

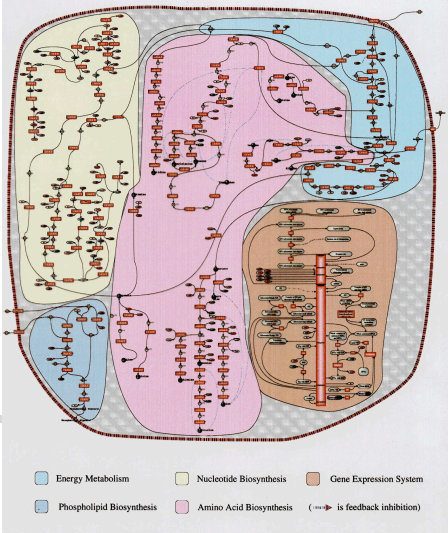
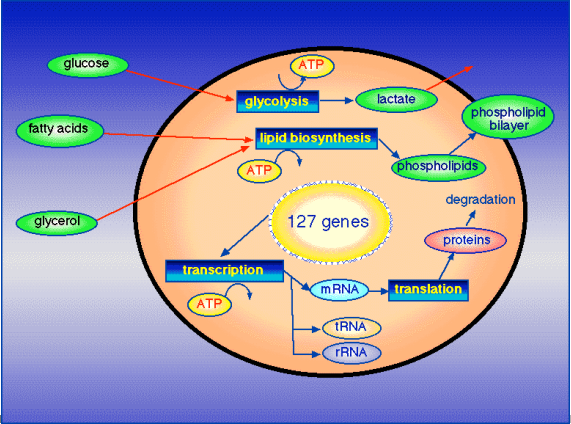
The background is a photograph of a modern, multi-story building with large glass windows, illuminated from within, reflecting on a body of water. The sky is a deep blue. In the foreground, there is a rocky shoreline. A large, white, semi-transparent circle is centered over the image, containing the text.

