



Archaea

Special Issue on  
**Exploring the Archaeal Hologenome and  
Metagenome**

# CALL FOR PAPERS

As defined by Eugene Rosenberg, the hologenome refers to the sum of the genetic information of a host organism plus all of its symbiotic microorganisms and viruses (the “holobionts”). More broadly, the term metagenome is used to describe all of the genetic material retrieved from any environmental sample. While the hologenomes and metagenomes of eukaryotic and bacterial systems have been published, studies in relation to the greater genomic relationships of Archaea have been comparatively underrepresented in the literature.

In this special issue, we invite authors to submit overview and original research articles relating to the diversity and evolution of archaeal hologenomes and metagenomes at the biochemical, ecological, genetic, genomic, or physiological levels.

Potential topics include, but are not limited to:

- ▶ Viruses and plasmids in relation to Archaea
- ▶ Archaeal horizontal gene transfer
- ▶ Comparative genomics within holobionts
- ▶ Diversity within and among holobionts
- ▶ Metagenomic studies of extremophile environments
- ▶ Environmental adaptations
- ▶ Evolutionary links between Archaea and Eukarya/Bacteria

Authors can submit their manuscripts via the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/archaea/holom/>.

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**Manuscript Due**

Friday, 20 November 2015

**First Round of Reviews**

Friday, 12 February 2016

**Publication Date**

Friday, 8 April 2016