
A Rule-based Model for LAT Phosphorylation and Aggregation

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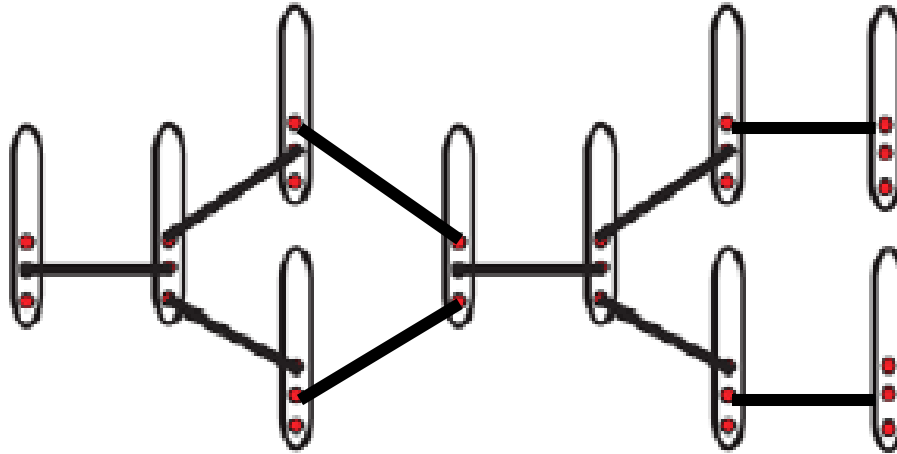
Cell Signaling Track (Q-bio 2)

6th Q-bio Summer School

Santa Fe campus

Introduction

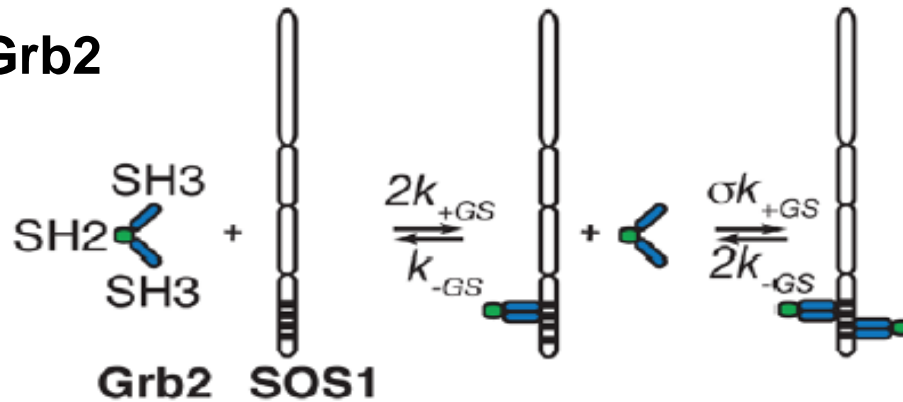
Biological Scenario: LAT aggregation



- LAT: the linker protein for activation of T cells
- Our Approach
 - To use a rule-based approach to represent the aggregation process of the LAT molecules