# E-CELL 3D

INSTITUTE FOR ADVANCED  
BIOSCIENCES, KEIO UNIVERSITY

KAZUHARU ARAKAWA

2007.07.20

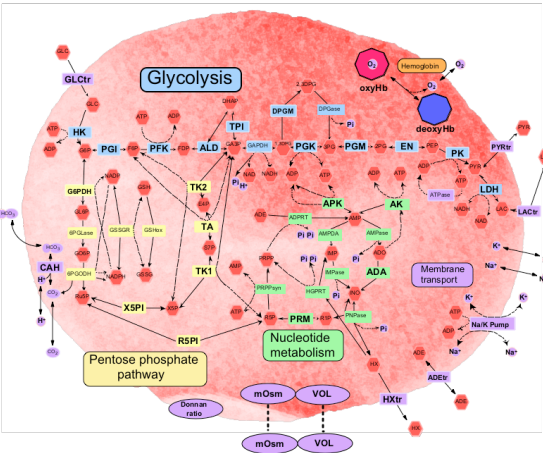


# Virtual Cell W/ 127 genes

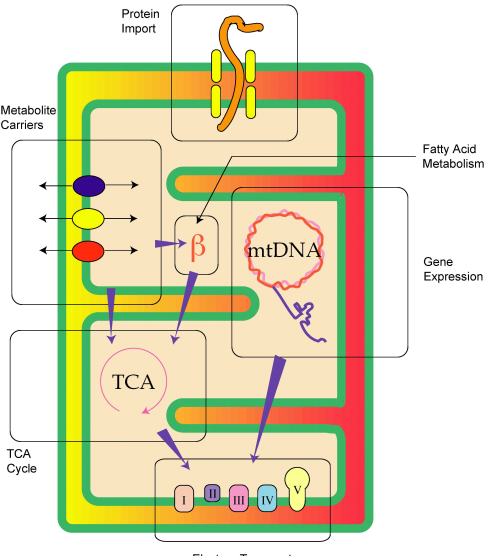
