

# Bioinformatics and the Exploration of Microbial Life



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### Education:

- B.A. Biology, William Jewell College, Liberty, MO; M.S. Microbiology, University of Illinois at Urbana-Champaign; Ph.D. Microbiology, University of Illinois at Urbana-Champaign; Postdoc. Evolutionary Microbiology, Carl R. Woese, University of Illinois

### Areas of Expertise

- Microbial Genome Analysis and Bioinformatics
- Transcription Mechanisms of Archaea and the human parasite, *Giardia lamblia*

### Grants and Awards:

- Best AA and DeJongh M. Development of a Software Environment for Comparative Genome Analysis and Annotation. Howard Hughes Medical Institute Faculty Development Grant for Interdisciplinary Research.
- Best AA, DeJongh M and Tintle N. Evaluation and Implementation of Structural Equation Modeling as a Statistical Method for Refining Theoretical Genome-scale Models with Experimental Data. HHMI Faculty Development Grant for Interdisciplinary Research.

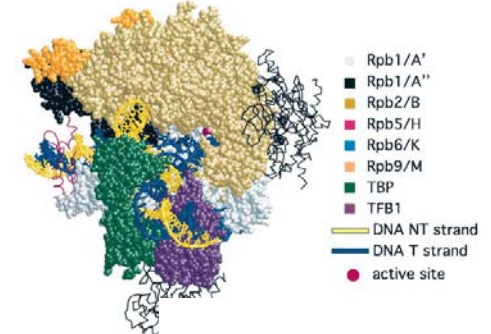
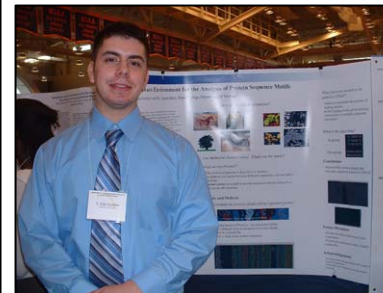
### Publications:

Sarría I\*, Holtrop M\* and Best AA. Unique transcription mechanism of *Giardia lamblia*. Annual Biomedical Research Conference for Minority Students, Nov. 2005

### Research Interests

My work combines the emerging field of bioinformatics with traditional molecular biology, biochemistry and genetics explorations of microbes. I seek to use the vast amounts of data produced by genome sequencing projects to guide wet-lab experimentation into fundamental biology of the human parasite, *Giardia lamblia*.

I am exploring the metabolic capabilities of bacteria that can remove toxic wastes from the environment. These studies combine computer modeling of metabolism with experimental verification of model predictions. This work improves our abilities to correctly catalogue the genes that all organisms have, a process called genome annotation.



QuickTime™ and a TIFF (Uncompressed) decompressor are needed to see this picture.



The SEED: an Annotation/Analysis Tool Provided by FIG

Contains 37 archaeal, 560 bacterial, 561 eukaryal, 1333 viral and 2 environmental genomes. Of these, 25 archaeal, 324 bacterial and 25 eukaryal genomes are more-or-less complete

Work on Subsystems

Searching for Genes or Functional Roles Using Text

If You Need to Pick a Genome for Options Below

