

Table S1. Box–Behnken design with three independent variables for arsenate removal.

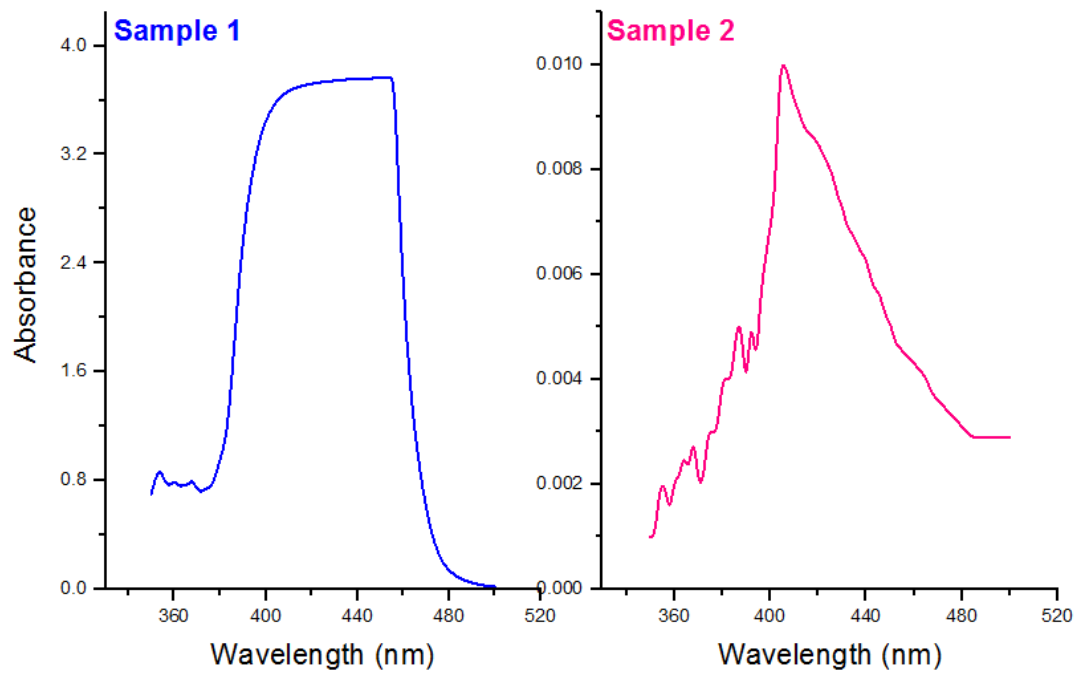
			Factors			Levels and Ranges			
			-1	0	+1				
A: Solution pH			4.5	6.5	8.5				
B: As concentration ($\mu\text{g/L}$)			20	70	120				
C: Contact time (min)			20	80	140				
Std.	Run	Block	A	B	C	Y_{Observed} (%)	$Y_{\text{Predicted}}$ (%)	Residual	Error (%)
9	1	1	4.5	70	80	91.62	92.36	-0.74	0.8
5	2	1	4.5	20	140	87.49	80.63	6.86	8.51
17	3	1	6.5	70	80	85.72	84.32	1.4	1.66
20	4	1	6.5	70	80	75.72	77.14	-1.42	1.84
6	5	1	8.5	20	140	14.4	15.18	-0.78	5.13
18	6	1	6.5	70	80	84.72	85.13	-0.41	0.48
16	7	1	6.5	70	80	86.72	88.65	-1.93	2.17
15	8	1	6.5	70	80	80.72	80.96	-0.24	0.29
8	9	1	8.5	120	140	2.6	2.43	0.17	6.99
1	10	1	4.5	20	20	8.89	8.13	0.76	9.35
14	11	1	6.5	70	140	87.1	88.57	-1.47	1.66
12	12	2	6.5	120	80	75.4	76.13	-0.73	0.96
2	13	2	8.5	20	20	1.47	1.32	0.15	11.36
7	14	2	4.5	120	140	100	99.13	0.87	0.87
11	15	2	6.5	20	80	64.99	65.97	-0.98	1.48

4	16	2	8.5	120	20	12.34	13.75	-1.41	10.25
19	17	2	6.5	70	80	83.82	82.68	1.14	1.37
3	18	2	4.5	120	20	41.3	43.57	-2.27	5.21
10	19	2	8.5	70	80	25.2	25.19	0.01	0.04
13	20	2	6.5	70	20	33.72	35.21	-1.49	4.23

Table S2. Analysis of variance (ANOVA) of the response surface model for the prediction of arsenic adsorption.

