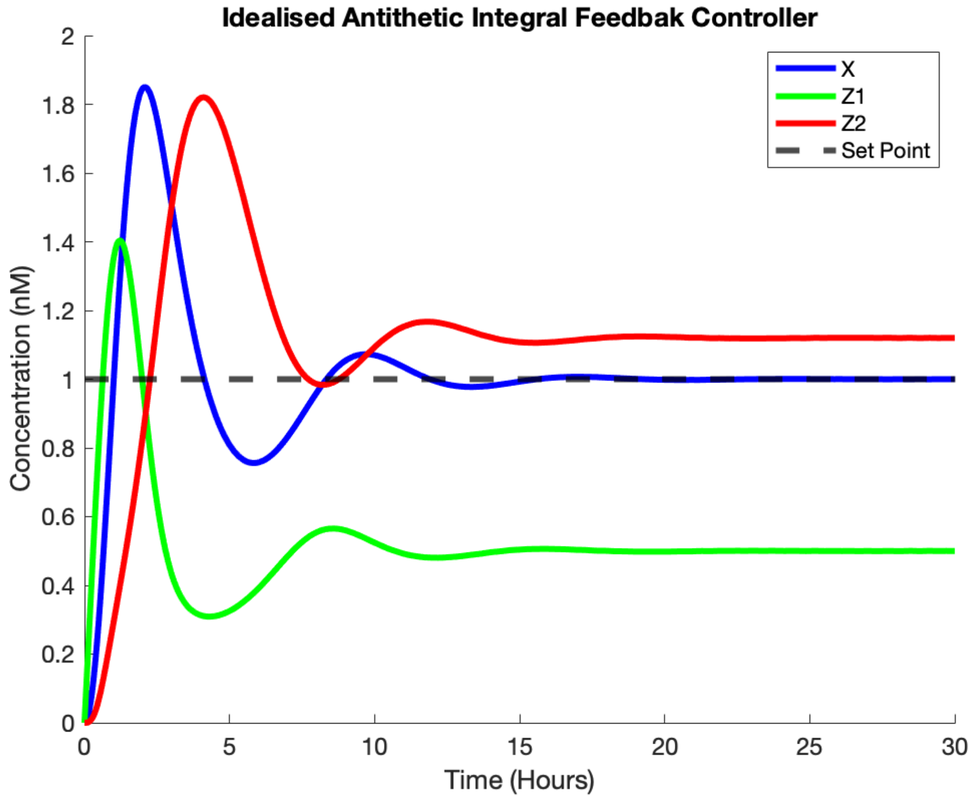
Antithetic

$$\frac{dZ_1}{dt} = \mu - \eta Z_1 Z_2 - \delta Z_1$$

$$\frac{dZ_2}{dt} = \theta X - \eta Z_1 Z_2 - \delta Z_2$$

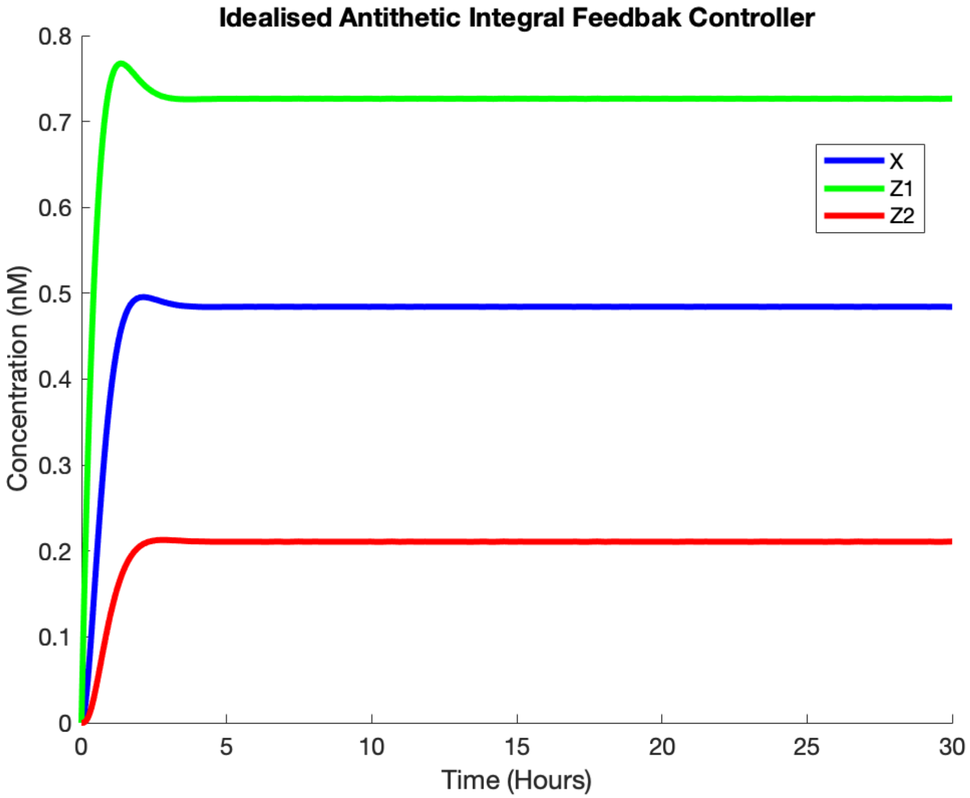
$$\frac{dX}{dt} = \mathrm{k} Z_1 - (\gamma + \delta) X$$

$$\text{setpoint} = \frac{\mu}{\theta}$$



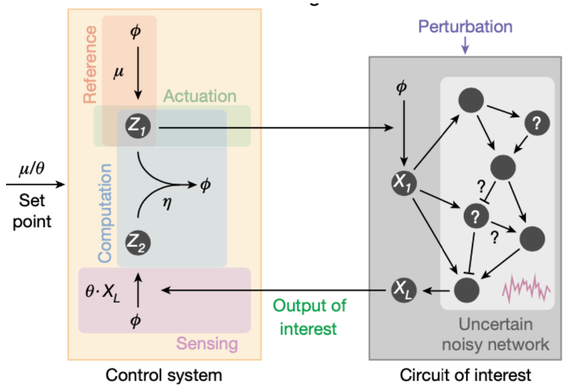
$\mu = 0.028$ nMmin^{-1}; $\eta = 0.05$ nM^{-1}min^{-1}; $\theta = 0.028$ min^{-1}

k $= 0.028$ min^{-1}; $\gamma = 0.014$ min^{-1}; $\delta = 0$ min^{-1}



$\mu = 0.028$ nMmin^{-1}; $\eta = 0.05$ nM^{-1}min^{-1}; $\theta = 0.028$ min^{-1}

k $= 0.028$ min^{-1}; $\gamma = 0.014$ min^{-1}; $\delta = 0.028$ min^{-1}



Antithetic with Damping

$$\frac{dZ_1}{dt} = \mu - \eta Z_1 Z_2 - \delta Z_1$$

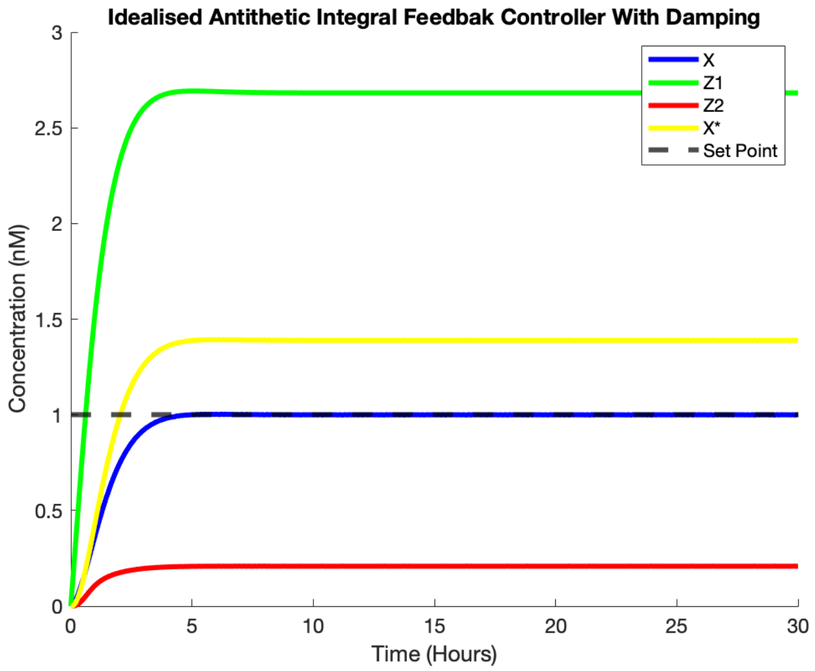
$$\frac{dZ_2}{dt} = \theta X - \eta Z_1 Z_2 - \delta Z_2$$

