**Entelos Position Paper for W3C Workshop on Semantic Web for Life Sciences**

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## About Entelos

Entelos, Inc. (www.entelos.com) uses its proprietary PhysioLab® technology to identify and validate targets, biomarkers and compounds for human efficacy. The PhysioLab systems biology platforms employ sophisticated mathematical models to integrate information from diverse scientific and clinical sources to represent the complex and dynamic relationships of human biology. Our primary mission is to increase the efficiency of pharmaceutical research and development and to expedite proprietary human therapeutics to the market. We have multiple disease level PhysioLab platforms in immunology, inflammation and metabolism and are currently developing new platforms in cardiovascular, CNS and Metabolic Syndrome.

## Entelos Interest in Semantic Web Technologies

Our primary interests in the semantic web are in three areas:

- Aiding the process of building models, through easier access to source information
- Providing a more universal mechanism to link models to data
- Providing a means for model-based knowledge to be more widely accessed

In the process of building our PhysioLab models, we depend on public sources including scientific papers and journals. The trend toward making papers and corresponding data directly available on the web is very promising. We look to semantic web technologies to make it easier to find and access the data in these sources. The first goal here would be to provide better search and data extraction tools for scientists, with a longer-term goal of permitting more automated/agent-type operations.

Biological models include items such as genes, proteins, or cells that can be found in a variety of databases. In addition, experimental data describing the behavior of these items under a variety of conditions may also be available. Models can be linked to these items and data, but the challenge is that they are frequently in disparate databases accessed through a variety of interfaces. Life Science Identifiers (LSIDs) offer the promise of creating a universal means for linking to such data and we are considering how we will use them in our technology platform.

Finally, each model, including its biological relationships and links to source data, is a great knowledgebase. Ideally these systems will also be published through semantic web technology to allow the relationships and knowledge in the model to be accessed through other systems and incorporated into larger biological knowledgebases.