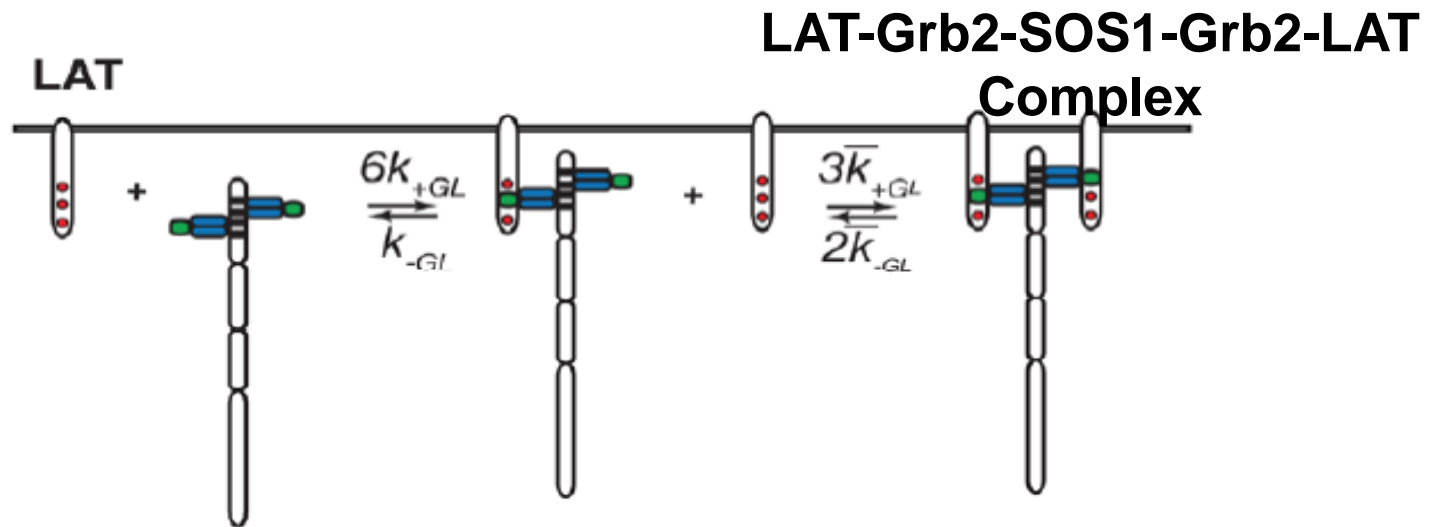
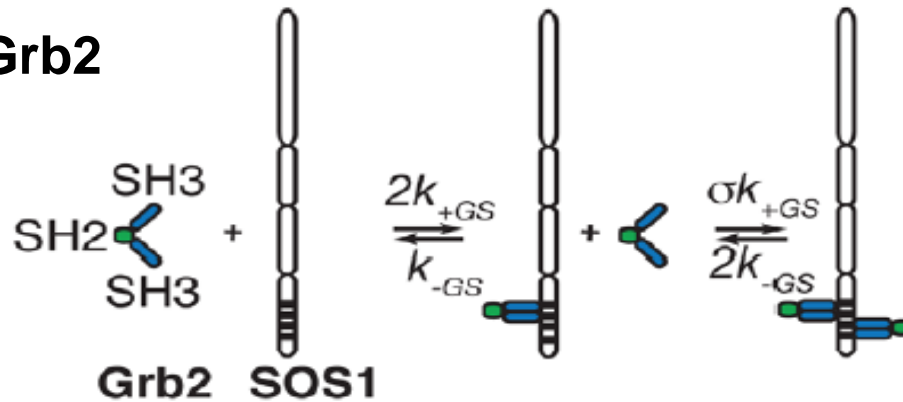
Interactions of LAT with Grb2 and SOS1

Grb2-SOS1-Grb2 Complex



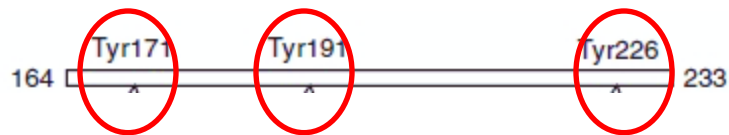
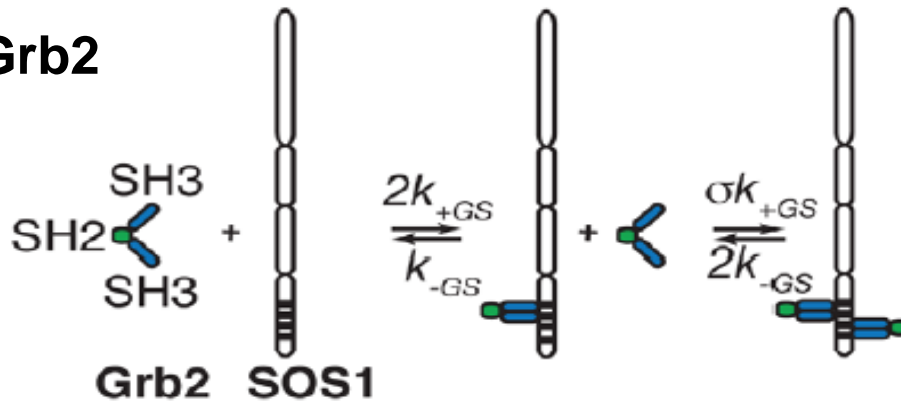
Interactions of LAT with Grb2 and SOS1

