Electronic Supplementary Material (ESI) for RSC Advances.

Table S1. Characteristics of cholesterol-lowering drugs.

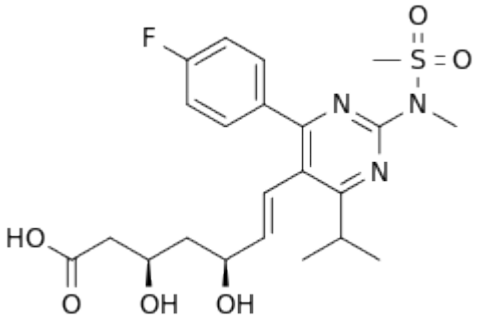
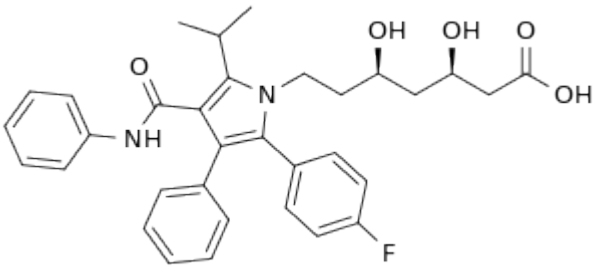
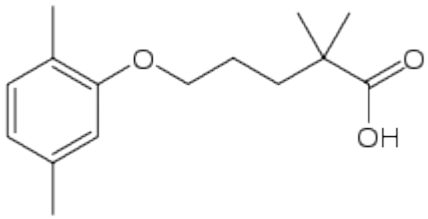
Analytes	Molecular structure	Molar mass (g mol $^{-1}$)	pK_a
Rosuvastatin		481.5	4.0
Atorvastatin		558.6	4.3
Gemfibrozil		250.3	4.5

Table S2. Peak areas (responses) for three acidic drugs after their preconcentration through TAALLME-SFO.

Run	X_1	X_2	X_3	X4	R_1 (Rosuvastatin)	R_2 (Atorvastatin)	R_3 (Gemfibrozil)
1	4.25	110	10.75	62.5	291294	116617	155231
2	3.5	100	11.5	50	533577	498584	370098
3	3.5	100	11.5	50	511579	527498	398135
4	4.25	110	12.25	37.5	566421	296093	191084
5	4.25	90	12.25	62.5	418686	382377	234108
6	3.5	100	11.5	25	548076	305656	197443
7	3.5	100	11.5	50	523577	518584	384875
8	3.5	80	11.5	50	358225	305489	167957
9	5	100	11.5	50	371122	204274	45923
10	3.5	120	11.5	50	450670	208166	264788
11	4.25	90	10.75	37.5	265823	200944	135137
12	4.25	90	12.25	37.5	455570	362483	117036
13	4.25	110	10.75	37.5	358351	85743	125921
14	2.75	90	10.75	62.5	320116	344372	66071
15	2.75	90	12.25	37.5	451832	346927	323141
16	4.25	110	12.25	62.5	455793	324349	345606
17	2.75	110	12.25	62.5	417723	401681	362198
18	2.75	110	12.25	37.5	505923	352491	310889
19	3.5	100	10	50	125393	272749	181363
20	2.75	90	12.25	62.5	472101	388211	324501
21	3.5	100	11.5	50	521579	507498	388135
22	3.5	100	11.5	75	437694	343802	256646
23	4.25	90	10.75	62.5	236752	194874	84583
24	3.5	100	13	50	482099	500206	536118
25	2.75	90	10.75	37.5	290114	365645	165563
26	2.75	110	10.75	37.5	370181	301881	95944
27	2	100	11.5	50	388195	431184	108234
28	3.5	100	11.5	50	527879	507498	369935
29	2.75	110	10.75	62.5	330422	362459	95960
30	3.5	100	11.5	50	522879	517498	369935

Table S3. ANOVA for central composite design.