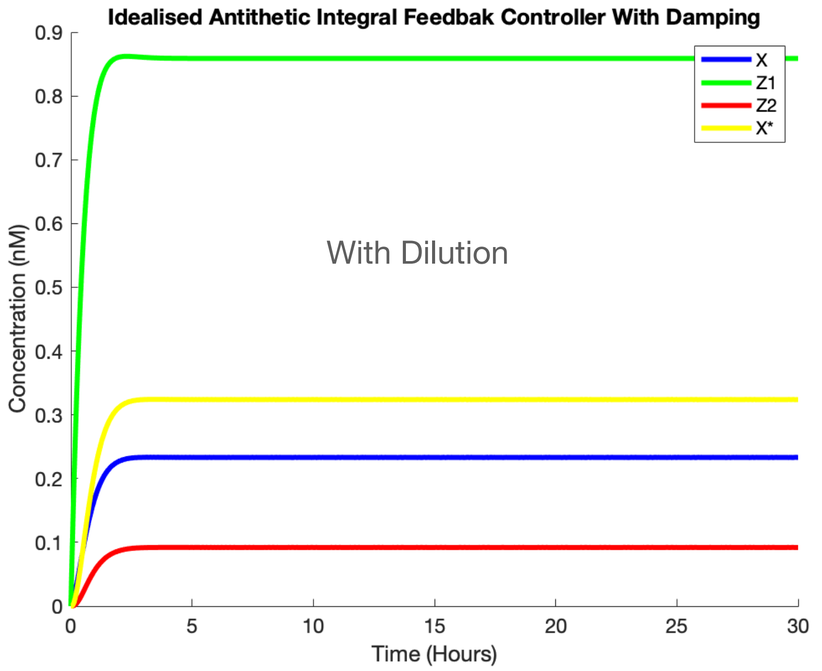
$$\frac{dX}{dt} = \mathrm{k} Z_1 - (\gamma + \delta) X - \alpha_1 X + \alpha_2 X^*$$

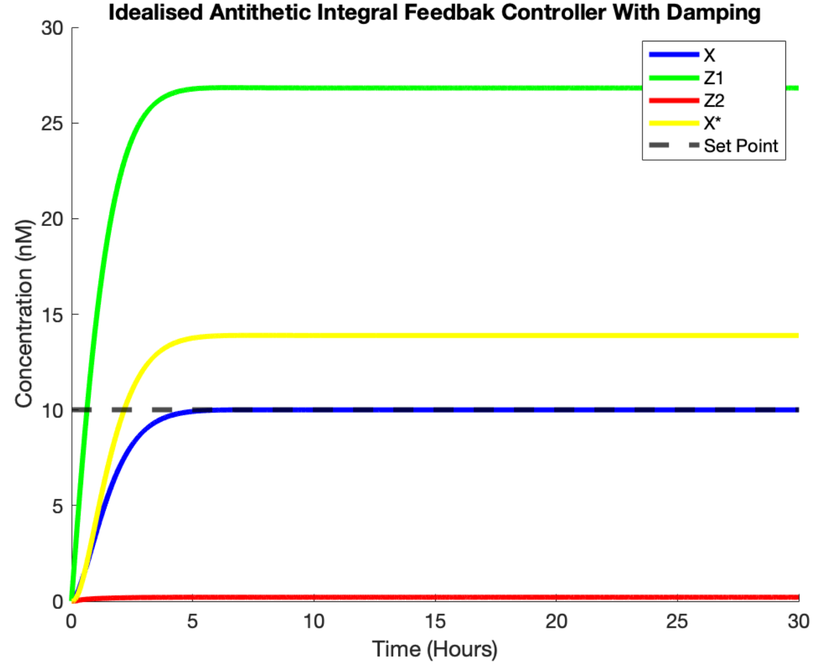
$$\frac{dX^*}{dt} = \alpha_1 X - \alpha_2 X^* - \gamma_* X^*$$

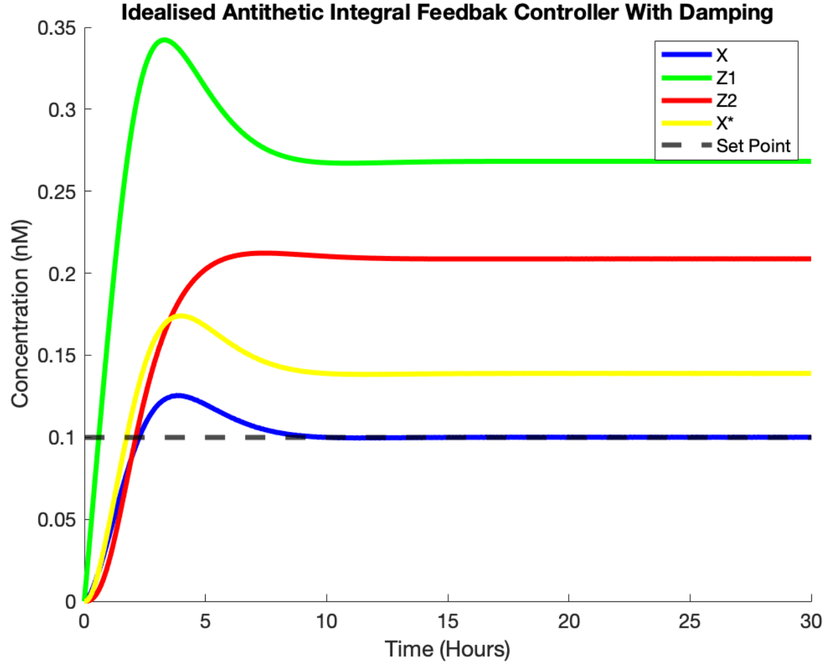
$$\text{setpoint} = \frac{\mu}{\theta}$$

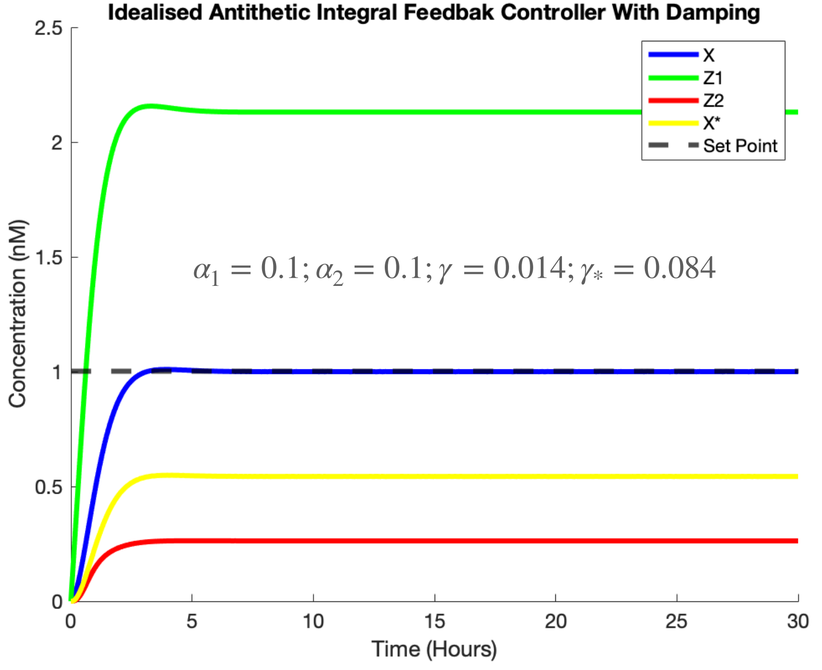
$$\alpha_1 = 0.2; \alpha_2 = 0.1; \gamma = 0.014; \gamma_* = 0.044$$



