```
model *BIOMD0000000012()
  ...
  // Assignment Rules:
  beta    :=tau_mRNA /tau_prot;
  alpha0  :=a0_tr *eff*tau_prot/(ln(2)*KM);
  a0_tr   :=ps_0 *60;
  alpha   :=a_tr *eff*tau_prot/(ln(2)*KM);
  a_tr    := (ps_a -ps_0 )*60;
  t_ave   :=tau_mRNA /ln(2);
  kd_mRNA :=ln (2)/tau_mRNA;
  kd_prot :=ln (2)/tau_prot;
  k_tl    :=eff /t_ave;
    // Reactions:
  Reaction1  :X  => ;kd_mRNA *X;
  Reaction2  :Y  => ;kd_mRNA *Y;
  Reaction3  :Z  => ;kd_mRNA *Z;
  Reaction4  :  =>PX ;k_tl *X;
  Reaction5  :  =>PY ;k_tl *Y;
  Reaction6  :  =>PZ ;k_tl *Z;
  Reaction7  :PX  => ;kd_prot *PX;
  Reaction8  :PY  => ;kd_prot *PY;
  Reaction9  :PZ  => ;kd_prot *PZ;
  Reaction10 :  =>X ;a0_tr +a_tr *KM^n/(KM^n +PZ ^n);
  Reaction11 :  =>Y ;a0_tr +a_tr *KM^n/(KM^n +PX ^n);
  Reaction12 :  =>Z ;a0_tr +a_tr *KM^n/(KM^n +PY ^n);
  ...
end
// Models
model1 =model  "BIOMD0000000012"
model2 =model model1 with ps_0  = 1.3e-05,ps_a  = 0.013
// Simulations
simulation1 =simulate uniform (0, 1000, 1000)
simulation1.algorithm =kisao .88
simulation2 =simulate uniform_stochastic (0, 1000, 1000)
simulation2.algorithm =kisao .27
// Tasks
task1 =run simulation1 on model1
task2 =run simulation1 on model2
// Outputs
plot "protein numbers per time point" task1.time vs task1.PX,task1.PY,task1.PZ
plot "protein numbers per time point - damped oscillations" task2.time vs task2.PX,
task2.PY,task2.PZ
plot "Normalized Plot"  task1.PX/max(task1.PX)  vs task1 PY /max(task1.PY),task1. PY
/max(task1.PY) vs task1.PZ/max(task1.PZ),task1.PZ/max(task1.PZ) vs task1.PX /
max(task1.PX)
// Names
model1 is "Repressilator-regular oscillations"
model2 is "Damped oscillations"
task1 is "Oscillation using a deterministic simulator"
task2 is "Damped oscillations using a deterministic simulator"
```