Source	Sum of Squares	DF	Mean Square	F-Value	p-value
Model	23009.52	9	2556.61	72.91	0.0001
A	7468.74	1	7468.74	212.98	0.0001
B	295.94	1	295.94	8.44	0.0157
C	3758.56	1	3758.56	107.18	0.0001
AB	262.78	1	262.78	7.49	0.0209
AC	2248.19	1	2248.19	64.11	0.0001
BC	226.53	1	226.53	6.46	0.0293
A ²	1181.61	1	1181.61	33.70	0.0002
B ²	219.97	1	219.97	6.27	0.0312
C ²	964.60	1	964.60	27.51	0.004
Residual	350.68	10	35.07		
Lack of Fit	267.67	5	53.53	3.22	11.23
Pure Error	83.01	5	16.60		
R-Squared					0.9850
Adj R-Squared					0.9715
Pred R-Squared					0.9130

p-value < 0.05 was set as significant



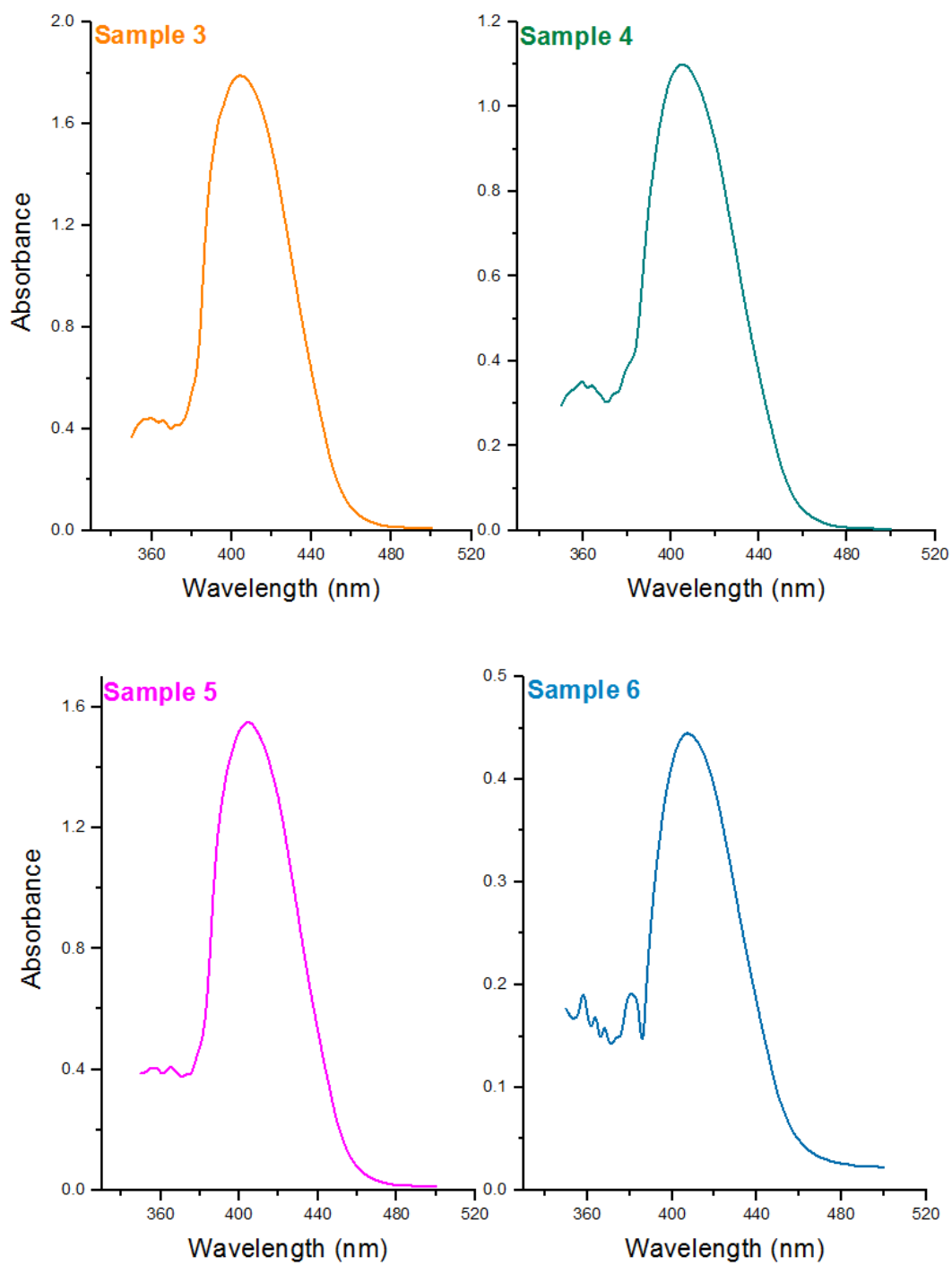


Fig. S1. UV/VIS spectra of AMPDSA samples after Schiff base reaction