# Growing Cell

# The E-CELL Project

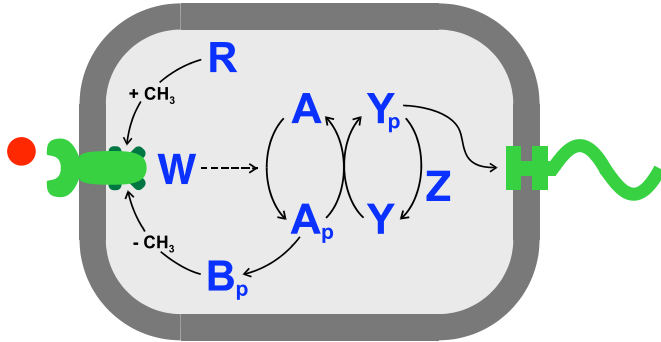
## Erythrocyte

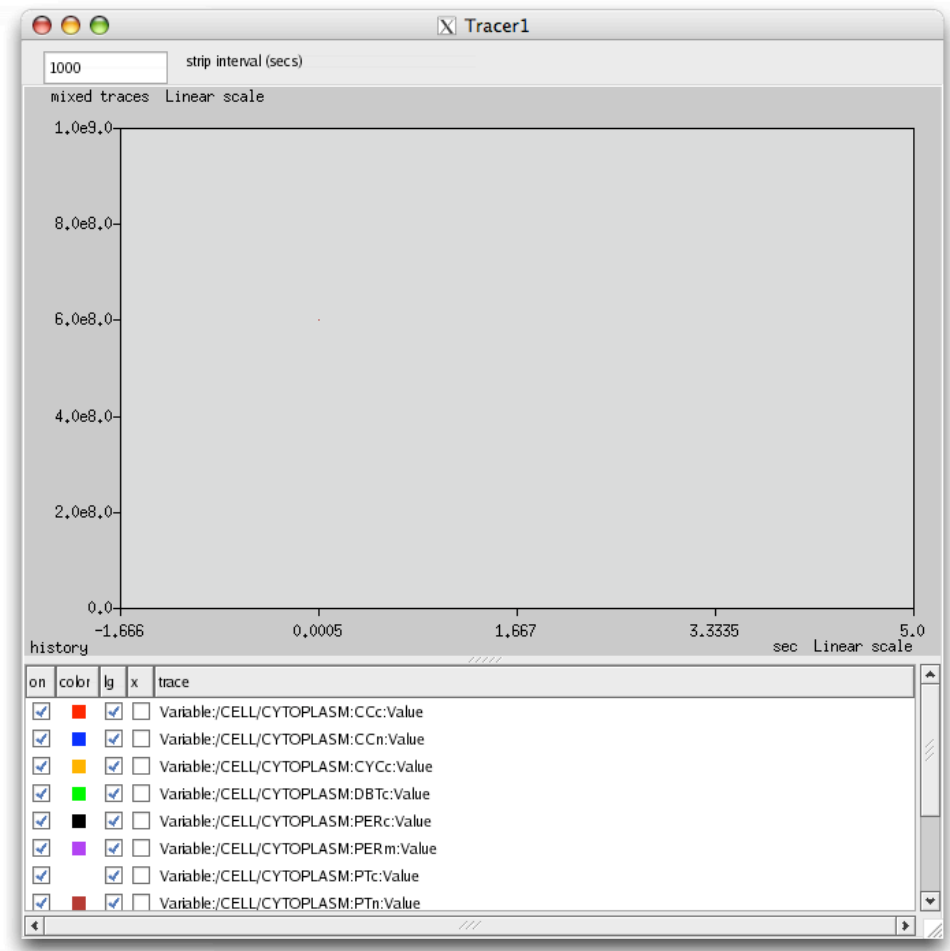
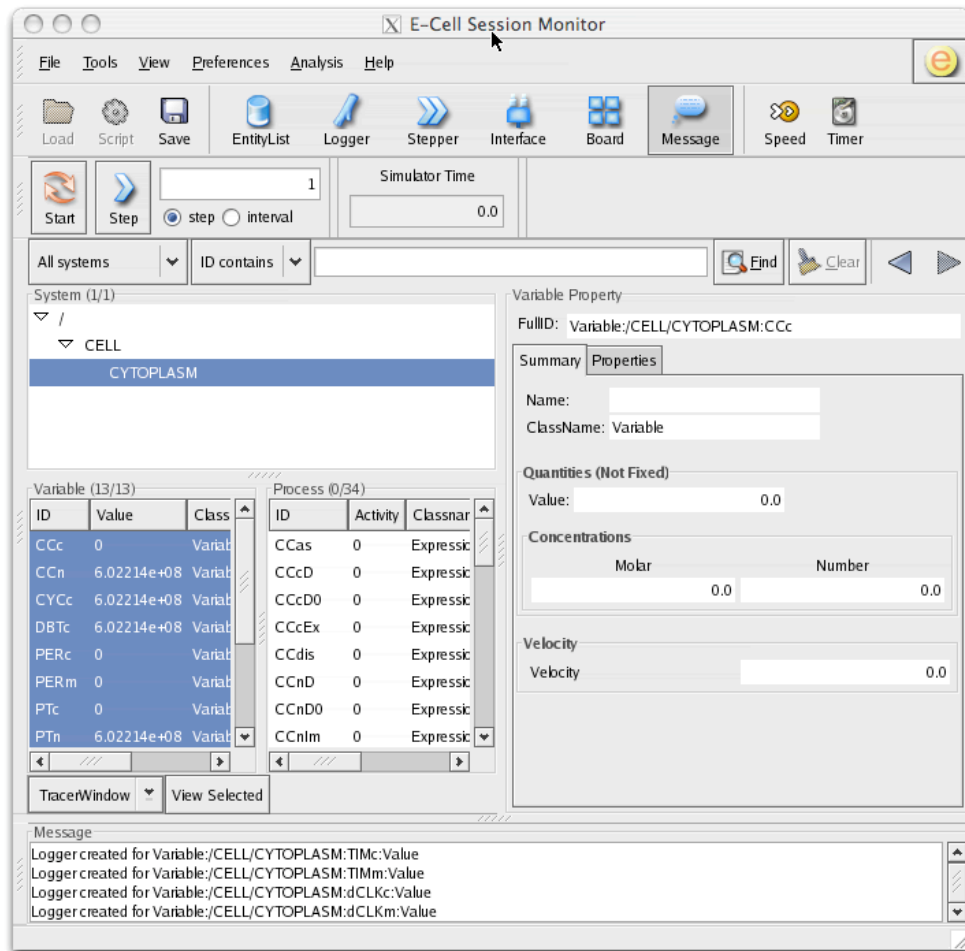


