupling efficiency

time [min]	A (water + 0.1 % FA) [%]	B (acetonitrile + 0.1 % FA) [%]
0.0	95	5
2.0	95	5
5.0	80	20
7.5	80	0
10.0	0	100
13.0	0	100
13.5	95	5
19.0	95	5

Table S1. LC-Gradient for LC-ESI-MS/MS quantitation of antibiotics used in this study.

Table S2. Operating MRM MS method parameters for quantitation of ampicillin (A), sulfanilamide (S1), tetracycline (T), sulfamerazine (S2), sulfadiazine (S3), chlortetracycline (CT), and oxytetracycline (OT).

tran	sitions	CE [V]	CXP [V]	DP [V]	EP [V]	Rt [min]
Qnt A	350.168 → 106.0	25	18			8.38
Q1 A	350.168 → 192.1	21	4	66	10	
Q2 A	350.168 → 159.9	17	10	00	10	
Q3 A	350.168 → 174.1	23	14			
Qnt S1	173.040 → 155.9	9	46	61	10	2.47
Q1 S1	173.040 → 92.1	25	6			
Q2 S1	173.040 → 108.1	21	8			
Q3 S1	$173.040 \rightarrow 65.1$	41	18			
Qnt T	445.180 → 410.0	27	12	91	10	9.51
Q1 T	445.180 → 427.4	19	14			
Q2 T	445.180 → 154.3	37	12			
Q3 T	445.180 → 241.1	55	20			
Qnt S2	265.157 → 156.0	25	24	46	10	8.50
Q1 S2	265.157 → 172.1	23	12			
Q2 S2	265.157 → 91.9	41	14			
Q3 S2	265.157 → 108.0	39	6			
Qnt S3	251.038 → 156.0	23	10	46	10	7.02
Q1 S3	251.038 → 91.9	41	14			
Q2 S3	251.038 → 108.2	35	6			
Q3 S3	251.038 → 65.0	63	8			
Qnt CT	479.141 → 197.0	65	30	56	10	10.35
Q1 CT	479.141 → 98.1	75	16			
Q2 CT	479.141 → 275.0	57	10			
Qnt OT	461.189 → 426.1	29	30	51	10	8.97
Q1 OT	461.189 → 444.1	27	24			
Q2 OT	461.189 → 283.0	57	40			
Q3 OT	461.189 → 201.2	53	8			

CE = collision energy, CXP = collision cell exit potential, DP = declustering potential, EP = entrance potential, Rt = retention time Qnt = quantifier, Q1-Q4 = qualifier

	Sulf-Apt-3	Sulf-Apt-4	Sulf-Apt-1	Sulf-Apt-2
Sulf-Apt-3	100.00	82.50	39.47	44.74
Sulf-Apt-4	82.50	100.00	47.37	47.37
Sulf-Apt-1	39.47	47.37	100.00	67.50
Sulf-Apt-2	44.74	47.37	67.50	100.00

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Table S3: Percent identity matrix of generated aptamers without primer regions designed with Clustal Omega.