



Sequencing the World of Possibilities for Energy and Environment

The mission of the U.S. Department of Energy Joint Genome Institute (DOE JGI) is to advance genomics in support of the DOE missions related to energy and the environment. Located in Walnut Creek, California, the DOE JGI is operated by the University of California for the U.S. Department of Energy and the facility provides integrated high-throughput DNA sequencing, synthesis and computational analysis that enable systems-based scientific approaches to these challenges (<http://jgi.doe.gov>).

The DOE JGI has an exciting opportunity available for a talented, highly motivated computational biologist to support the New Lineages of Life project.

Computational Biologist Postdoctoral Fellow

The recovery of genomes directly from environmental samples using deep metagenomic sequencing and single-cell genomics has illuminated the phylogenetic breadth of major uncultivated microbial lineages in the tree of life. As a member of the New Lineages of Life project, the fellow will be expected to reconstruct and characterize genomes from candidate phyla and novel microbial lineages through the large-scale analysis of metagenomic data and assemble a genomic reference catalogue of microbial “dark matter.” The successful candidate will work as part of a large multidisciplinary team of biologists, computer scientists, software developers and postdoctoral researchers.

Qualifications:

- Recent Ph.D. (within the last 4 years) in microbiology, molecular biology, biochemistry or a related discipline
- Experience in analysis of microbial genomes and metagenomes is essential with a proven track record in this area reflected in recent or pending publications
- Substantial knowledge and understanding of bioinformatics tools for sequence similarity search, multiple sequence alignment, profile search, clustering and phylogenetic analyses using ribosomal genes and conserved marker genes is required
- Significant experience in methods and tools for next-generation sequencing, metagenome assembly and binning, and genome reconstruction
- Excellent written and oral communication skills
- Ability to independently carry out high-quality research with tenacity and creativity
- Strong understanding in a scripting language (Perl, Python) is a must, knowledge of Unix tools, relational databases and R
- Good knowledge of tools for microbial ecology studies
- Experience in or familiarity with statistical analysis

How to Apply: Interested applicants should apply online
<https://lbl.taleo.net/careersection/2/jobdetail.ftl?lang=en&job=82858>



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