## Mitochondria



## Chemotaxis









*Demo*



*J. theor. Biol.* (2001) **210**, 401–406

doi:10.1006/jtbi.2000.2226, available online at <http://www.idealibrary.com> on IDEAL<sup>®</sup>



### **Robust Oscillations within the Interlocked Feedback Model of *Drosophila* Circadian Rhythm**

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A mechanism for generating circadian rhythms has been of major interest in recent years. After the discovery of *per* and *tim*, a model with a simple feedback loop involving *per* and *tim* has been proposed. However, it is recognized that the simple feedback model cannot account for phenotypes generated by various mutants. A recent report by Glossop, Lyons & Hardin [*Science*



# Dynamic Modeling of the Central Carbon Metabolism of *Escherichia coli*

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*Received 16 August 2001; accepted 29 January 2002*

*DOI: 10.1002/bit.10288*

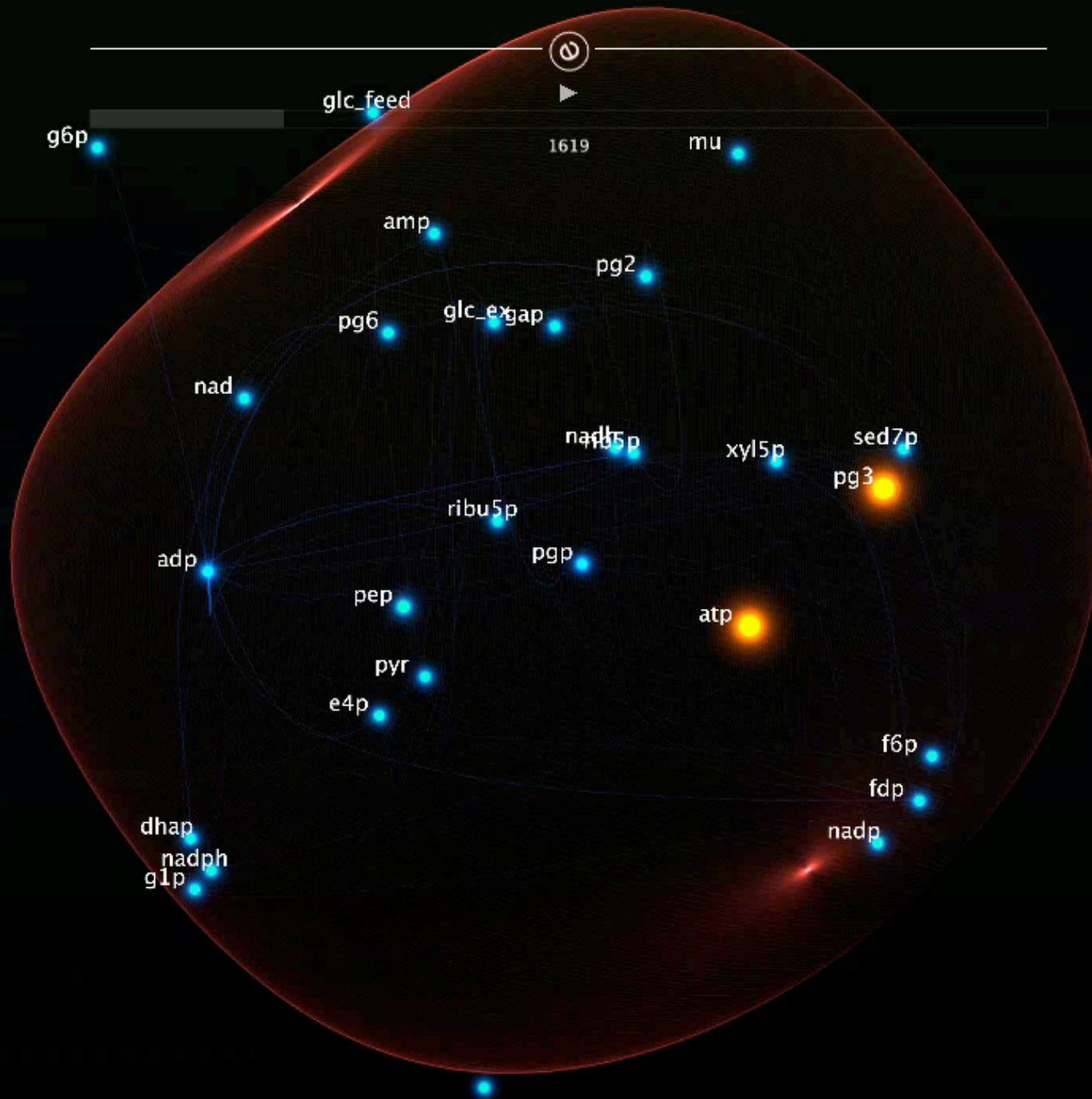
**Abstract:** Application of metabolic engineering principles to the rational design of microbial production processes crucially depends on the ability to describe quantitatively the systemic behavior of the central carbon metabolism to redirect carbon fluxes to the product-forming pathways. Despite the importance for several production processes, development of an essential dynamic model for central carbon metabolism of *Escherichia coli* has been severely hampered by the current lack of kinetic information on the dynamics of the metabolic reactions. Here we present the design and experimental validation of such a dynamic model, which, for the first time, links the sugar transport system (i.e., phosphotransferase system [PTS]) with the reactions of glycolysis and the pentose-phosphate pathway. Experimental observations of intracellular concentrations of metabolites and cometabolites at transient conditions are used to validate the structure of the model and to estimate the kinetic parameters. Further analysis of the detailed characteristics of the system offers the possibility of studying important questions regarding the stability and control of metabolic fluxes. © 2002 Wiley Periodicals, Inc. *Biotechnol Bioeng* 79: 53–73, 2002

action pathways. Indeed, success in the development of rigorous dynamic models for metabolic systems has been severely hampered by the current lack of kinetic information on the dynamics of the reactions (Edwards and Palsson, 2000).