Source of variation	Sum of squares	Degree of freedom	Mean square	F-value	P-value
		Drug 1			
Model	3.27E+11	14	2.34E+10	141.4079	< 0.0001
Residual	2.48E+09	15	1.65E+08		
Lack-of-fit	2.21E+09	10	2.21E+08	4.148341	0.0649
Pure error	2.67E+08	5	53382561		
$R^2 = 0.99$	Adj-$R^2 = 0.98$	Pred-$R^2 = 0.96$			
		Drug 2			
Model	4.19E+11	14	2.99E+10	121.9317	< 0.0001
Residual	3.68E+09	15	2.45E+08		
Lack-of-fit	3.15E+09	10	3.15E+08	2.971664	0.1205
Pure error	5.3E+08	5	1.06E+08		
$R^2 = 0.99$	Adj-$R^2 = 0.98$	Pred-$R^2 = 0.95$			
		Drug 3			
Model	4.61E+11	14	3.29E+10	70.79638	< 0.0001
Residual	6.98E+09	15	4.65E+08		
Lack-of-fit	6.26E+09	10	6.26E+08	4.350142	0.0592
Pure error	7.19E+08	5	1.44E+08		
$R^2 = 0.98$	Adj-$R^2 = 0.97$	Pred-$R^2 = 0.92$			

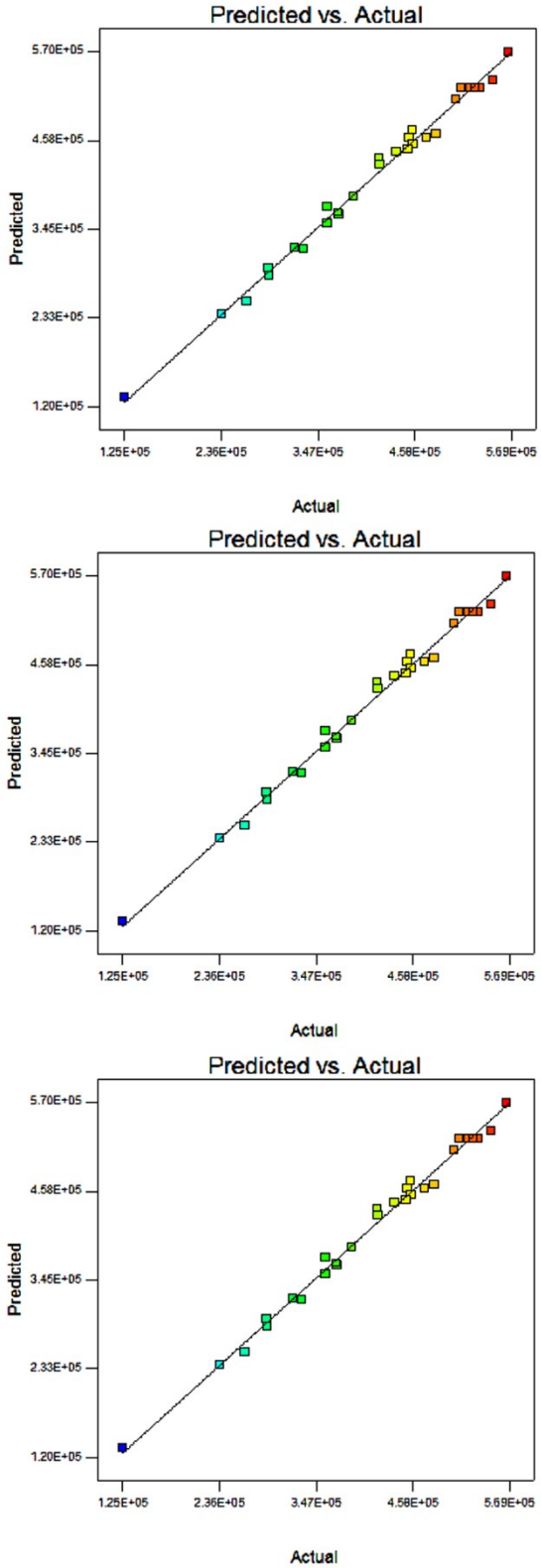


Fig. S1. 2D plots of experimental peak areas versus predicted peak areas obtained through corresponding fitted models for the target analytes (a, b, and c are related to rosuvastatin, atorvastatin and gemfibrozil, respectively).