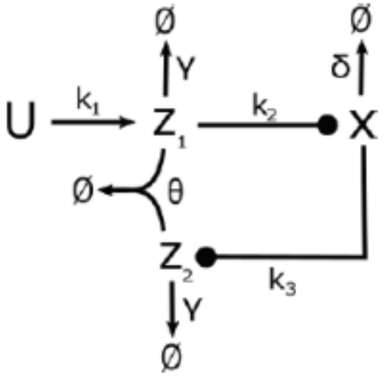








Antithetic sRNA Implementation



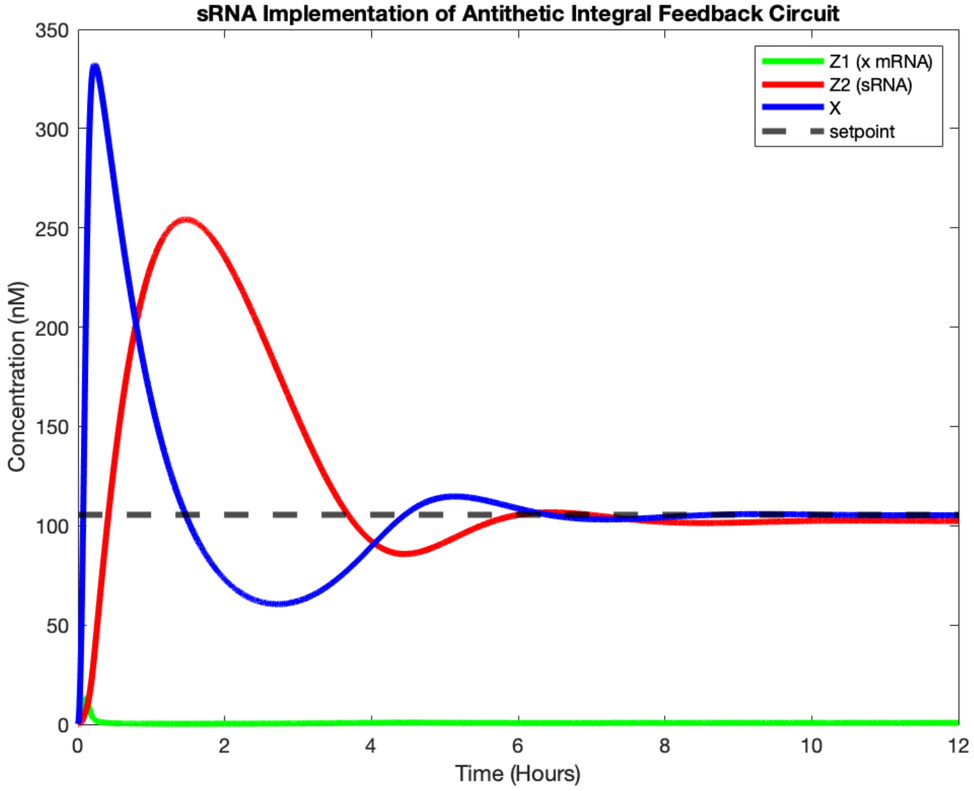
$$\frac{dZ_1}{dt} = \tau_1 + \frac{k_1 U}{K_U + U} - \gamma_m Z_1 - \theta Z_1 Z_2$$

$$\frac{dZ_2}{dt} = \tau_2 + \frac{k_3 X}{K_X + X} - \gamma_s Z_2 - \theta Z_1 Z_2$$

$$\frac{dX}{dt} = \tau_3 C + k_2 Z_1 - \delta X$$

$$\frac{dC}{dt} = \theta Z_1 Z_2 - \delta_C C$$

Without Dilution/Degradation



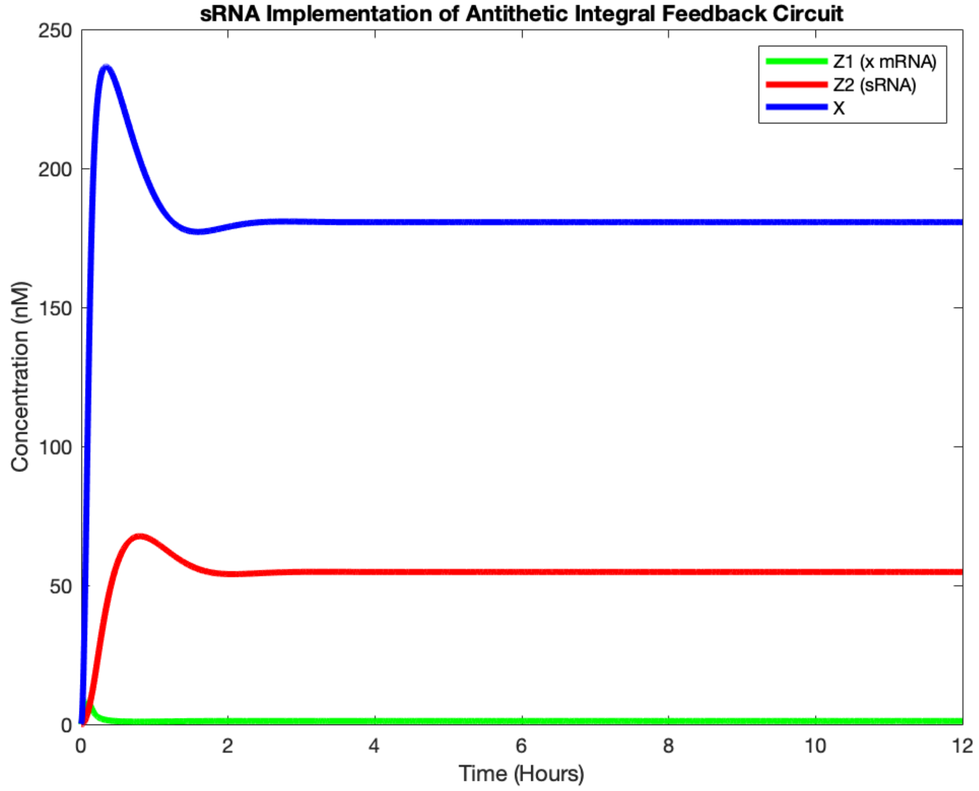
$$\tau_1 = 0; \tau_2 = 0; \tau_3 = 0; \gamma_m = 0; \gamma_s = 0$$

$$k_1 = 0.1 \text{ nMs}^{-1}; k_2 = 0.06 \text{ s}^{-1}; k_3 = 1.5 \text{ nMs}^{-1}$$

$$\theta = 0.05 \text{ nM}^{-1}\text{s}^{-1}; \delta = 0.00039 \text{ s}^{-1}; \delta_C = 0.0041 \text{ s}^{-1}$$

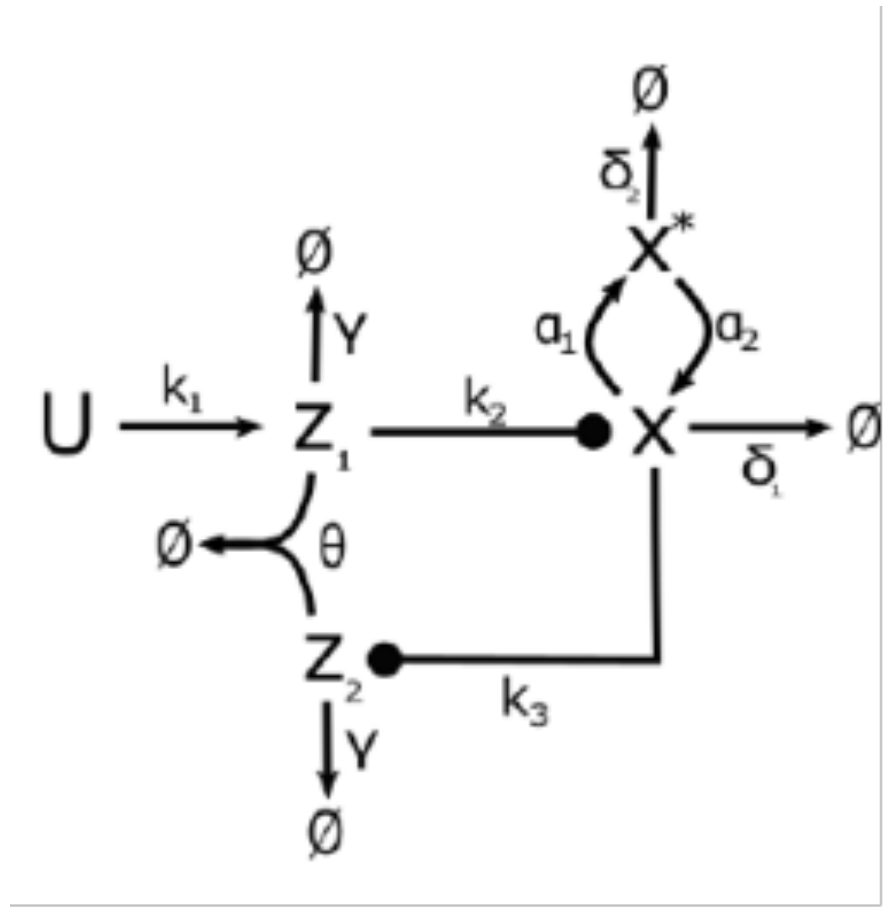
$$K_U = 178000 \text{ nM}; K_X = 2600 \text{ nM}$$