Because the many biochemical details of the metabolic networks appear overwhelming at first sight, there is a demand for decreasing the enormous complexity of the problem. Concepts generated toward this end must be examined in the context of the intended purpose of the model. When focusing on objectives of flux amplification for increase of specific productivities in the industrial manufacturing of metabolites, the task is most often specifically reduced to an amplification of the central metabolic pathways (Stephanopoulos and Simpson, 1997). Of course, modeling of the many interconnected reactions of the main supply route to product-forming pathways remains a demanding undertaking, but the model of the system required for



xyl5p  
sed7p  
ribu5p  
rib5p  
pyr  
  
pg6  
**pg3**  
**pg2**  
**pep**  
nadoh  
nadp  
nadh  
nad  
mu  
**glc\_feed**  
glc\_ex  
gap  
g6p  
g1p  
fdp  
f6p  
emptySet  
e4p  
dhap  
**atp**  
amp



1619

StepSize 11

Research

Open Access

## Dynamic simulation of red blood cell metabolism and its application to the analysis of a pathological condition

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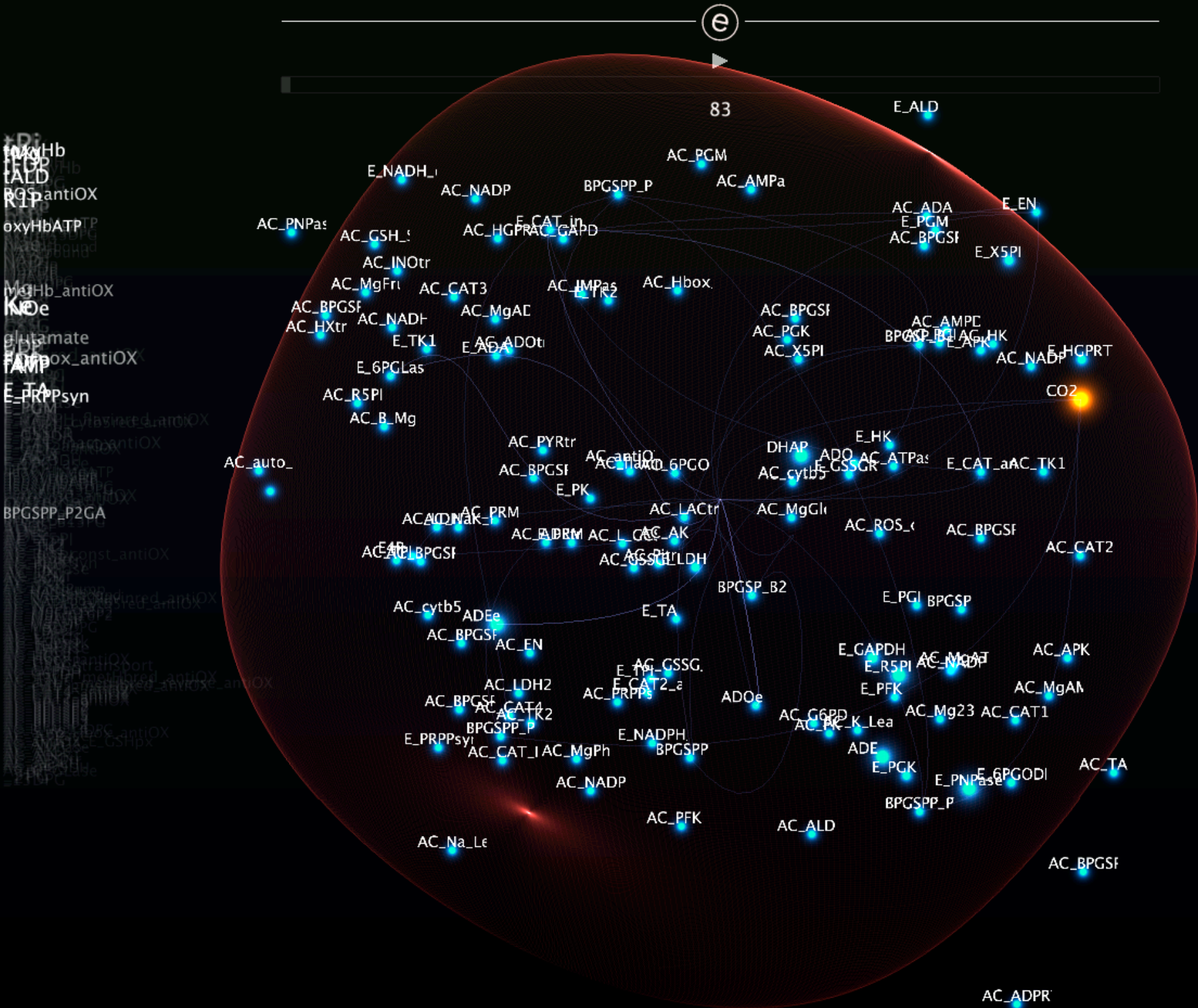
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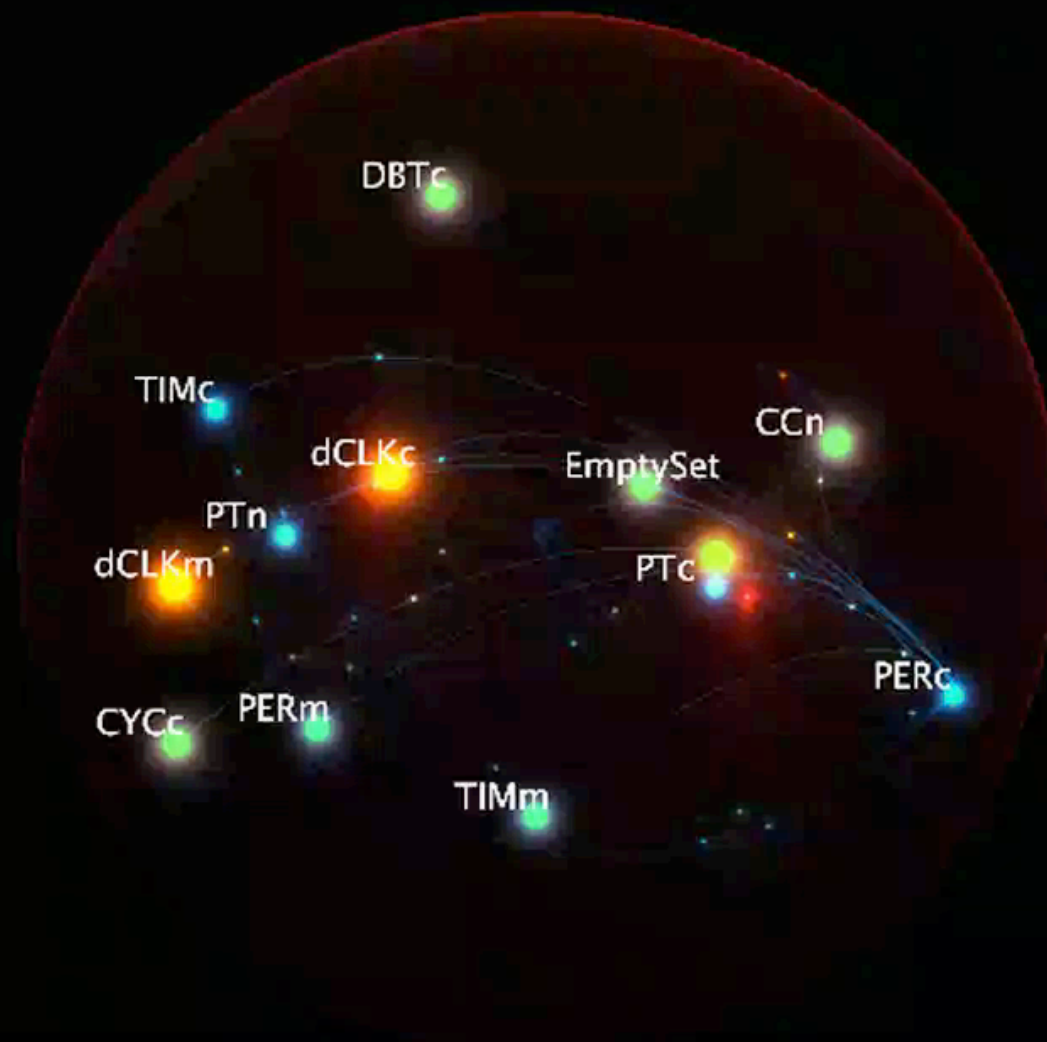
### Abstract

