

## Online Links

*Aspergillus fumigatus*

[http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genomeprj&cmd=Retrieve&dopt=Overview&list\\_uids=9521](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genomeprj&cmd=Retrieve&dopt=Overview&list_uids=9521)

*Pyrococcus furiosus*

[http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genomeprj&cmd=Retrieve&dopt=Overview&list\\_uids=287](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genomeprj&cmd=Retrieve&dopt=Overview&list_uids=287)

## IN BRIEF

## TECHNIQUES AND APPLICATIONS

Defining genes in the genome of the hyperthermophilic archaeon *Pyrococcus furiosus*: implications for all microbial genomes

Poole, F. L. II *et al. J. Bacteriol.* **187**, 7325–7332 (2005)

Does automated genome annotation produce reliable and reproducible results? Not necessarily, according to Farris L. Poole and co-workers. A comparison of the genome annotations of the archaeon *Pyrococcus furiosus* from three different databases revealed significant discrepancies. In particular, the number and size of the open reading frames differed among the different databases. Transcriptional analyses and recombinant protein production confirmed the presence of at least 17 genes in *P. furiosus* that had not been identified in the original annotation. It is therefore imperative that all microbial genome annotations are carefully scrutinized and, ideally, backed up by experimental analyses.

## ENVIRONMENTAL MICROBIOLOGY

Fungal contamination of bedding

Woodcock, A. A. *et al. Allergy* 20 Oct 2005 (doi:10.1111/j.1398-9995.2005.00941.x)

Woodcock and colleagues identify a fungal ‘field of dreams’. The authors show that regularly used pillows in the UK harbour up to 16 different species of fungus, most commonly *Aspergillus fumigatus*. Synthetic and feather pillows might therefore represent a previously unidentified source of fungal infection, with implications for susceptible patients with respiratory disease.

## SYMBIOSIS

A secondary symbiosis in progress?

Okamoto, N. & Inouye, I. *Science* **310**, 287 (2005)

This study describes the formative stages of a secondary endosymbiosis between a protist, here referred to as Hatena (‘enigmatic’ in Japanese), and its symbiont — a green algae of the genus *Nephroselmis*. The study illustrates the profound morphological changes in both the host and the symbiont that accompany endosymbiosis. Ultrastructural data and observations of natural populations are used to outline the life cycle of Hatena.

## EPIDEMIOLOGY

Comparative phylogenomics of the food-borne pathogen *Campylobacter jejuni* reveals genetic markers predictive of infection source

Champion, O. L. *et al. Proc. Natl Acad. Sci. USA* **102**, 16043–16048 (2005)

Although poultry has traditionally been regarded as the main source of human *Campylobacter jejuni* infection, this is currently unproven, owing to the limitations of traditional typing methods. In this study, Champion *et al.* combine DNA-microarray-based genotyping with Bayesian-based algorithms to determine the phylogeny of *C. jejuni*. The population structure of *C. jejuni* comprises a livestock-associated and a non-livestock-associated clade. Surprisingly, most human isolates were found in the non-livestock sources, suggesting an environmental reservoir of the pathogen and highlighting the utility of this approach.