

Figure S1: Effect of changing inhibition parameters $km1$ and $km2$ on time course profiles for CycA (Fig S1a), CycB (Fig S1b) and CycE (FigS1c). In all the three figures $km2=0.01$ (red line), $km2=0.1$ (green line), $km2=1$ (blue line) and $km2=10$ (black line).

Fig S1a

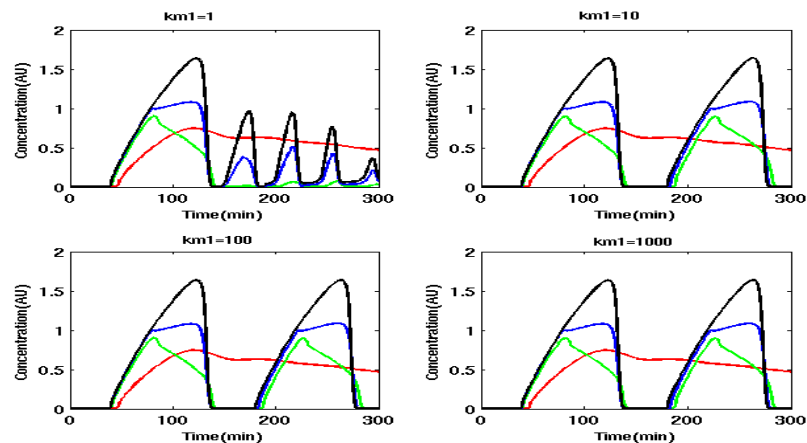


Fig S1b