With Dilution/Degradation



$$\gamma_m = 0.0041 \text{ s}^{-1}; \gamma_s = 0.0008 \text{ s}^{-1}$$

Antithetic sRNA Implementation with Damping



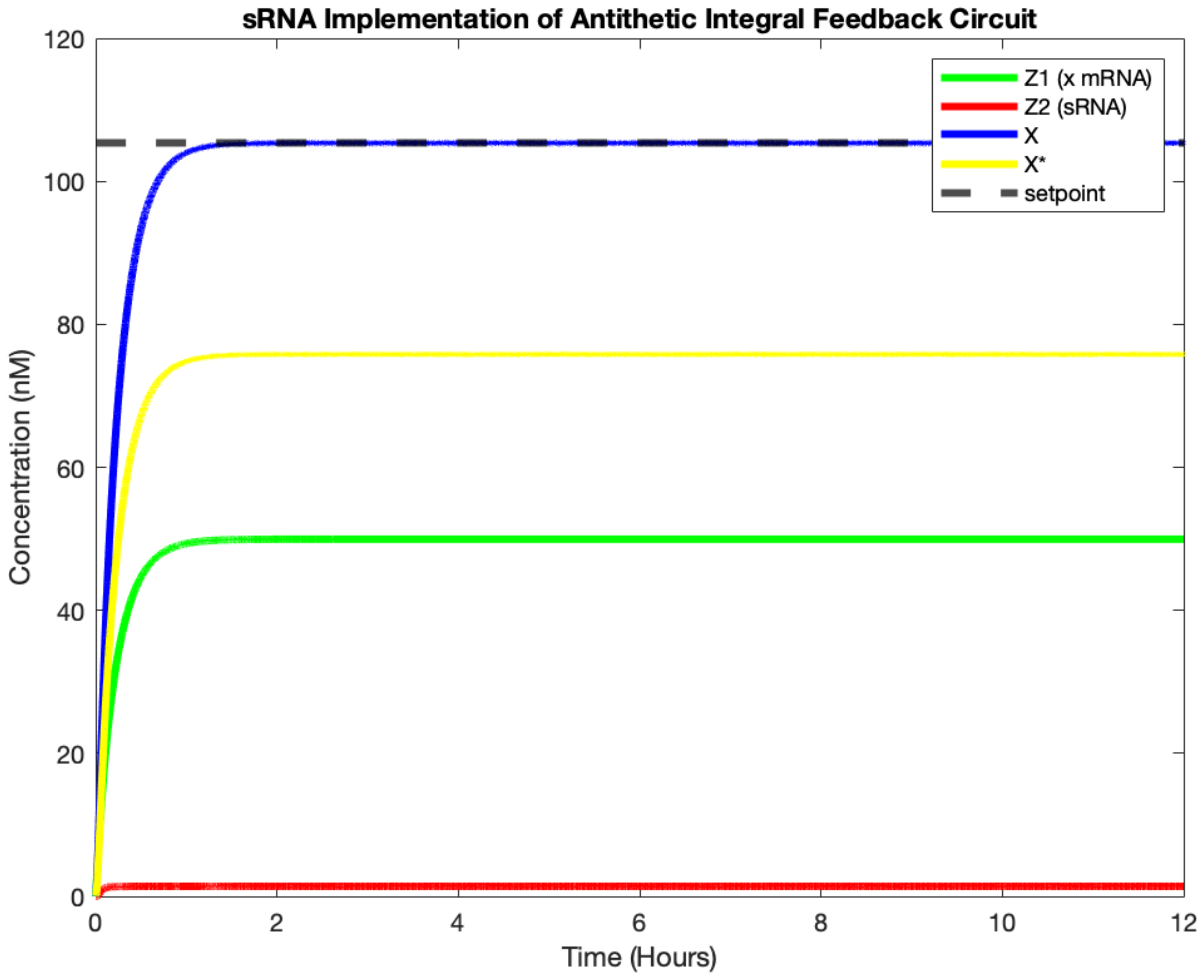
$$\frac{dZ_1}{dt} = \tau_1 + \frac{k_1 U}{K_U + U} - \gamma_m Z_1 - \theta Z_1 Z_2$$

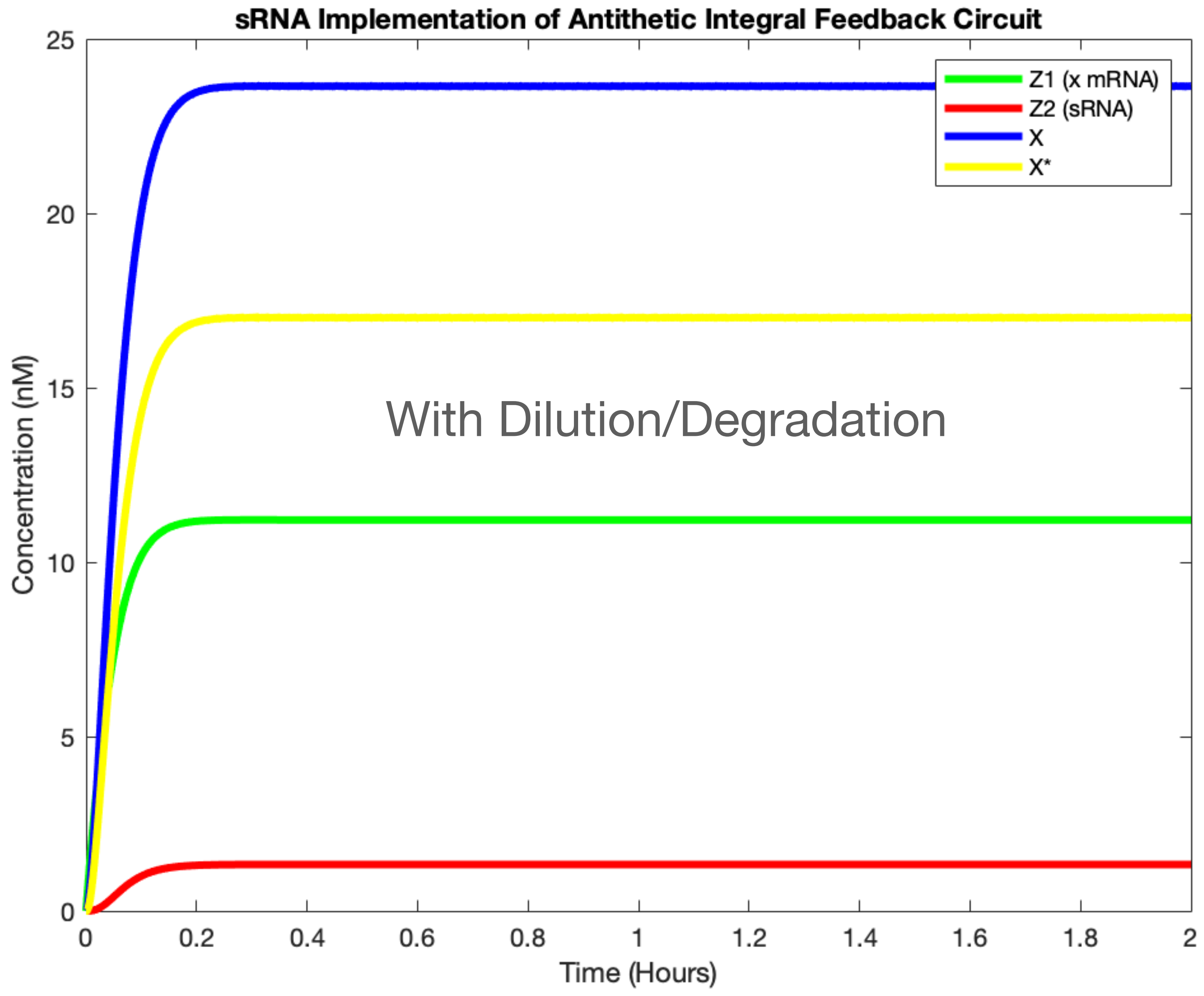
$$\frac{dZ_2}{dt} = \tau_2 + \frac{k_3 X}{K_X + X} - \gamma_s Z_2 - \theta Z_1 Z_2$$