Grb2-SOS1-Grb2 Complex

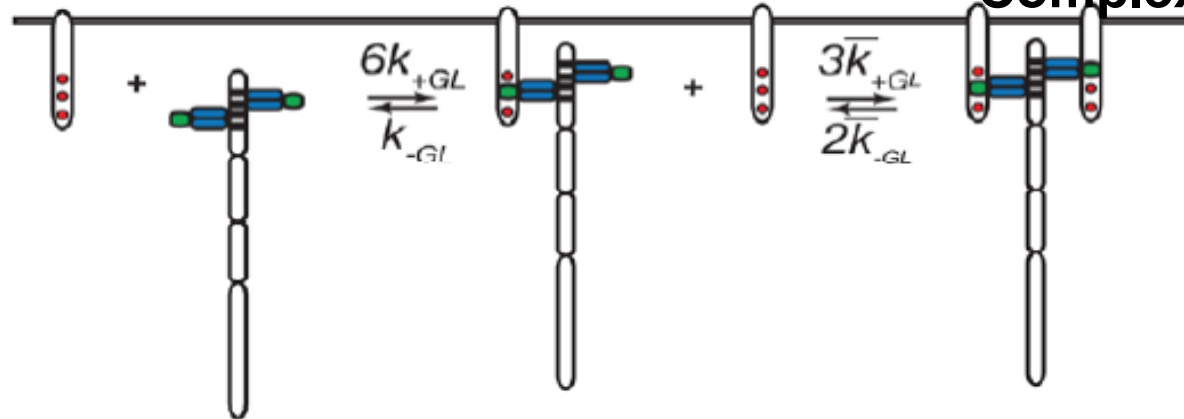


Interactions of LAT with Grb2 and SOS1

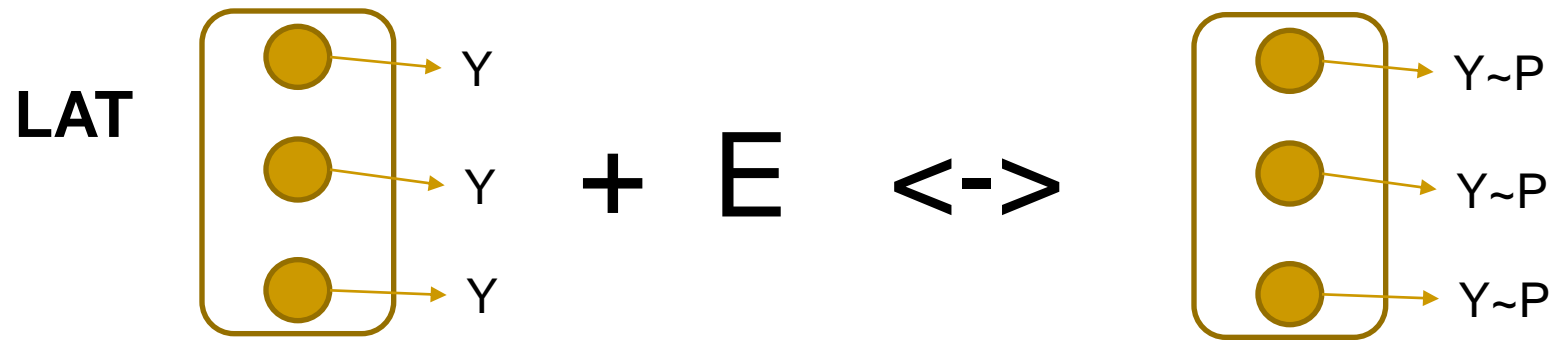
Grb2-SOS1-Grb2 Complex



LAT-Grb2-SOS1-Grb2-LAT Complex



Rule-based Model for LAT



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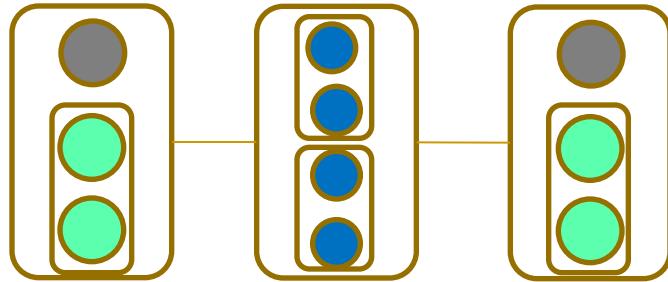
66 - begin reaction rules
67 #PHOSPHORYLATION RULES
68 #Encounter Complex
69 LAT(E~0,A~0) <-> LAT(E~1,A~0) Ekp,Ekm
70 LAT(E~1,A~1) -> LAT(E~0,A~0) Ekm
71
72 #Binding Reactions
73 LAT(E~1,A~0,Y~U) <-> LAT(E~1!1,A~0,Y~U!1) Ekf1,Ekb
74 LAT(E~1,A~0,Y~P,Y~U,Y~U) <-> LAT(E~1!1,A~0,Y~P!1,Y~U,Y~U) Ekf2,Ekb
75 LAT(E~1,A~0,Y~P,Y~P,Y~U) <-> LAT(E~1!1,A~0,Y~P,Y~P!1,Y~U) Ekf3,Ekb
76 LAT(E~1,A~0,Y~P,Y~P,Y~P) <-> LAT(E~1!1,A~0,Y~P,Y~P,Y~P!1) Ekf4,Ekb