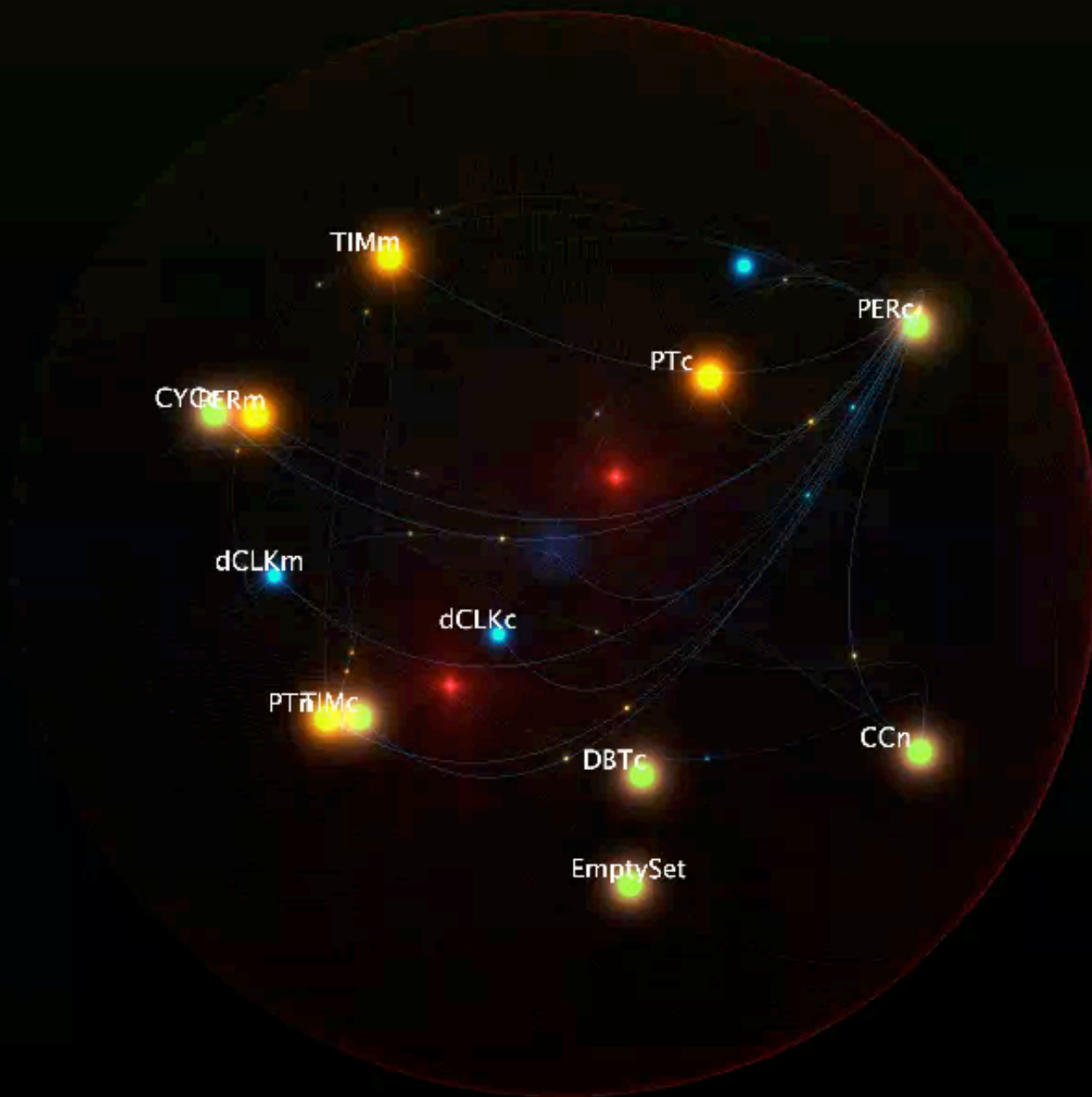
**Background:** Cell simulation, which aims to predict the complex and dynamic behavior of living cells, is becoming a valuable tool. In silico models of human red blood cell (RBC) metabolism have

