Parameter	Unit	Value	Source
α	μM	3.00×10^{6}	Ref. 1
$k_{e,1}$	$1/h$	1.20×10^{3}	
$k_{e,2}$	$1/h$	7.56×10^{4}	Ref. 1
$m_{e,1}$		325	Ref. 2
$m_{e,2}$		11738	Ref. 3
$K_{m,s}$	μM	1.00×10^{2}	
$K_{m,m}$	μM	2.00×10^{1}	Ref. 1
$K_{i,r}$	μM	6.00×10^{1}	
k_r	$1/h$	3.60×10^{3}	Ref. 1
d_r	$1/h$	1.26×10^{2}	Ref. 1
Y_m	$1/\mu M$	3.33×10^{-7}	
M_e	μM	0.00	
$K_{i,a}$	μM	1.00	

Supplementary Table 4: Parameter values used in the simulation of the single-strain model. Note that these values are specific to *E. coli*. The value of $m_{e,2}$ was calculated by multiplying the literature value (7336 amino acids in ribosomal proteins) by a factor of 1.6 to account for tRNA-affiliated proteins. The yield coefficient of amino acid is the inverse of the total amino acid concentration of an *Escherichia coli* cell, i.e., $Y_m = 1/\alpha$. By choosing $M_e = 0$, we assume that the metabolite released to the environment does not accumulate and can be quickly metabolized by other cell types.

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