77
78 #Catalysis + Enzyme Inactivation
79 LAT(E~1!1,A~0,Y~U!1) -> LAT(E~1,A~1,Y~P,Y~U,Y~U) Ekc
80 LAT(E~1!1,A~0,Y~P!1,Y~U,Y~U) -> LAT(E~1,A~1,Y~P,Y~P,Y~U) Ekc
81 LAT(E~1!1,A~0,Y~P,Y~P!1,Y~U) -> LAT(E~1,A~1,Y~P,Y~P,Y~P) Ekc
82
83 #Refractory Period
84 LAT(E~1,A~1) -> LAT(E~1,A~0) Emu
  
```

Phosphorylation of LAT sites

Heterogeneous LAT mixture:
monovalent, bivalent, and trivalent

Rule-based Model for LAT

GRB2 **SOS1** **GRB2**



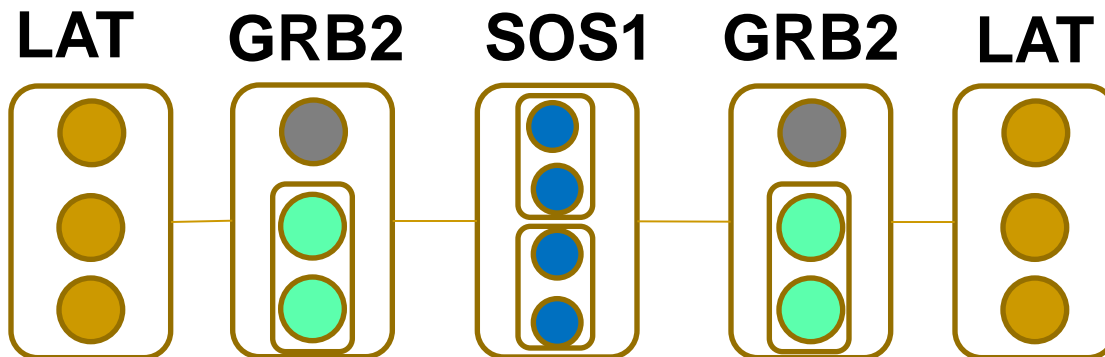
**Binding of GRB2
and SOS1**

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86 # LAT AGGREGATION RULES
87 # 1a: Free GRB2 binds free SOS1
88 GRB2(SH2,SH3) + SOS1(PRS,PRS) <-> GRB2(SH2,SH3!1).SOS1(PRS!1,PRS)  kgsp, kgsm
89
90 # 1b: Free GRB2 binds SOS1 bound to GRB2