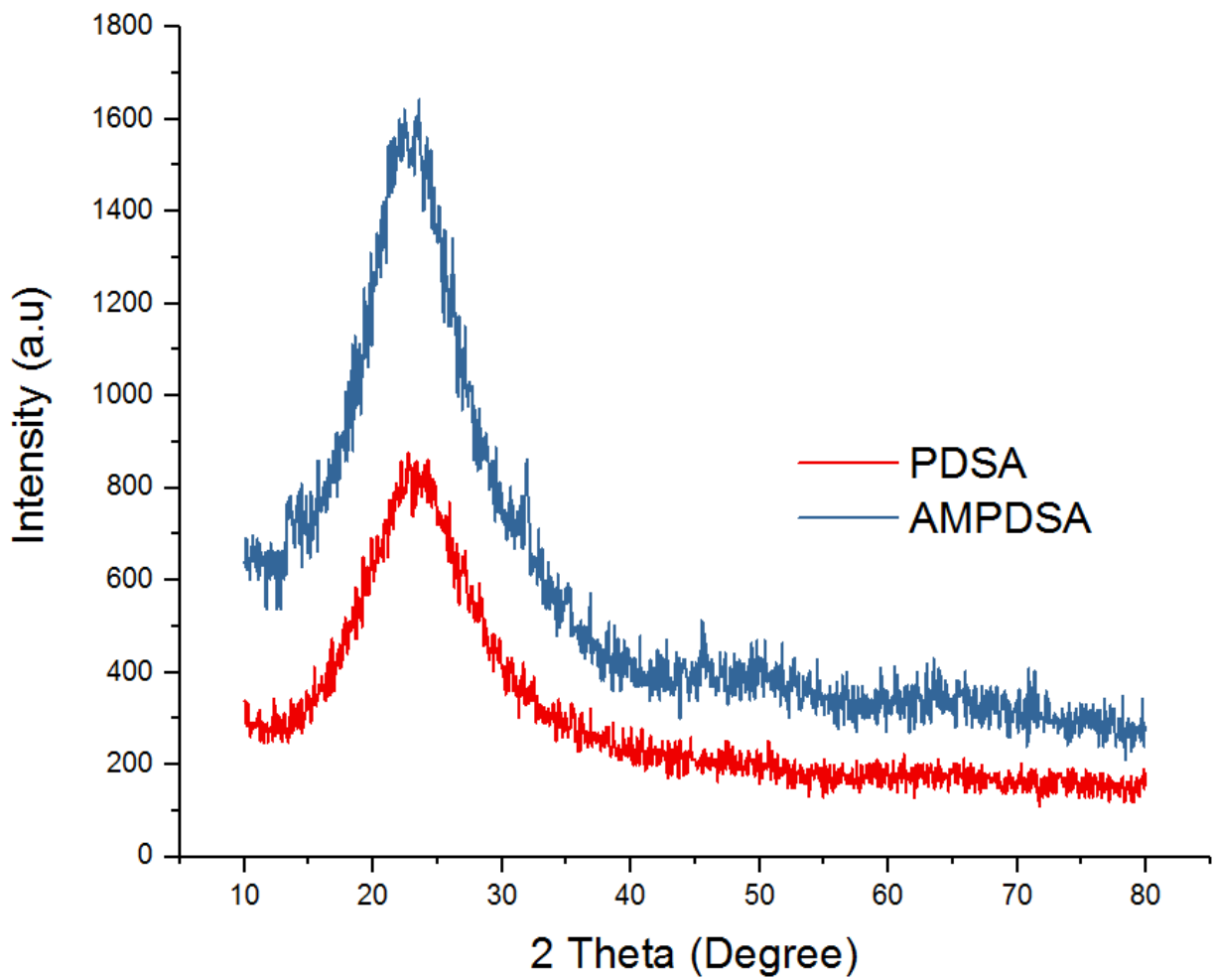


Fig. S2. XRD pattern of PDSA and AMPDSA

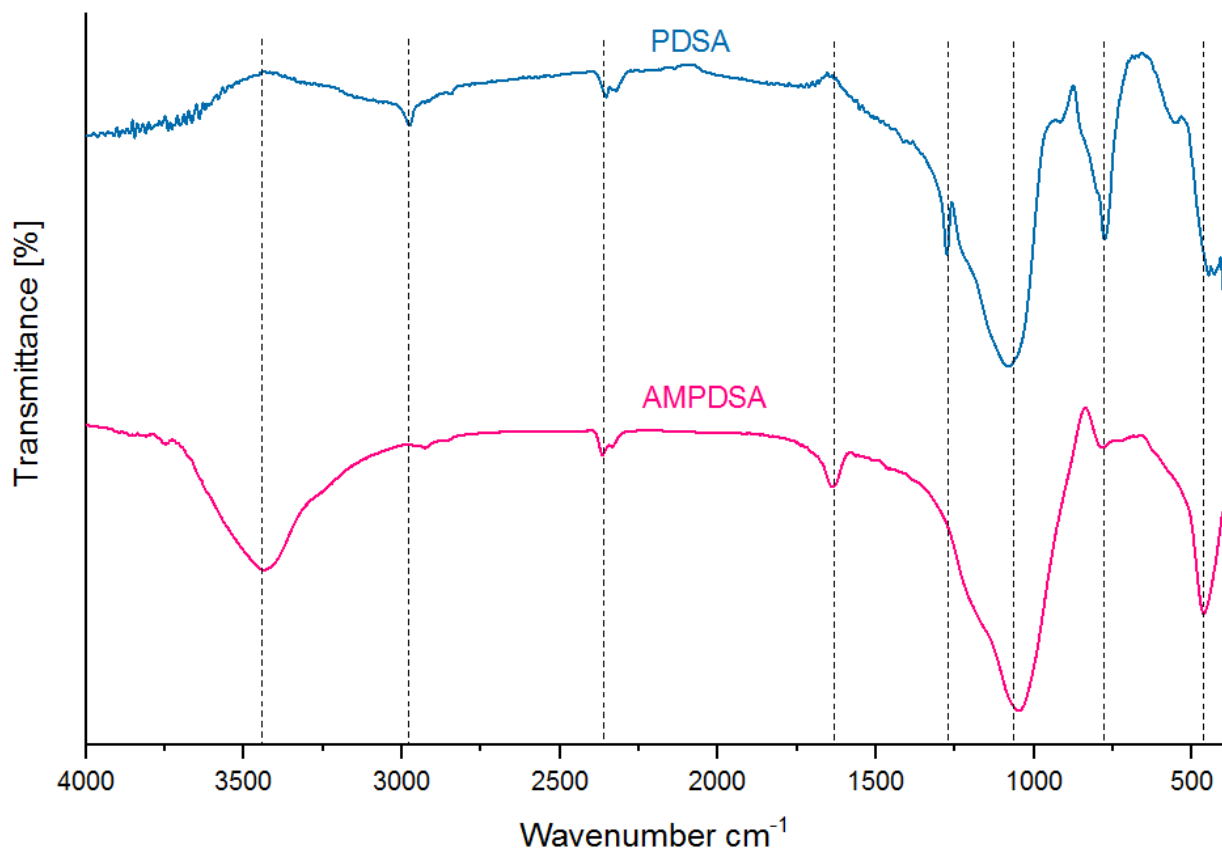
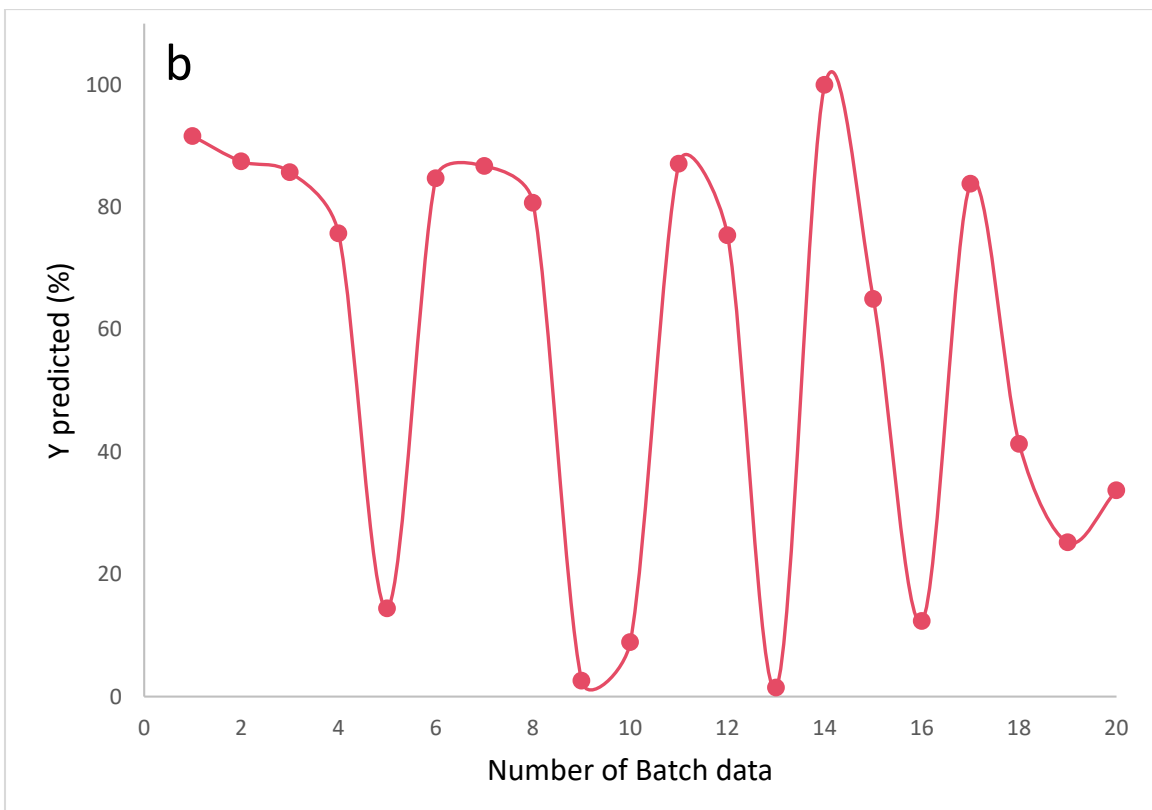
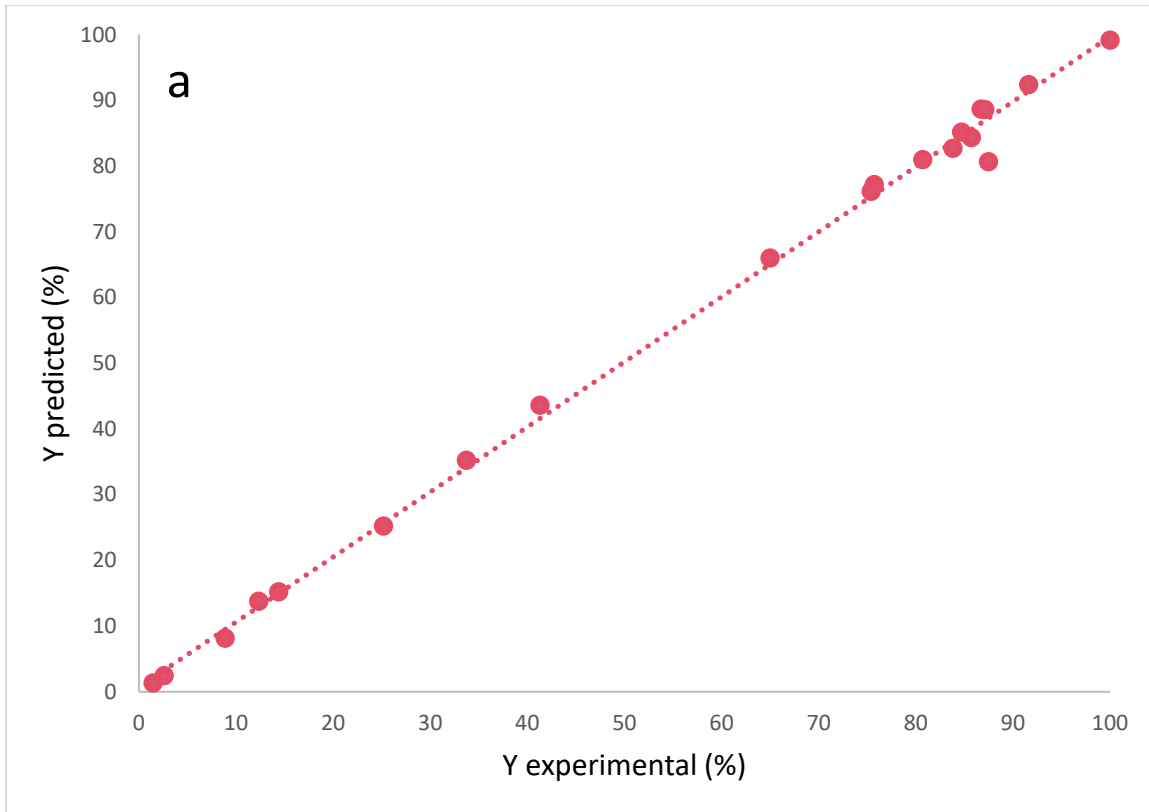


