

## ***Pilot Usability Study***

**Welcome. The purpose of this interview is to examine the usability of this collaborative gene annotation tool, not you. Any problem you encounter will help us improve it. You can quit at any time.**

**Tell us your thoughts as you are working. If you forget to think aloud, we may remind you. Please ask questions as they occur to you, but we will not be able to answer them until the end of the test.**

**Your feedback is highly appreciated. Thank you for participating in this test.**

## A. ORIENTATION

We are currently developing an add-on to the existing JGI IMG portal, which you should already be familiar with. Basically, we have received many requests, throughout the lifetime of the IMG system, for a system which would allow users to annotate genes, upload these annotations for others to see, view other people's annotations, and discuss any points of contention. This prototype system implements only collaborative functional annotation; for the present time, structural annotation remains outside of the scope of this project. You can think of this as an additional feature set which will be tightly integrated with the existing IMG system. However, since we want your feedback on the new features, and not the existing system, we will be directing you to certain "starting pages," from which you will try to execute certain tasks. Do you have any questions?

## A. TASKS

### Task Set 1

- \* Start from the gene list: <http://groups.sims.berkeley.edu/annotation/>
  - View the annotation history for the first gene on the list.

*Record*

Start time:

End time:

Number/location of click-throughs:

- Modify the existing annotation for that gene with data from a homolog:
  - GO function; EC number; Gene Name.
- \* Submit your annotation.

*Record*

Start time:

End time:

Number of errors:

Other resources referenced:

*Notes:*

**Task Set 2.**

- \* Start from the gene list: <http://groups.sims.berkeley.edu/annotation/>
- \* Express your opposition to the annotation for the first gene on the list.

*Record*

Start time:

End time:

Number of clicks:

Notes:

**Task Set 3.**

- \* Start from the Gene Cart: <http://groups.sims.berkeley.edu/annotation/genecart.php>
- \* Change an annotation by adding a COG group.
- \* Add this gene to your list of watched annotations.

*Record*

Start time:

End time:

Number of clicks:

Notes:

**Task Set 4.**

- \* Start from the Gene Cart: <http://groups.sims.berkeley.edu/annotation/genecart.php>
- \* Comment on annotations for multiple genes.

*Record*

Start time:

End time:

Number of clicks:

Notes:

**Task Set 5.**

\* Starting from anywhere on the site, find where you can view your watched annotations.

*Record*

Start time:

End time:

Number of clicks:

Notes:

**Task Set 6.**

How would you go about determining whether this annotation is a valid one or not?

## **B. DEBRIEFING**

What did you think of this application?

What were the best (most useful?) parts? What were the worst (least useful?) ?

Did these sets of tasks feel natural to you? Why or why not?

Do you feel there are other tasks that you think this interface should support?

Do you feel there is anything that should be removed from the current design?

What other kinds of functionality would you like to see in a collaborative gene annotation tool, either in the current system or in a no-holds-barred system of the future?

While using this system, did you ever feel lost?

## D. DEMOGRAPHICS

1. Your age is

- 15-25       25-35       35-45       45-55       55-65       >65

2. Please check off the highest level of education you have completed.

- Bachelors       Masters       PhD Candidacy       PhD  
 Other. Please Specify: \_\_\_\_\_

3. What is your field of study or work?

\_\_\_\_\_

4. How often have you used JGI's IMG system before?

- never       rarely       a few times a month       a few times a week or more

5. What other comparative genomics tools are you familiar with?

6. How familiar are you with functional gene annotation?

- Not at all.  
 I refer to annotations made by other people in my work.  
 I have annotated a gene before.  
 I annotate genes regularly.  
 I have experience in professional annotation or the equivalent.

Feel free to elaborate on your experience: \_\_\_\_\_

7. What kind of computer user are you? (Please select one)

- I use computers only when I have to.  
 I use computers routinely but don't know much about them.  
 I use computers routinely and have a good understanding of them, but I do not do programming.  
 I use computers often and do computer programming.

**Thank you very much!**