91 GRB2(SH2,SH3) + SOS1(PRS,PRS!1).GRB2(SH2,SH3!1) <-> GRB2(SH2,SH3!2).SOS1(PRS!2,PRS!1).GRB2(SH2,SH3!1)  kxgsp, kxgsm
92
93 # 1c: Membrane-associated GRB2 binds free SOS1
94 GRB2(SH3,SH2!+) + SOS1(PRS,PRS) <-> GRB2(SH3!1,SH2!+).SOS1(PRS!1,PRS)  kgsp,kgsm
95
96
97 # 1d: Membrane-associated GRB2 binds SOS1 bound to GRB2
98 GRB2(SH3,SH2!+) + SOS1(PRS,PRS!1).GRB2(SH3!1,SH2) <-> GRB2(SH3!2,SH2!+).SOS1(PRS!2,PRS!1).GRB2(SH3!1,SH2)  kxgsp,kxgsm
99
100 # 1e: Free GRB2 binds membrane-associated SOS1
101 GRB2(SH3,SH2) + SOS1(PRS,PRS!1).GRB2(SH3!1,SH2!+) <-> GRB2(SH3!2,SH2).SOS1(PRS!2,PRS!1).GRB2(SH3!1,SH2!+)  kxgsp,kxgsm
102
103 # 1f: Membrane-associated GRB2 binds membrane-associated SOS1
