

**Table S1.**  $A$  (maximum OD<sub>595</sub>),  $\mu_m$  (maximum specific growth rate; h<sup>-1</sup>) and  $\lambda$  (lag time; h) values and error standard of the modified Gompertz model obtained from 3 independently growth curves of *Staphylococcus aureus* subsp. *aureus* USA300\_FPR3757 (SaWT) (A) and SaROEO at different concentrations of OEO. The goodness of the fit is shown by  $R^2$  and adjusted  $R^2$  values and the root mean square error ( $RMSE$ ).

### A) SaWT

OEO ( $\mu$ L/L)	Values			Standard error			Goodness of fit		
	$A$	$\mu_{max}$	$\lambda$	$A$	$\mu_{max}$	$\lambda$	$R^2$	Adj. $R^2$	$RMSE$
<b>0</b>	1.294	0.248	2.902	0.012	0.019	0.228	0.9841	0.9832	0.0550
<b>250</b>	1.276	0.238	6.468	0.014	0.015	0.215	0.9897	0.9891	0.0517
<b>500</b>	1.293	0.229	8.239	0.013	0.011	0.162	0.9942	0.9938	0.0407
<b>750</b>	1.324	0.181	11.410	0.030	0.008	0.170	0.9920	0.9916	0.0470
<b>1000</b>	1.262	0.183	15.000	0.032	0.006	0.099	0.9964	0.9961	0.0251
<b>1250</b>	1.185	0.161	17.430	0.038	0.008	0.149	0.9893	0.9887	0.0295

### B) SaROEO

OEO ( $\mu$ L/L)	Values			Standard error			Goodness of fit		
	$A$	$\mu_{max}$	$\lambda$	$A$	$\mu_{max}$	$\lambda$	$R^2$	Adj. $R^2$	$RMSE$
<b>0</b>	1.268	0.254	3.319	0.010	0.018	0.191	0.9888	0.9881	0.0465
<b>250</b>	1.287	0.217	4.776	0.013	0.014	0.215	0.9895	0.9889	0.0494
<b>500</b>	1.295	0.218	6.311	0.019	0.015	0.251	0.9871	0.9863	0.0576
<b>750</b>	1.271	0.244	6.876	0.018	0.021	0.271	0.9835	0.9825	0.0660
<b>1000</b>	1.280	0.2518	7.884	0.018	0.020	0.243	0.9862	0.9854	0.0614
<b>1250</b>	1.280	0.240	7.761	0.017	0.017	0.226	0.9888	0.9881	0.0555
<b>1500</b>	1.272	0.210	8.062	0.019	0.014	0.237	0.9882	0.9875	0.0564
<b>1750</b>	1.254	0.237	8.447	0.019	0.019	0.236	0.9858	0.9850	0.0622
<b>2000</b>	1.246	0.244	8.563	0.018	0.019	0.225	0.9850	0.9842	0.0636
<b>2500</b>	1.212	0.250	9.482	0.023	0.019	0.240	0.9848	0.9839	0.0624
<b>3000</b>	1.198	0.227	9.516	0.019	0.017	0.204	0.9868	0.9860	0.0581
<b>4000</b>	1.112	0.208	10.300	0.020	0.015	0.196	0.9893	0.9887	0.0485
<b>5000</b>	1.052	0.193	10.850	0.014	0.010	0.139	0.9953	0.9950	0.0316

**Table S2.** Primers used for PCR amplification and Sanger sequencing to verify the mutations in SaROEO.

SaROEO mutations	Forward primer (5' → 3')	Reverse primer (5' → 3')
SAUSA300_RS03770	ATCGCATGGGATGATGCTT	TGGGCTACAACTCATATTGCTT
SAUSA300_RS05495	GCACCGACTAGTACCGCATT	GTACAGCCCCCTCAAGCATT
<i>hepT</i>	AAATCACTTCCGACCGGCTT	CGTAGTTTACAGGGGGCGT
<i>accA</i>	ACCGCCAAGTGGTTCAGAAA	TTGCGCGTTGCAAGAAAGA