

**Table S1.** Analysis of variance (ANOVA) of the regression model from the PBD for medium components contribution to a) cell growth and b) maximum biosurfactant productivity

(a)					
Source	DF*	SS*	MS*	F-value	$\rho$ -value
Model	3	67.34	22.45	18.45	0.0003
A: KH <sub>2</sub> PO <sub>4</sub>	1	13.65	13.65	11.22	0.0085
E: Yeast extract	1	39.60	39.60	32.56	0.0003
G: Na-EDTA	1	14.08	14.08	11.58	0.0078
Residual	9	10.95	1.22		
Total	12	78.29			

Notes: DF, degrees of freedom; SS, sum of squares; MS, mean sum of squares.

S: 1.10, R<sup>2</sup>: 0.8602, R<sup>2</sup> (pred): 0.8135, R<sup>2</sup> (adj): 0.7004

(b)					
Source	DF*	SS*	MS*	F-value	$\rho$ -value
Model	3	0.099	0.033	18.67	0.0003
A: KH <sub>2</sub> PO <sub>4</sub>	1	0.027	0.027	15.50	0.0034
C: MgSO <sub>4</sub> .7H <sub>2</sub> O	1	0.049	0.049	27.94	0.0005
E: Yeast extract	1	0.023	0.023	13.01	0.0057
Residual	9	0.016	1.77×10 <sup>-3</sup>		
Total	12	0.11			

Notes: DF, degrees of freedom; SS, sum of squares; MS, mean sum of squares.

S: 0.042, R<sup>2</sup>: 0.8615, R<sup>2</sup> (pred): 0.8154, R<sup>2</sup> (adj): 0.7111

**Table S2.** Analysis of variance (ANOVA) of the regression model from the CCD for medium components contribution to a) cell growth and b) biosurfactant productivity in uncoded units

(a)					
Source	*DF	*SS	*MS	F-value	p-value
Block	2	0.45	0.23		
Model	9	98.91	10.99	29.94	0.0001
C: Yeast extract	1	2.13	2.13	5.82	0.0204
D: Sodium-EDTA	1	2.27	2.27	6.19	0.070
E: MgSO <sub>4</sub> .7H <sub>2</sub> O	1	5.15	5.15	14.02	0.0006
C*D: Yeast extract*Sodium-EDTA	1	1.71	1.71	4.66	0.0367
A <sup>2</sup> : PFAD*PFAD	1	16.75	16.75	45.63	0.0001
B <sup>2</sup> : KH <sub>2</sub> PO <sub>4</sub> *KH <sub>2</sub> PO <sub>4</sub>	1	5.70	5.70	15.52	0.0003
C <sup>2</sup> : Yeast extract*Yeast extract	1	44.70	44.70	121.78	0.0001
D <sup>2</sup> : Sodium-EDTA*Sodium-EDTA	1	7.44	7.44	20.27	0.0001
E <sup>2</sup> : MgSO <sub>4</sub> .7H <sub>2</sub> O* MgSO <sub>4</sub> .7H <sub>2</sub> O	1	32.06	32.06	87.34	0.0001
Residual	41	15.05	0.37		
Lack of Fit	33	12.86	0.39	1.43	0.3119
Pure Error	8	2.19	0.27		
Total	52	114.42			

Notes: DF, degrees of freedom; SS, sum of squares; MS, mean sum of squares

S: 0.61, R<sup>2</sup>: 0.8679, R<sup>2</sup> (pred): 0.7369, R<sup>2</sup> (adj): 0.8389

(b)					
Source	*DF	*SS	*MS	F-value	p-value
Block	2	2.58×10 <sup>-3</sup>	1.29×10 <sup>-3</sup>		
Model	9	0.40	0.045	19.39	0.0001
A: PFAD	1	0.039	0.039	16.92	0.0002
D: Sodium-EDTA	1	0.026	0.026	11.46	0.0016
E: MgSO <sub>4</sub> .7H <sub>2</sub> O	1	6.91×10 <sup>-3</sup>	6.91×10 <sup>-3</sup>	3.00	0.0905
A*B: PFAD*KH <sub>2</sub> PO <sub>4</sub>	1	9.61×10 <sup>-3</sup>	9.61×10 <sup>-3</sup>	4.18	0.0474
A <sup>2</sup> : PFAD*PFAD	1	0.025	0.12	50.79	0.0019
B <sup>2</sup> : KH <sub>2</sub> PO <sub>4</sub> * KH <sub>2</sub> PO <sub>4</sub>	1	0.11	0.025	11.06	0.0001
C <sup>2</sup> : Yeast extract*Yeast extract	1	0.019	0.11	48.80	0.0066
D <sup>2</sup> : Na-EDTA*Na-EDTA	1	0.12	0.019	8.19	0.0001
E <sup>2</sup> : MgSO <sub>4</sub> .7H <sub>2</sub> O* MgSO <sub>4</sub> .7H <sub>2</sub> O	1	0.40	0.12	51.14	0.0001
Residual	41	0.094	2.30×10 <sup>-3</sup>		
Lack of Fit	33	0.086	2.60×10 <sup>-3</sup>	2.44	0.0935
Pure Error	8	8.52×10 <sup>-3</sup>	1.07×10 <sup>-3</sup>		
Total	52	0.50			

Notes: DF, degrees of freedom; SS, sum of squares; MS, mean sum of squares

S: 0.048, R<sup>2</sup>: 0.8097, R<sup>2</sup> (pred): 0.6877, R<sup>2</sup> (adj): 0.7680