104 GRB2(SH3,SH2!+) + SOS1(PRS,PRS!1).GRB2(SH3!1,SH2!+) <-> GRB2(SH3!2,SH2!+).SOS1(PRS!2,PRS!1).GRB2(SH3!1,SH2!+)  kxgspsr,kxgmsr
105

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Rule-based Model for LAT



**Binding of pLAT
with GRB2 and
SOS1**

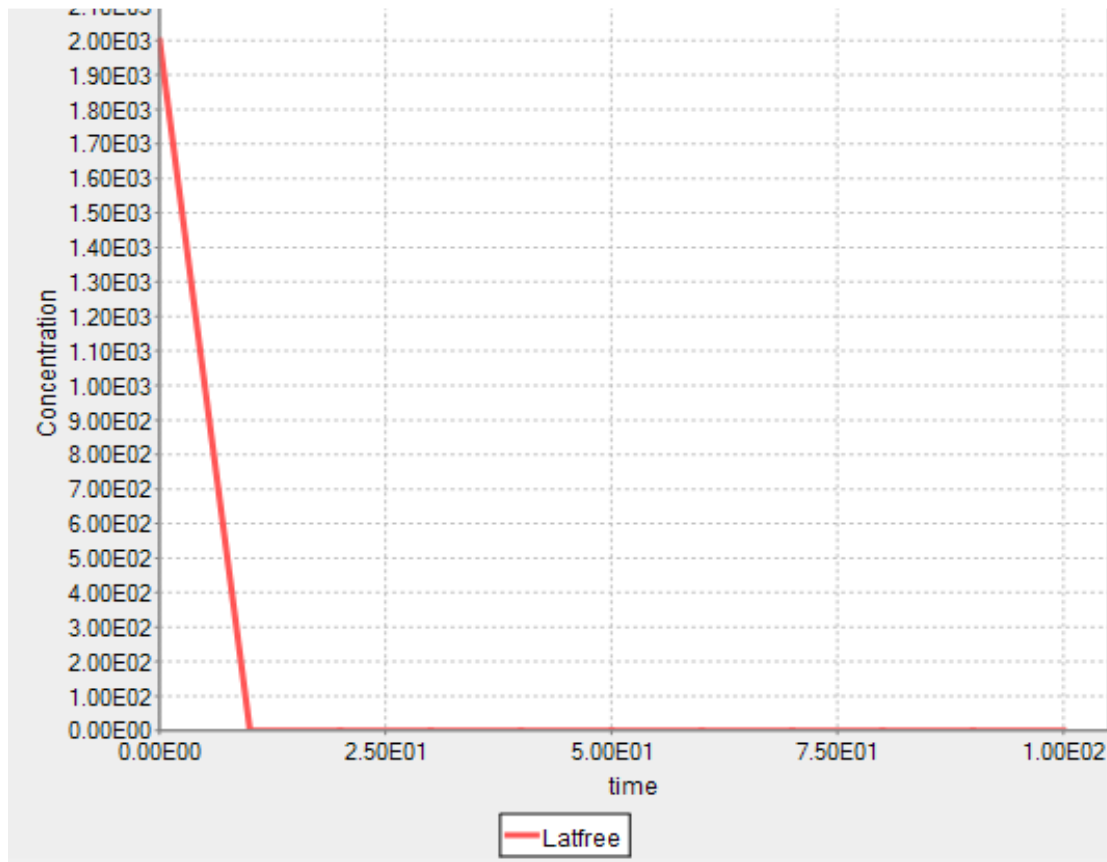
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106 # 2a: LAT binds free GRB2
107 LAT(Y~P)+GRB2(SH2,SH3) <-> LAT(Y~P!1).GRB2(SH2!1,SH3) kglp,kglm
108
109 # 2b: monoLAT binds GRB2 bound to SOS1
110 LAT(Y~P)+GRB2(SH2,SH3!1).SOS1(PRS!1,PRS) <-> LAT(Y~P!2).GRB2(SH2!2,SH3!1).SOS1(PRS!1,PRS) kglp,kglm
111
112 # 2c: LAT binds membrane-associated GRB2
113 LAT(Y~P)+GRB2(SH2,SH3!1).SOS1(PRS!1,PRS!2).GRB2(SH2,SH3!2) <-> LAT(Y~P!3).GRB2(SH2!3,SH3!1).SOS1(PRS!1,PRS!2).GRB2(SH2,SH3!2) kglp,kglm
114 |