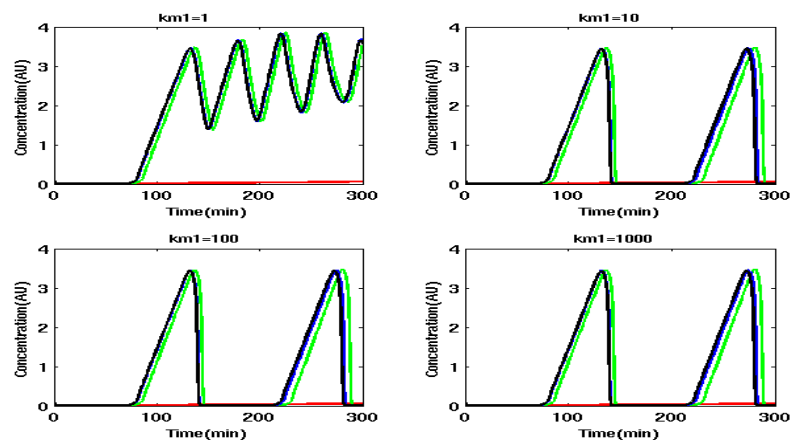


Fig S1c

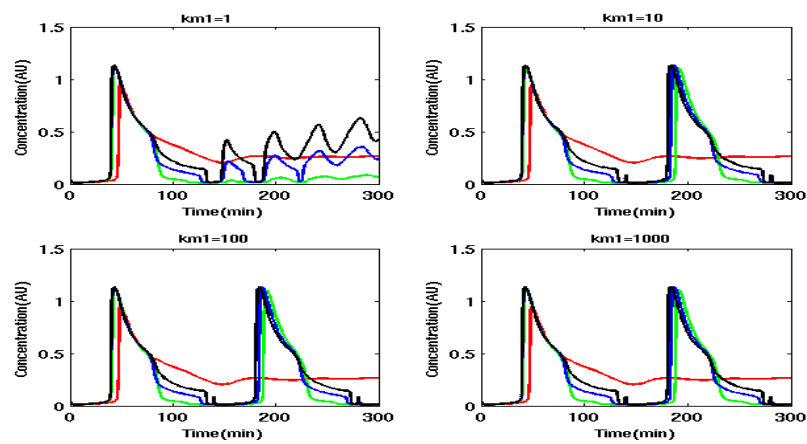
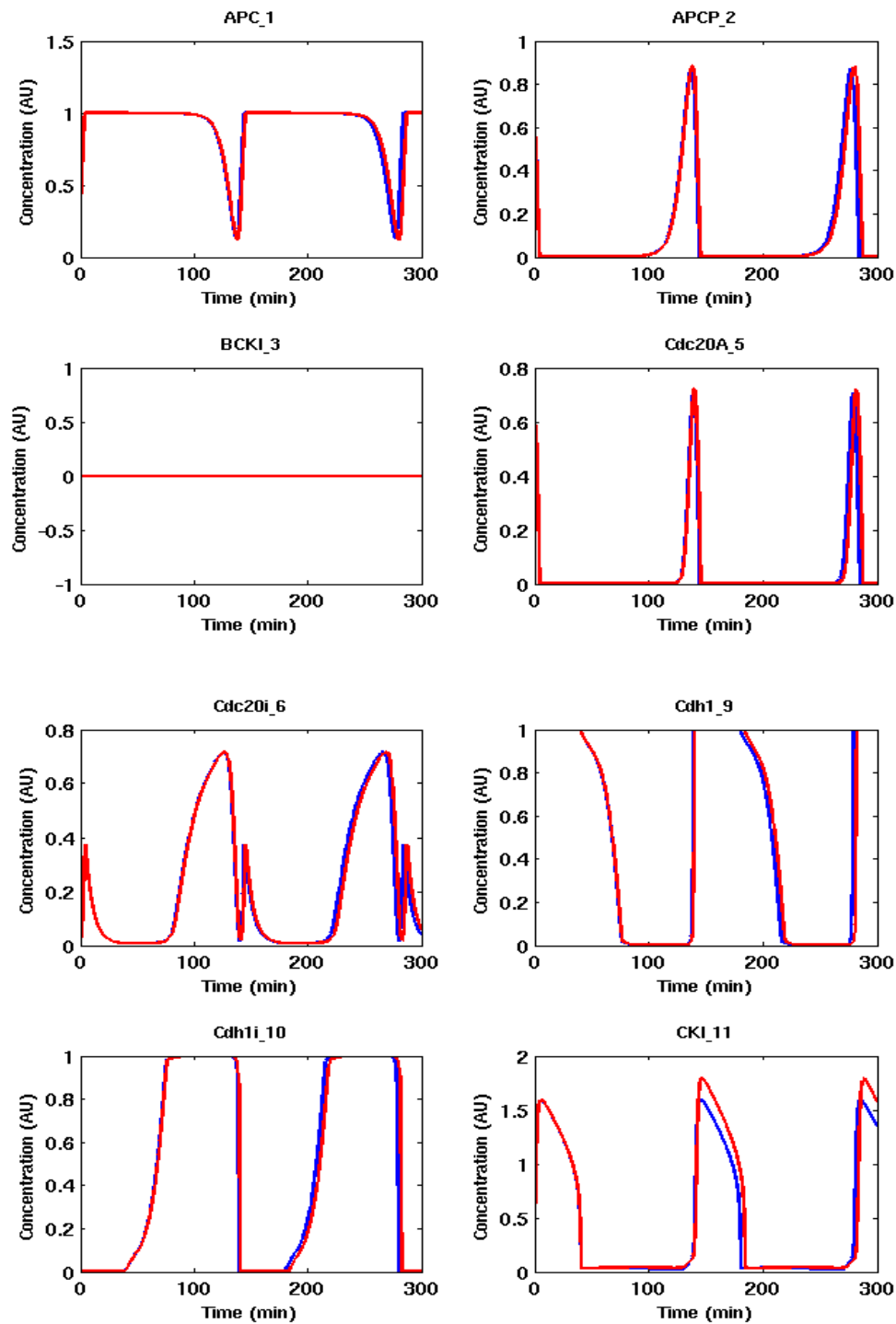
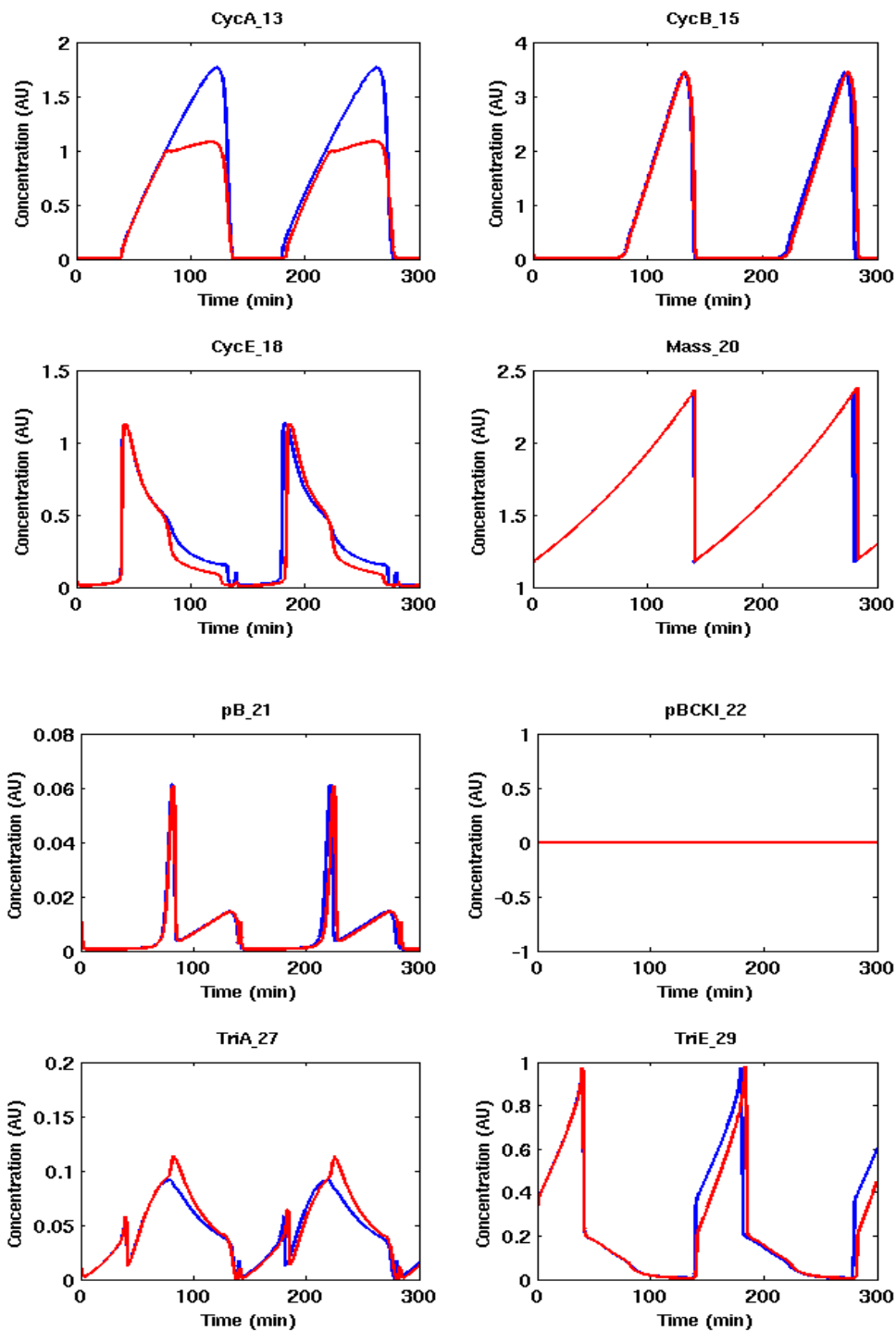