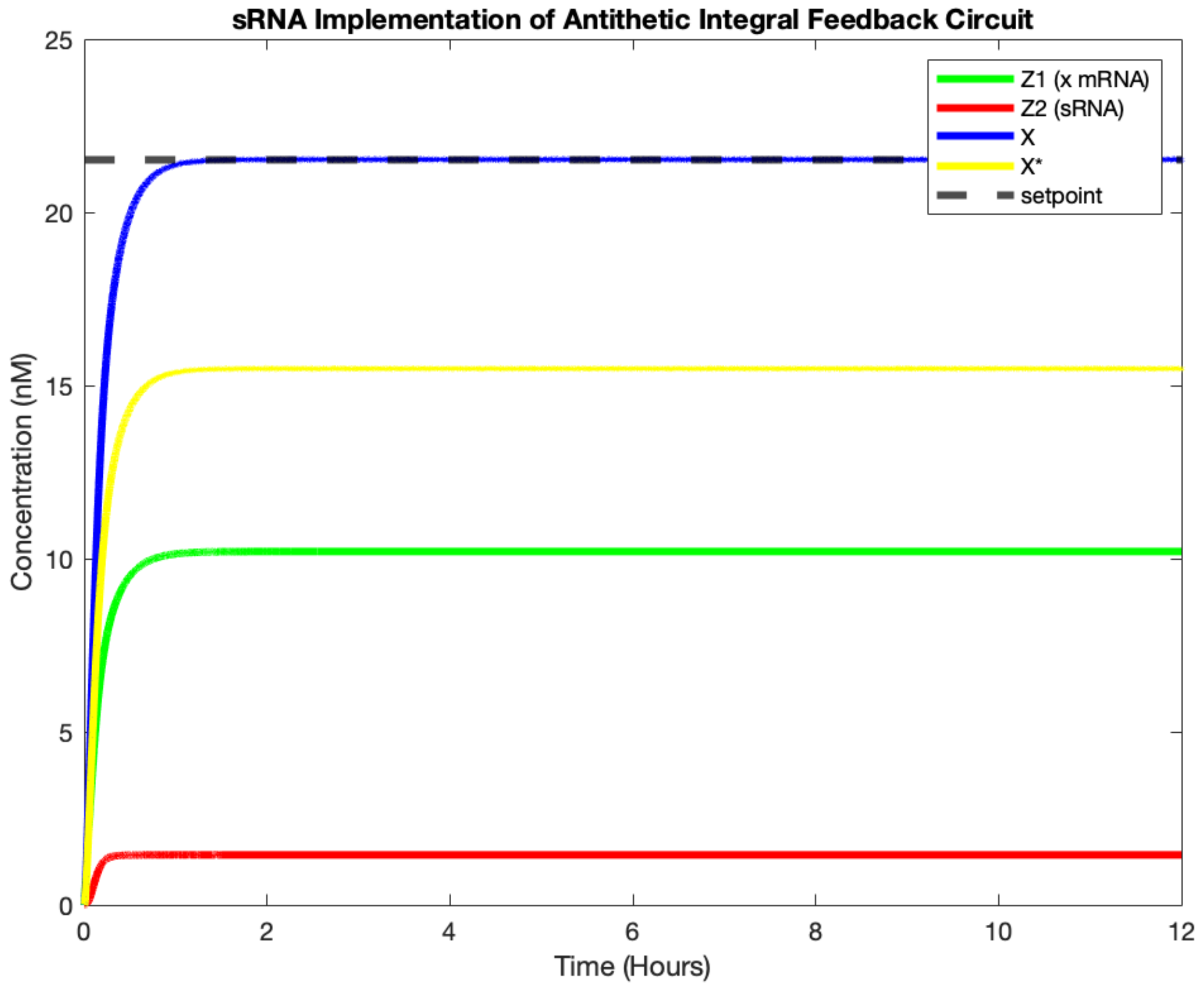
$$\frac{dX}{dt} = \tau_3 C + k_2 Z_1 - \delta X - \alpha_1 X + \alpha_2 X^*$$

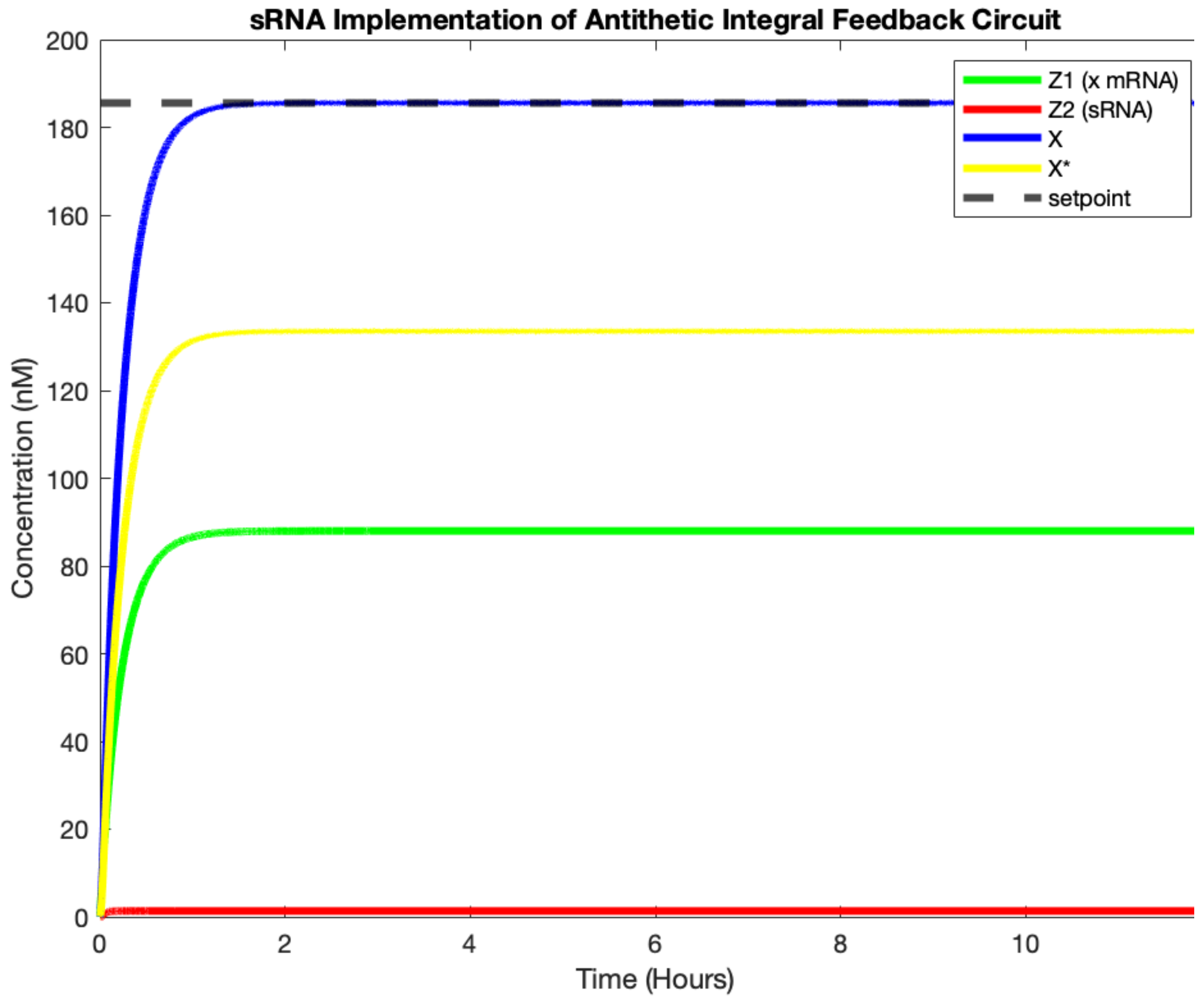
$$\frac{dC}{dt} = \theta Z_1 Z_2 - \delta_C C$$

