Table S1. Molar composition of the prepolymerization mixtures used in the experimental design and resulting binding affinites of the corresponding nanoMIPs.

Polymer	AA %mol	tBAM %mol	NIPAM %mol	BIS %mol	K_{eq} ± 1 s.e. (10^6 M^{-1})
P1	10	57	30	3	2.05 ± 1.12
P2	20	46	30	4	2.44 ± 0.68
P3	20	48	30	2	4.01 ± 0.62
P4	30	35	30	5	3.99 ± 0.57
P5	30	37	30	3	1.39 ± 0.27
P6	30	39	30	1	3.00 ± 0.75
P7	40	26	30	4	3.08 ± 0.83
P8	40	28	30	2	0.63 ± 0.76
P9	50	17	30	3	0.37 ± 0.73

Table S2. Non linear fitting of langmuirian binding models for ciprofloxacin-imprinted nanoMIPs.

Polymer	K_{eq} ± 1 s.e. (10^6 M^{-1})	B_{max} ± 1 s.e. (nmol g^{-1})	r^2	Fit std. error	F-value
P1	2.05 ± 1.12	8.3 ± 2.1	0.905	0.417	76.0
P2	2.44 ± 0.68	7.6 ± 1.1	0.950	0.294	153.5
P3	4.01 ± 0.62	8.8 ± 0.7	0.981	0.245	409.5
P4	3.99 ± 0.57	5.4 ± 0.3	0.973	0.160	283.5
P5	1.39 ± 0.27	10.7 ± 1.4	0.990	0.150	806.2
P6	3.00 ± 0.75	18.8 ± 2.9	0.979	0.442	381.9
P7	3.08 ± 0.83	9.5 ± 1.4	0.951	0.397	153.9
P8	0.63 ± 0.76	19.8 ± 20.8	0.952	0.236	153.5
P9	0.37 ± 0.73	43.8 ± 77.8	0.920	0.583	91.48

Table S3. Non linear fitting of 6-parameters polynomial model for the two-factor central composite (d=2, n=9) experimental design.

Model: $z = a_0 + a_1x + a_2y + a_3x^2 + a_4y^2 + a_5xy$ ($r^2 = 0.921$, fit std. error = 0.607, F-value = 6.980)

Parameters	value ± 1 s.e.	t-value	P
a_0	15.686 ± 3.697	4.243	0.0240
a_1	-5.792 ± 1.351	-4.287	0.0233
a_2	-0.322 ± 0.140	-2.304	0.1046
a_3	0.496 ± 0.150	3.306	0.0455
a_4	-0.001 ± 0.001	-0.381	0.7287
a_5	0.101 ± 0.033	3.073	0.0544

Polymer	z value (K_{eq})	z predicted	Residual	Residual %
P1	2.05	2.54	-0.49	23.8
P2	2.44	1.89	0.55	22.4
P3	4.01	3.47	0.54	13.5
P4	3.99	4.14	-0.15	-3.7
P5	1.39	1.71	-0.32	-22.7
P6	3.00	3.24	-0.24	-8.00
P7	3.08	2.84	0.24	7.70
P8	0.63	0.36	0.26	41.7
P9	0.37	0.39	-0.02	-5.31

Table S4. Recovery of ciprofloxacin in human urine after dilution 9 + 1 v/v with 50 mmol L−1 MES buffer, pH 4.5 and MISPE. t-values for pairwise comparison of samples at different concentration.

μg mL^{-1}	**0.2**	**0.5**	**1.0**	**1.5**	**2.0**
0.2	-	0.432	0.821	0.477	0.910
0.5	0.432	-	0.316	0.938	0.290
1.0	0.821	0.316	-	0.352	0.880
1.5	0.477	0.938	0.352	-	0.334
2.0	0.910	0.290	0.880	0.334	-