Figure S2- Time course profiles of unmodified model and model with hsa-miR-25 regulation for all 16 species (Blue line indicates profile of species in unmodified model; red line indicates profile of species in model with hsa-miR-25 regulation.)





Average inhibition

The ratio of average expression in the presence of miRNA mediated regulation and that in the absence of miRNA regulation was considered as average inhibition. To incorporate average inhibition the original rate expression was modified as,

$$cdc14 = (\text{Rate expression for } cdc14 \text{ used in Tyson model}) \times \text{average_inhibition}$$

$$TFE = (\text{Rate expression for TFE used in Tyson model}) \times \text{average_inhibition}$$

The target production rates in basic model were reduced by the average inhibition by miRNA dependent reduction for the respective targets. The average inhibition for CDC14 for all three km1 values was up to 10%. Repressing cdc14 to higher values results in perturbation in cell cycle. On the other hand, average inhibition observed for TFE for the two km2 values was upto 60%.

Figure S3: Comparison of time course simulation profiles of three cyclin species for cell cycle model and cell cycle with average inhibition. (Average inhibition: $cdc14 = cdc20A \times 0.9214$; $TFE = GK(Vatf, Vitf, Jatf, Jitf) \times 0.6779$).

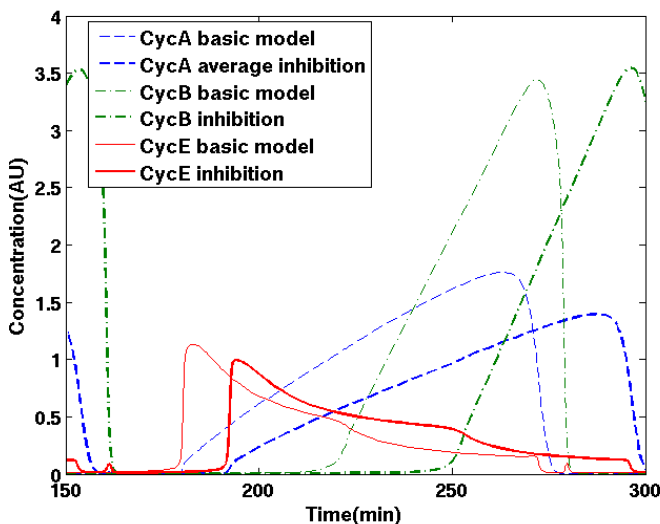


Figure S4: Time course profile of target protein with intronic miRNA regulation and with host protein mediated inhibition when the inhibitory effect is removed by setting the specific rate of synthesis (k_2 and k_5) to zero. Initial conditions- (a) all components at zero level. (b) Target protein at unregulated steady state, all other components at zero level. (c) Target mRNA at unregulated steady state level, all other components at zero level. (d) Target mRNA and protein at unregulated steady state, all other components at zero level. (e) Regulator molecule (miRNA and host protein) at steady state, all other components at zero level.

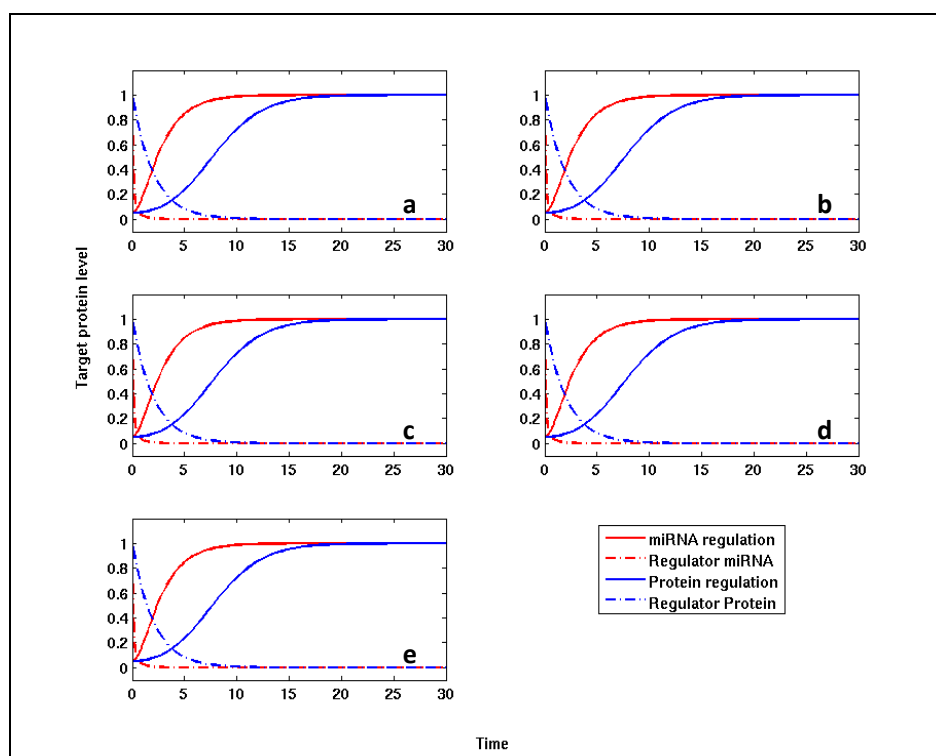


Figure S5: Time course profile of target protein with intronic miRNA regulation and with host protein mediated inhibition when the inhibitory effect is removed by blocking the synthesis of miRNA and regulator protein. The degradation reaction rate constant for regulator protein (k_{10}) is set to the same value as the miRNA degradation reaction rate constant (k_8). Initial conditions are same as in FigureS4.