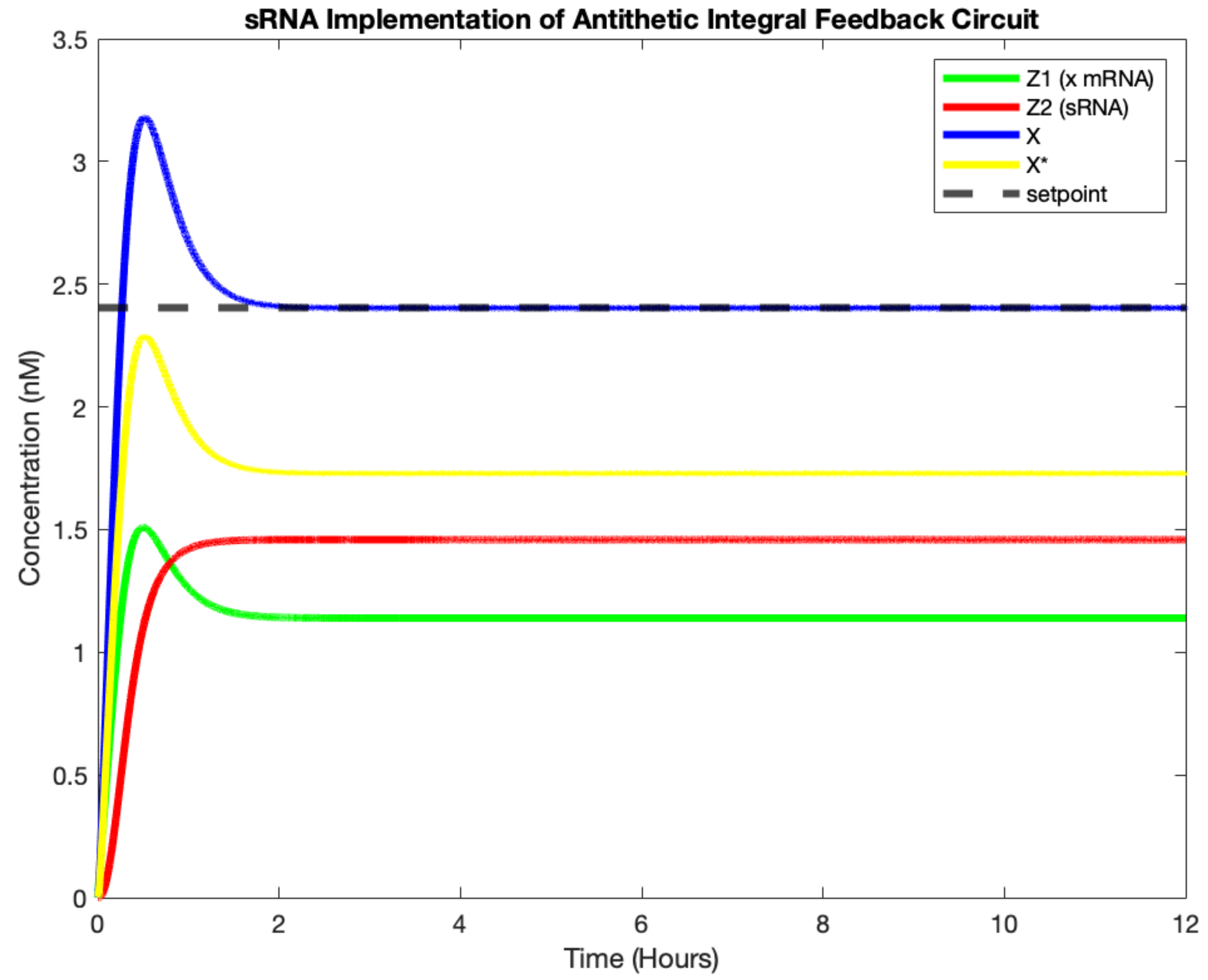
$$\frac{dX^*}{dt} = \alpha_1 X - \alpha_2 X^* - \delta_* X^*$$











Can tune this to make it work by increasing alpha 1 but always stops working at some point and leads to more X* than X in the system

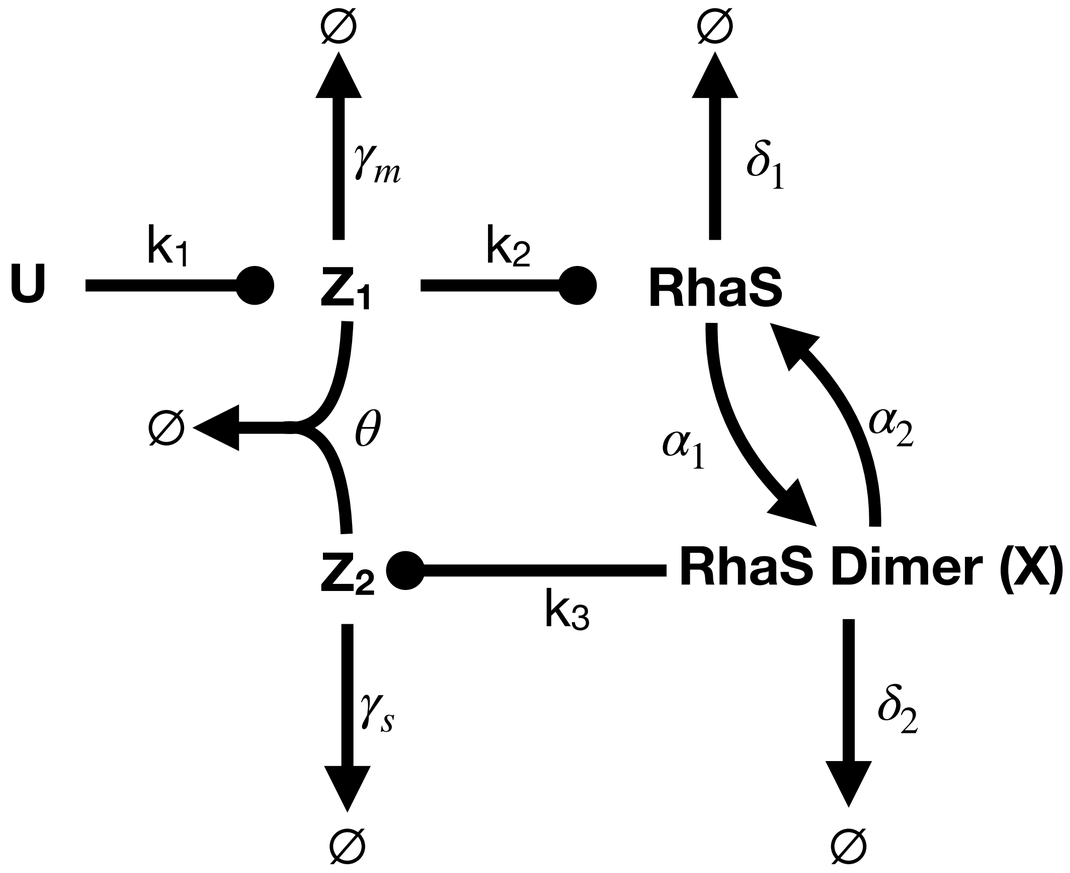
$\alpha_1 = 0.1\ \mathrm{s}^{-1}; \alpha_2 = 0.1\ \mathrm{s}^{-1}; \delta = 0.00039\ \mathrm{s}^{-1}; \delta_* = 0.039\ \mathrm{s}^{-1}$

