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## Marine micro-eukaryote phylogenetics

A selection of evaluations from Faculty of 1000 covering phylogenetic analysis of marine micro-eukaryotes; quantitative proteomics; the proteomics of tubulin-binding; rooting the tree of life with wobble; sizing protein aggregates.

**Phylogenetic and ecological analysis of novel marine stramenopiles.** Massana R, Castresana J, Balagué V, Guillou L, Romari K, Groisillier A, Valentin K, Pedrós-Alió C. *Appl Environ Microbiol* 2004, **70**:3528-3534.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-9-345.asp#Massana>

## Quantitative proteomics

**A model for random sampling and estimation of relative protein abundance in shotgun proteomics.** Liu H, Sadygov RG, Yates JR. *Anal Chem* 2004, **76**:4193-4201.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-9-345.asp#Liu>

## The tubulin-binding proteome

**Large-scale identification of tubulin binding proteins provides insight on subcellular trafficking, metabolic channeling, and signaling in plant cells.** Chuong SD, Good AG, Taylor GJ, Freeman MC, Moorhead GB, Muench DG. *Mol Cell Proteomics* 2004, Jul 12.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-9-345.asp#Chuong>

# Rooting the tree of life with wobble

**Anticodon and wobble evolution.** Tong KL, Wong JT. *Gene* 2004, **333**:169-177.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-9-345.asp#Tong>

# Sizing protein aggregates

**Liquid-chromatography-coupled SAXS for accurate sizing of aggregating proteins.** Mathew E, Mirza A, Menhart N. *J Synchrotron Radiat* 2004, **11**:314-318.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-9-345.asp#Mathew>