115 # 2d: LAT binds membrane-associated GRB2
116 LAT(Y~P)+GRB2(SH2,SH3!1).SOS1(PRS!1,PRS!2).GRB2(SH2!3,SH3!2).LAT(Y~P!3) <-> LAT(Y~P!4).GRB2(SH2!4,SH3!1).SOS1(PRS!1,PRS!2).GRB2(SH2!3,SH3!2).LAT(Y~P!3) kxglp,kxglm

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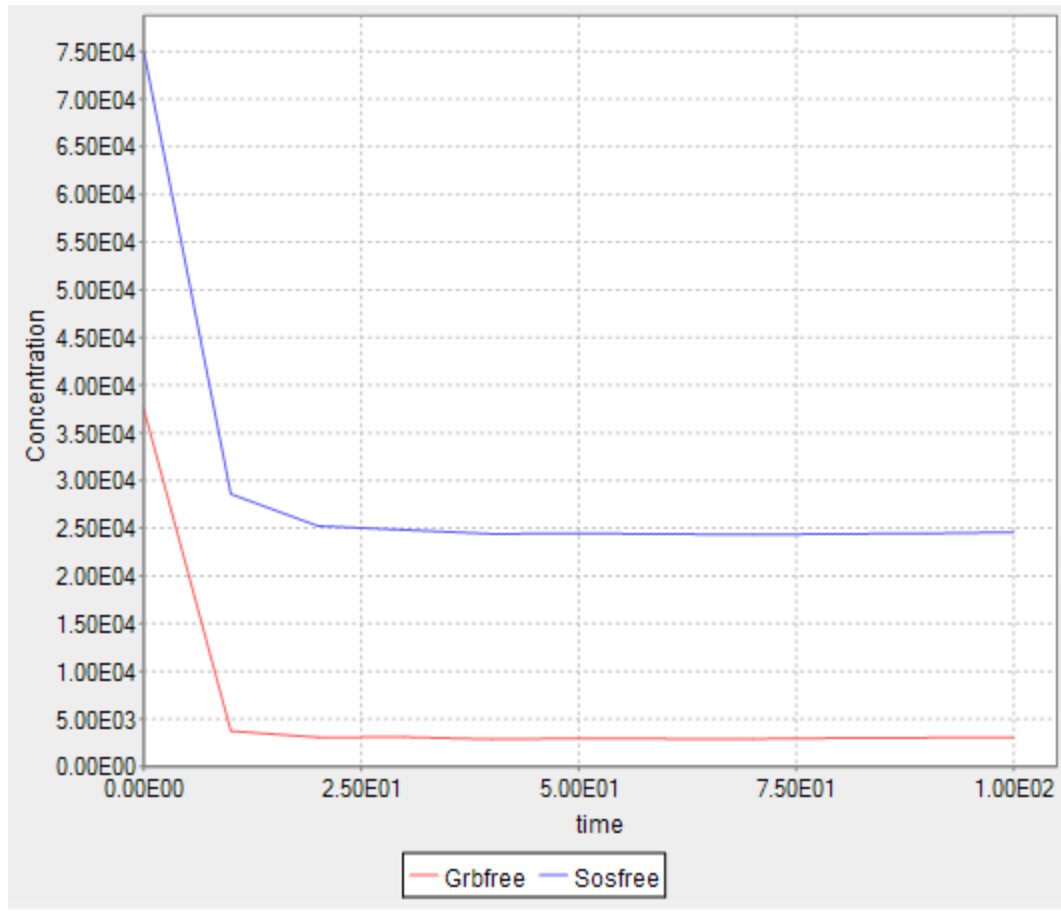
Preliminary Results

Species LATfree (LAT(Y~U,Y~U,Y~U))



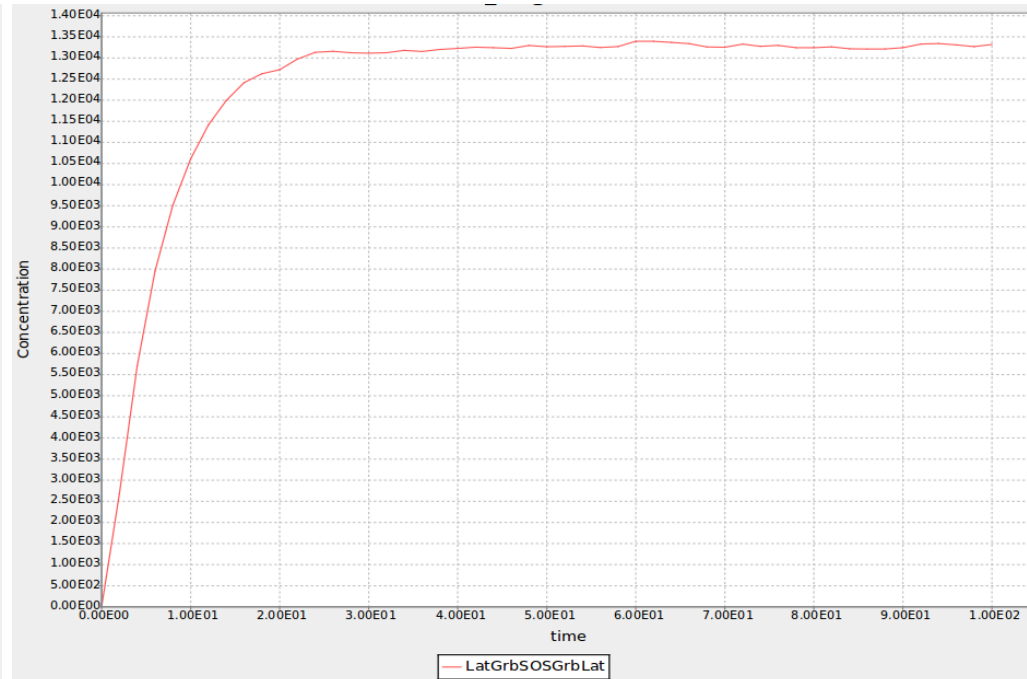
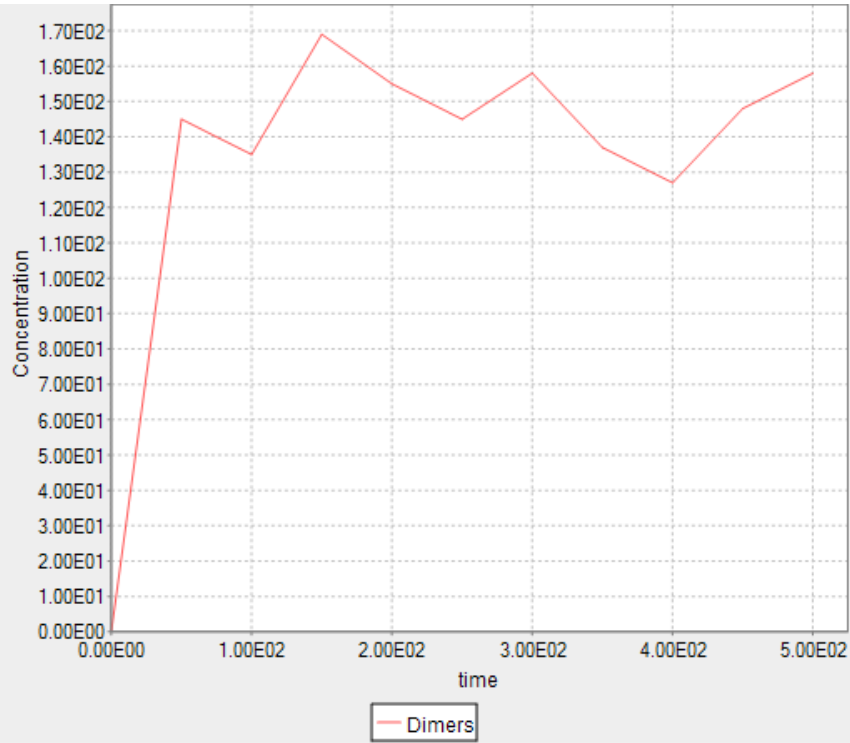
Preliminary Results

- Species GRB2free (GRB2(SH2,SH3))
- Species SOS1free (SOS1(PRS,PRS))



Preliminary Results

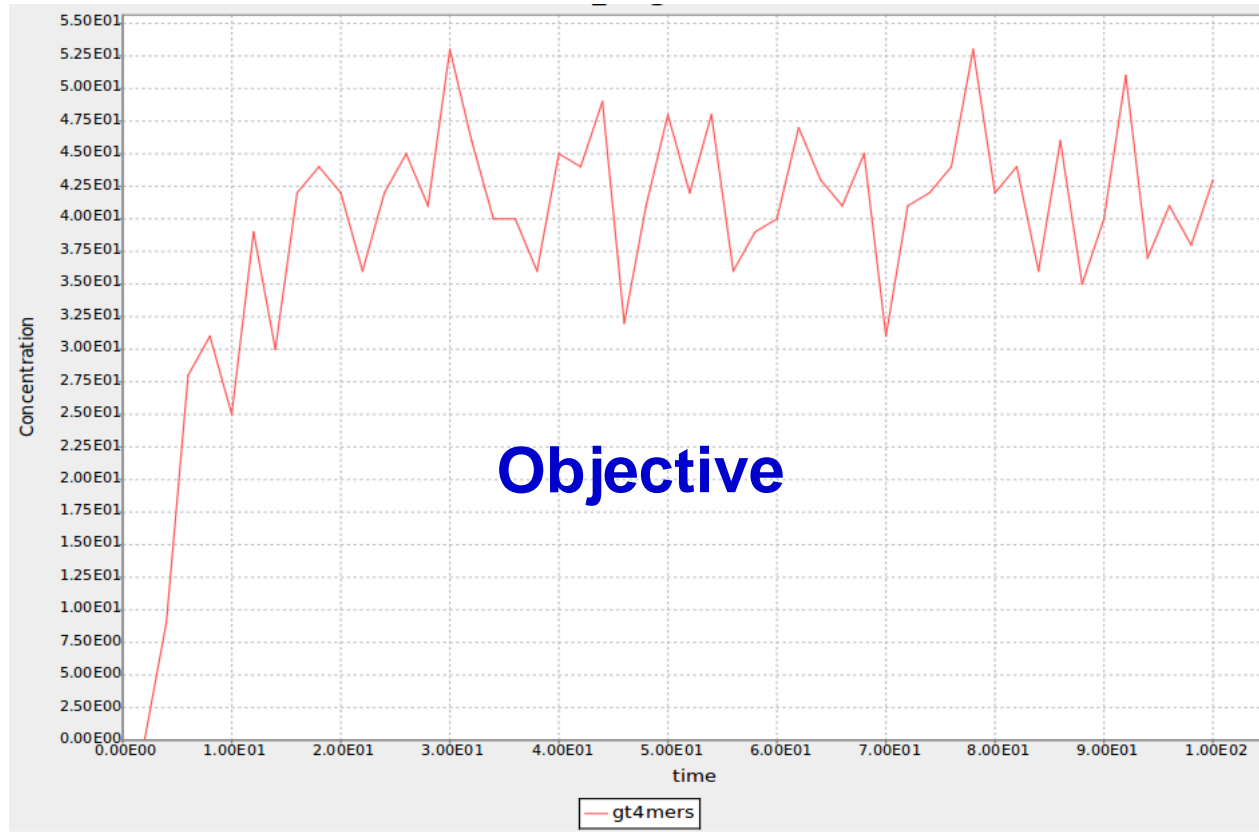
Aggregate with two LAT molecules



Source code taken from
(<http://public.tgen.org/dynstoc/download/models/lat.bngl>,
DYNSTOC: a tool for simulating large-scale rule-based models)

Preliminary Results

Aggregate with more than four LAT molecules



Source code taken from
(<http://public.tgen.org/dynstoc/download/models/lat.bngl>,
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Conclusion

- Rule-based modeling allows the formalization of mechanistic hypothesis.
- A useful mechanistic modeling based on local interactions.
- Allows the construction of abstract models that can be gradually refined.
- Currently, we have achieved to produce LAT aggregates with only two LAT molecules.
- If phosphorylation code, and aggregation code are run separately, the produce results that verifies the hypothesis of LAT phosphorylation and aggregation respectively.

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