sRNA RhaS PI Controller

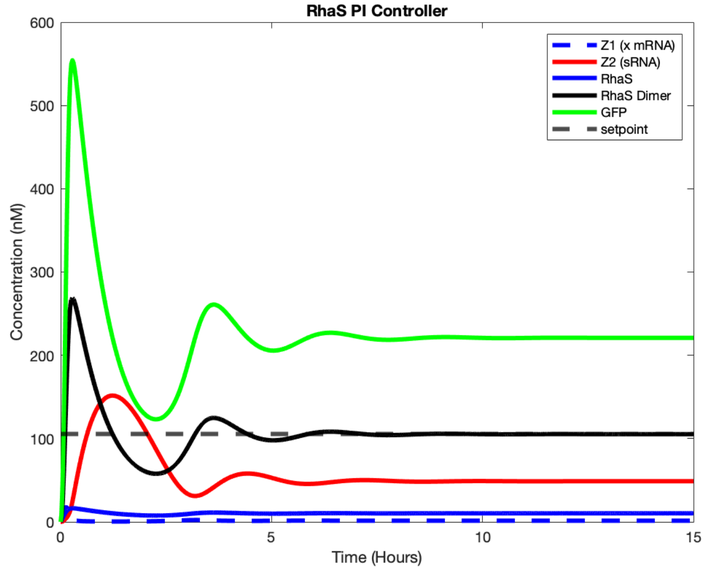
$$\frac{dZ_1}{dt} = \frac{k_1 U}{K_U + U} - \gamma_m Z_1 - \theta Z_1 Z_2 \qquad \frac{dZ_2}{dt} = \frac{k_3 X}{K_X + X} - \gamma_s Z_2 - \theta Z_1 Z_2$$

$$\frac{d\text{RhaS}}{dt} = k_2 Z_1 - \delta_1 \text{RhaS} - 2\alpha_1 \text{RhaS}^2 + 2\alpha_2 X$$

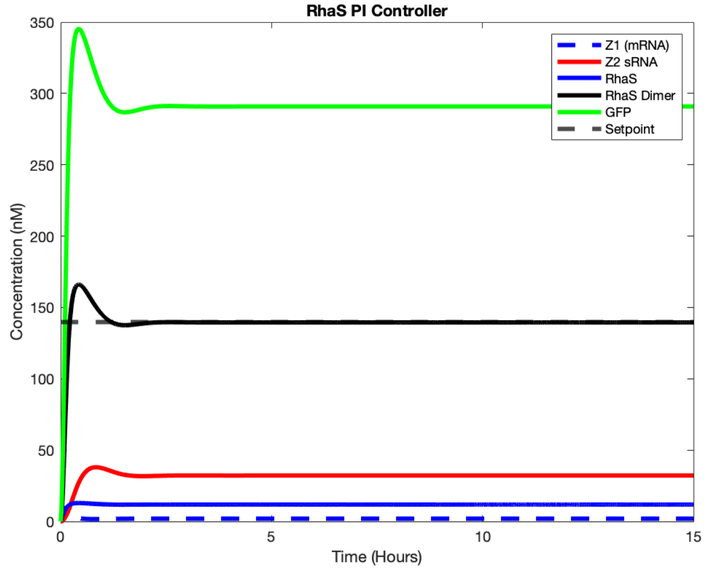
$$\frac{dX}{dt} = \alpha_1 \text{RhaS}^2 - \alpha_2 X - \delta_2 X$$



