

Additional File 3. Parameters used for the simulations

Parameter name	Parameter value	Description	Units
ba, br, bd	0.36	transcription rate	min ⁻¹
α	20	coefficient of active promoter	
k_{-a}, k_r	1.8	protein–promoter unbinding rate	min ⁻¹
t_a, t_r, t_d	90	translation rate	min ⁻¹
d_a, d_r, d_d	0.54	mRNA degradation rate	min ⁻¹
k_{fa}, k_{fr}, k_{fd}	0.9	folding rate	min ⁻¹
k_{da}, k_{dr}, k_t	0.018	multimerization rate	min ⁻¹ molecules ⁻¹
k_{-da}, k_{-dr}, k_t	0.00018	multimer dissociation rate	min ⁻¹
k_l	0.36	loop forming rate	min ⁻¹
k_{ul}	0.18	loop dissociation rate	min ⁻¹
γ	1080	maximum degradation rate	molecules · min ⁻¹
c_e	0.1	dissociation constant	molecules
λ	2.5	coefficient of degradation rate	
ε	0.2	coefficient of degradation rate	
N_a	50	copy number of activator gene	
N_r	25	copy number of repressor gene	
N_d	50	copy number of downstream gene	
C_r^{max}	0.2	maximum affinity of LacI for the promoter	molecules ⁻¹
C_r^{min}	0.01	minimum affinity of LacI for the promoter	molecules ⁻¹

[IPTG]	0–10	IPTG concentration	mM
k_{r1}	0.035	correction constant of IPTG	mM
b_1	2	Hill coefficient of inhibition by LacI	
C_a^{max}	1	maximum affinity of AraC for the promoter	molecules ⁻¹
C_a^{min}	0	minimum affinity of AraC for the promoter	molecules ⁻¹
[ara]	0–2	arabinose concentration	% (w/v)
k_{a1}	2.5	correction constant of arabinose	% (w/v)
c_1	2	Hill coefficient of activation by AraC	
b_2	2	Hill coefficient of inhibition by LacI	