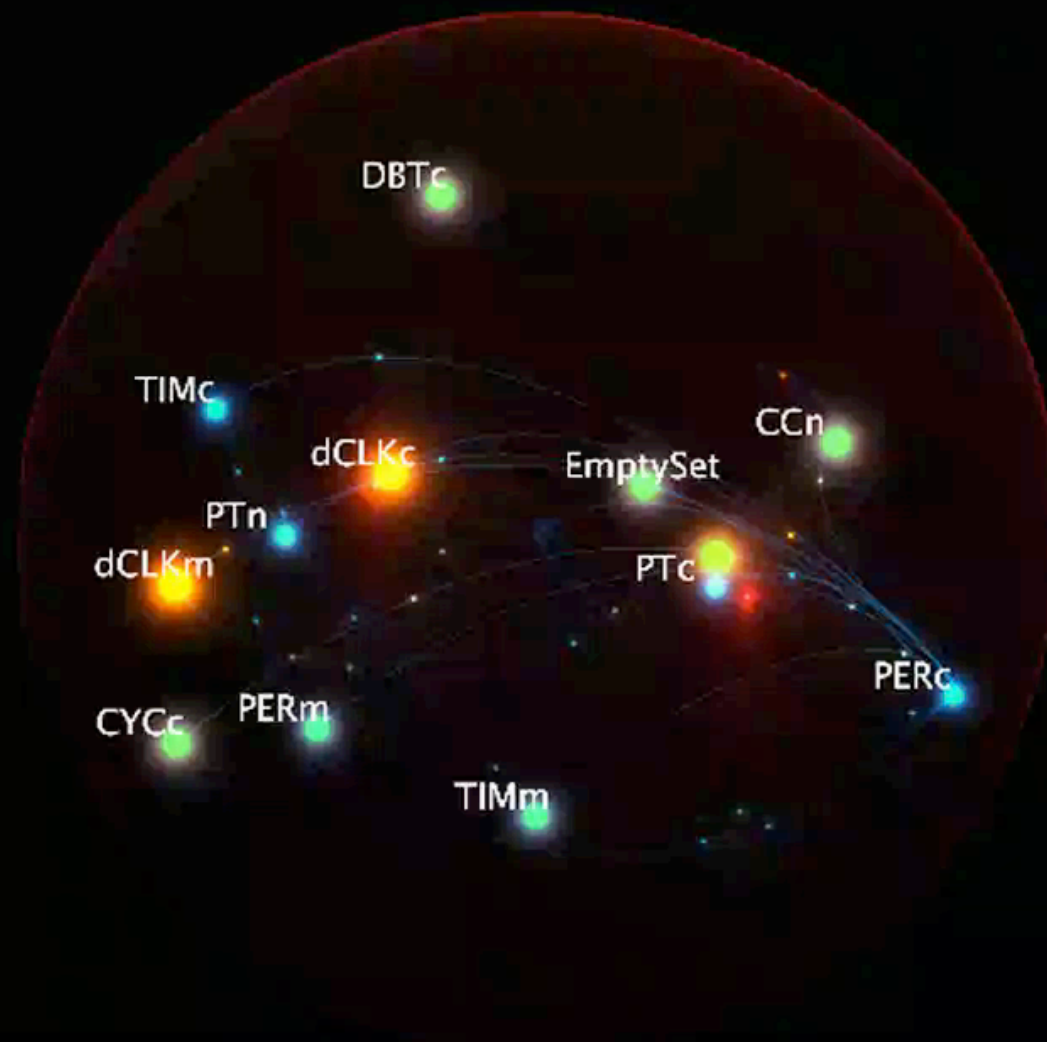


















*Demo*





# Visualization

<http://ecell3d.iab.keio.ac.jp/>

ISMB Poster C58

ISMB Demonstration  
Monday 23rd 3:50~4:15 Hall L