Fig. S3. FTIR spectra of PDSA and AMPDSA



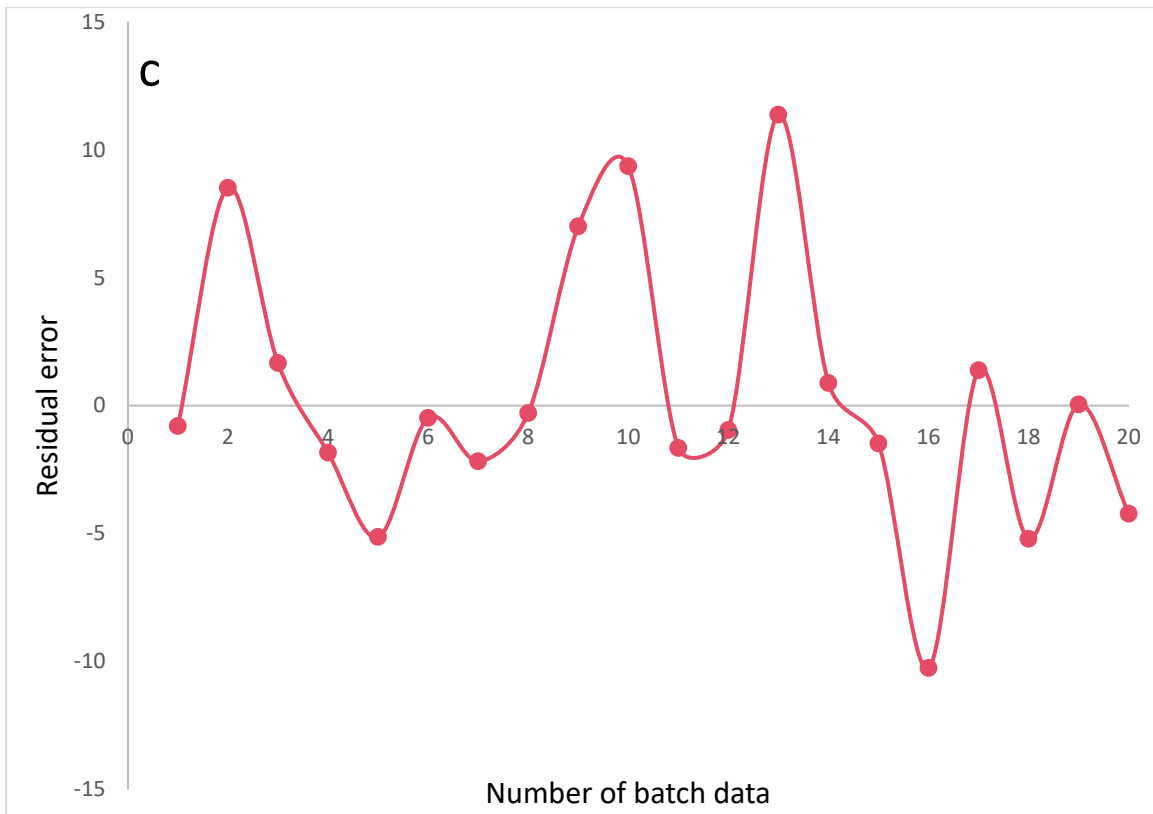


Fig. S4. Correlations between the predicted values and the batch experimental data (a), number of batch data with predicted values (b) and residual errors (c)