Leszek Piotr Pryszcz

Lista publikacji

z dnia 31 października 2015

Publikacje w czasopismach

1. Pryszcz, L. P., *et al.,* 2015, ***The genomic aftermath of hybridization in the opportunistic pathogen Candida metapsilosis***, *PLOS Genetics 11: e1005626*

2. González-Torres, P., Pryszcz, L. P., *et al.,* 2015, ***Interactions between closely related bacterial strains revealed by deep transcriptome sequencing***, *AEM*, AEM.02690-15

3. Gerecova, G., Nebohacova, M., Zeman, I., Pryszcz, L. P., *et al*. 2015, ***Metabolic gene clusters encoding the enzymes of two branches of the 3-oxoadipate pathway in the pathogenic yeast Candida albicans***. *FEMS Yeast Research 15(3) pii: fov006*

4. Pryszcz, L. P., *et al.*, 2014, ***Genome comparison of Candida orthopsilosis clinical strains reveals the existence of hybrids between two distinct subspecies***, *Genome Biol Evol.* 6:1069-78

5. Huerta-Cepas, J., Capella-Gutierrez, S., Pryszcz, L. P., Marcet-Houben, M., & Gabaldón, T., 2014, ***PhylomeDB v4: zooming into the plurality of evolutionary histories of a genome***, *Nucleic Acids Res.* 42: D897-902

6. Pryszcz, L. P., *et al.*, 2013, ***Genome sequencing of clinical and environmental strains reveals unexpected genomic variability in the pathogenic yeast Candida parapsilosis***, *Genome Biol Evol.* 5: 2382-92

7. Hagen, F, *et al*., 2013, ***Ancient Dispersal of the Human Fungal Pathogen Cryptococcus gattii from the Amazon Rainforest***, *PLOS ONE*, 8: e71148

8. Hatzihristidis, T., Liu, S., Pryszcz, L. P., *et al*., 2013, ***PTP-central: A Comprehensive Resource of Protein Tyrosine Phosphatases in Eukaryotic Genomes***, *Methods,* S1046-2023(13)00280-6

9. Valach, M., Pryszcz, L. P., Tomaska, L., Gacser, A., Gabaldon, T. and Nosek, J., 2012, ***Mitochondrial genome variability within the Candida parapsilosis species complex***, *Mitochondrion*, 12: 514-519

10. Huerta-Cepas, J., Capella-Gutierrez, S., Pryszcz, L. P., Denisov, I., Kormes, D., Marcet-Houben, M., & Gabaldón, T., 2011, ***PhylomeDB v3.0: an expanding repository of genome-wide collections of trees, alignments and phylogeny-based orthology and paralogy predictions***, *Nucleic Acids Res.* 39: D556-60

11. Pryszcz, L. P., Huerta-Cepas, J., & Gabaldón, T., 2011,. ***MetaPhOrs: orthology and paralogy predictions from multiple phylogenetic evidence using a consistency-based confidence score***, *Nucleic Acids Res.* 39: e32