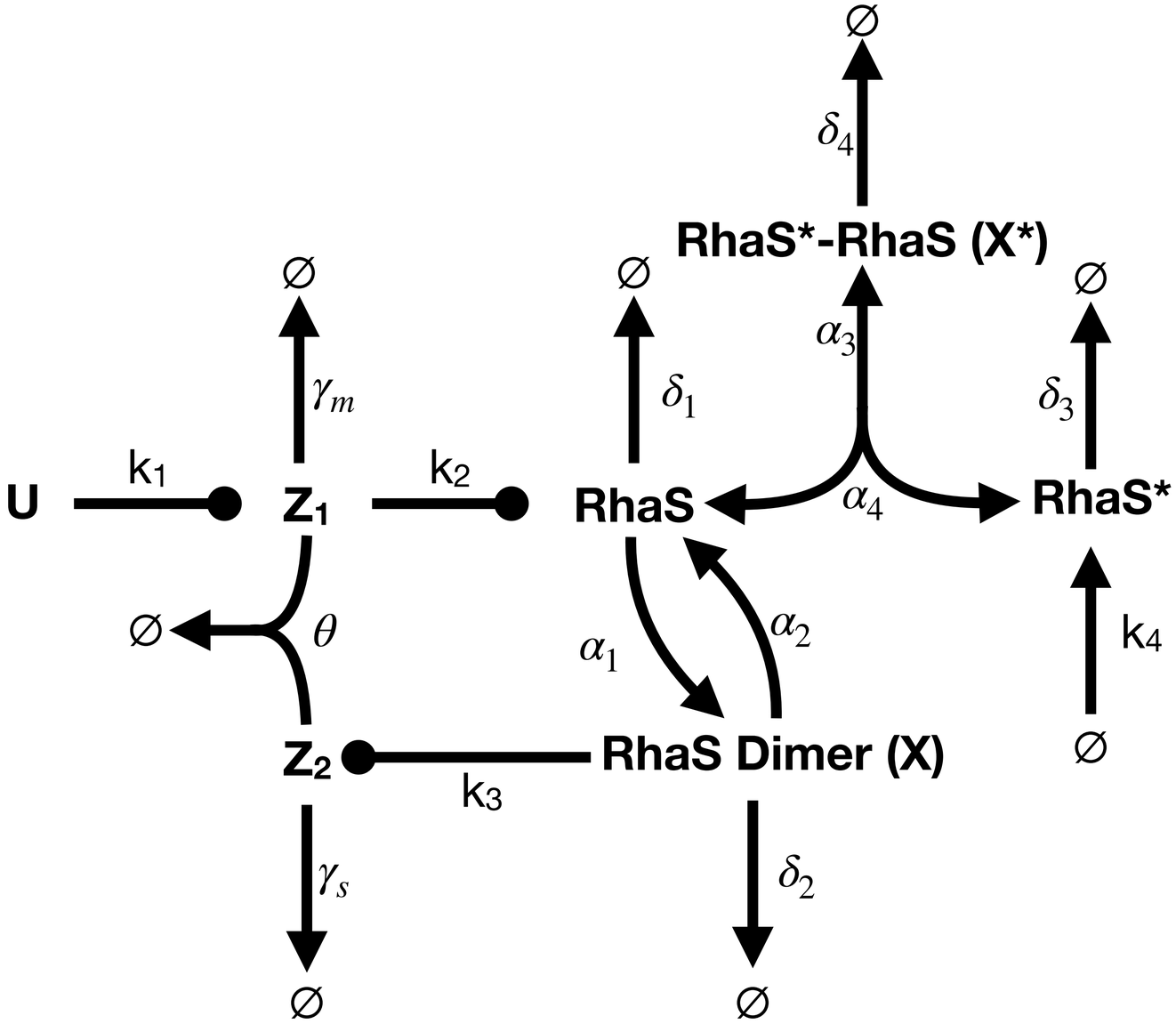
No Dilution/ degradation of Z1 and Z2



Dilution/degradation of Z1 and Z2



sRNA RhaS PID Controller



$$\frac{dZ_1}{dt} = \frac{k_1 U}{K_U + U} - \gamma_m Z_1 - \theta Z_1 Z_2$$

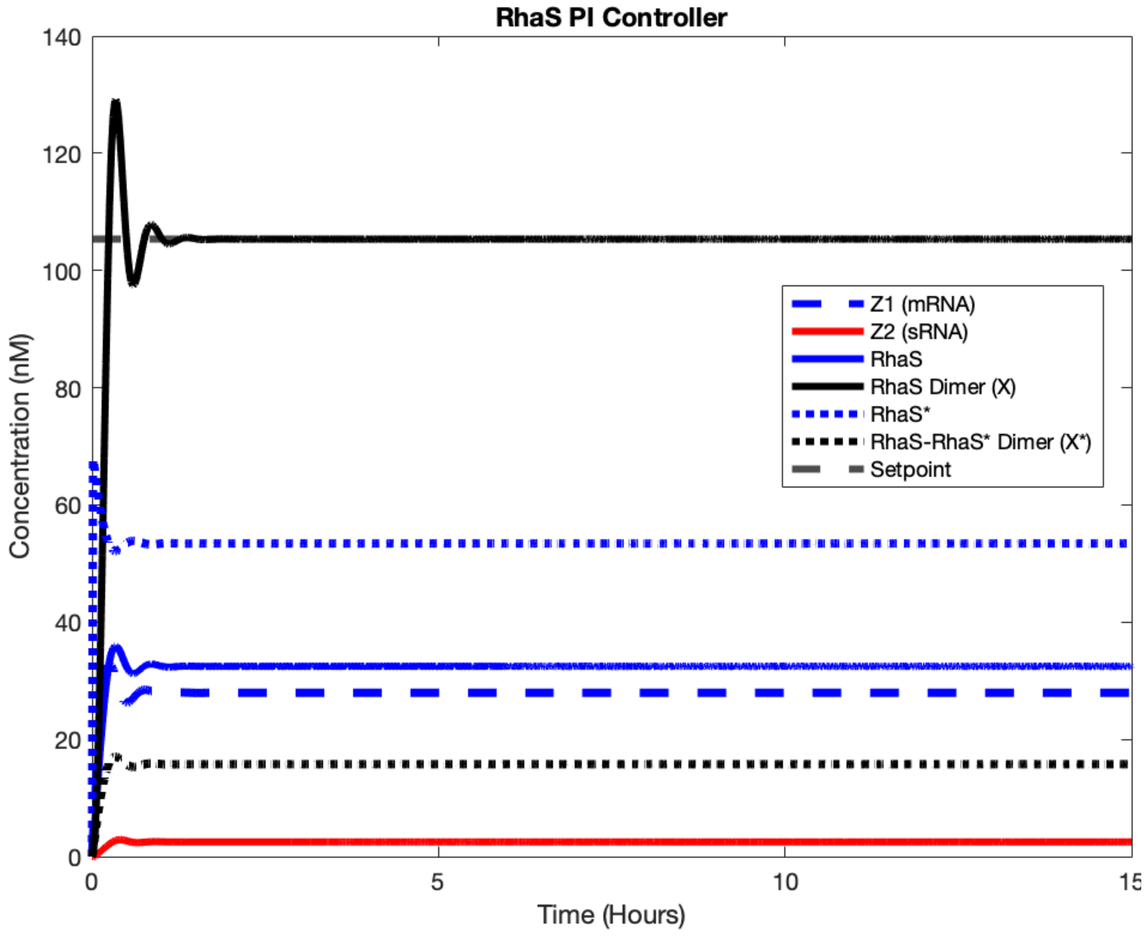
$$\frac{dZ_2}{dt} = \frac{k_3 X}{K_X + X} - \gamma_s Z_2 - \theta Z_1 Z_2$$

$$\frac{d\text{RhaS}}{dt} = k_2 Z_1 - \delta_1 \text{RhaS} - 2\alpha_1 \text{RhaS}^2 + 2\alpha_2 X - \alpha_3 \text{RhaS}\ \text{RhaS}^* + \alpha_4 X^* + \text{deg} X^*$$

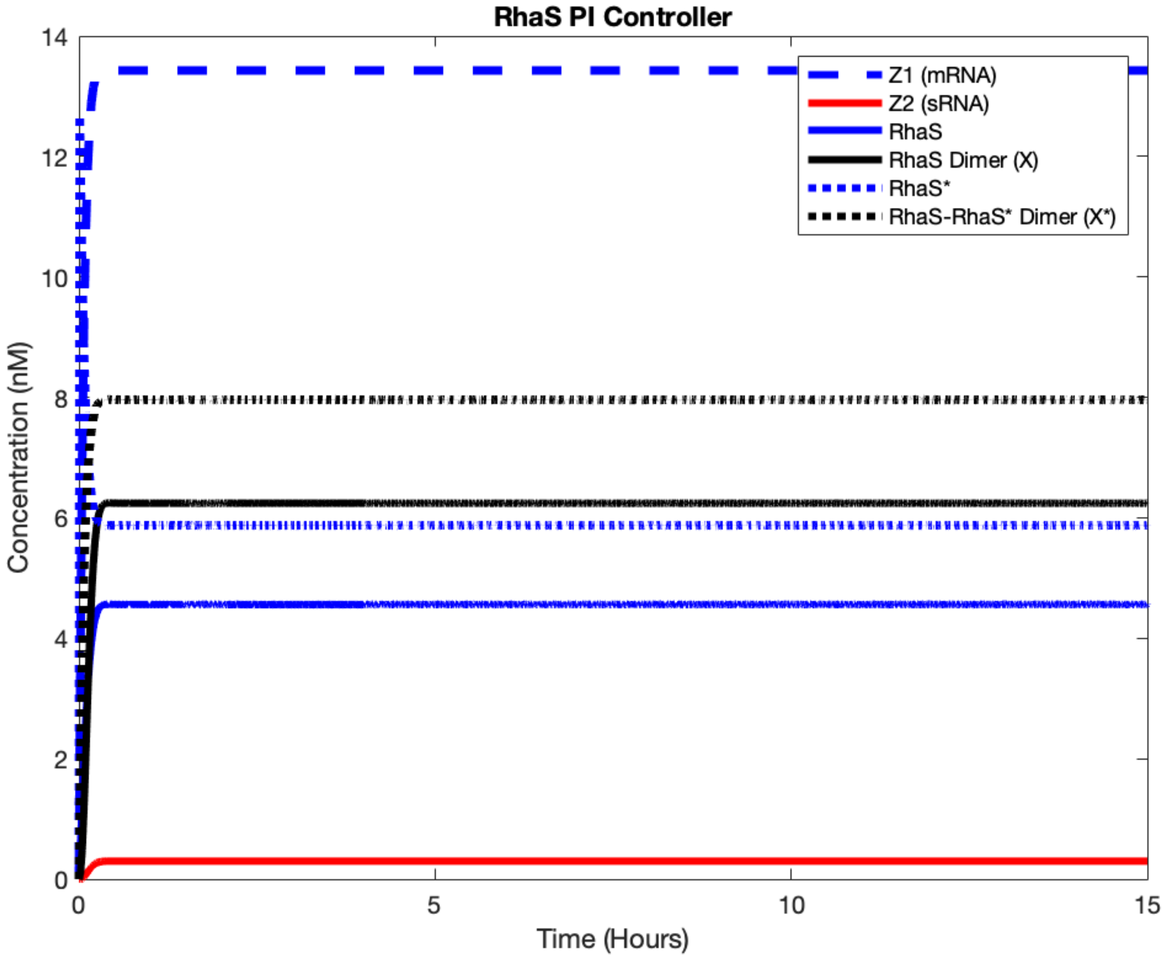
$$\frac{d\text{RhaS}^*}{dt} = k_4 - \delta_3 \text{RhaS}^* - \alpha_3 \text{RhaS}\ \text{RhaS}^* + \alpha_4 X^*$$

$$\frac{dX}{dt} = \alpha_1 \text{RhaS}^2 - \alpha_2 X - \delta_2 X$$

$$\frac{dX^*}{dt} = \alpha_3 \text{RhaS}\ \text{RhaS}^* - \alpha_4 X^* - \delta_4 X^*$$

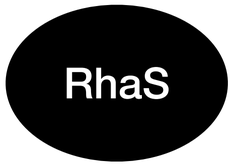


Gammas = 0
Closest I got



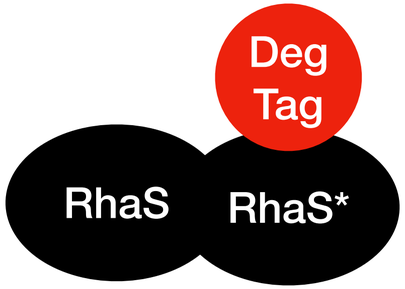
Gammas non 0

Still a bit confused as to how degradation of the mixed dimer would work



Degraded at dilution rate

Degraded at dilution rate
+ deg tag rate



Degraded at dilution rate
+ deg tag rate ?

At half deg tag rate because you're degrading more protein?

Are both parts degraded or is RhaS released?

Changed the model so some RhaS is released on degradation of the dimer

Ciaran suggested a Possible solution to the GFP problem if it is a problem is to have a TF being controlled by Z2 that produces the RhaS mRNA
And then have the buffering act upon that transcription factor rather than the output