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Summary

Profiling honeybee brains; phylogenetic analysis in legumes; marine and freshwater bacterioplankton transcriptomes; RNA secondary structure prediction; unraveling the tissue origin of cancer samples

Profiling honeybee brains

Behavior and the limits of genomic plasticity: power and replicability in microarray analysis of honeybee brains. Cash AC, Whitfield CW, Ismail N, Robinson GE. *Genes Brain Behav* 2005, 4:267-271.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-9-345.asp#Cash>

Phylogenetic analysis in legumes

Placing paleopolyploidy in relation to taxon divergence: a phylogenetic analysis in legumes using 39 gene families. Pfeil BE, Schlueter JA, Shoemaker RC, Doyle JJ. *Syst Biol* 2005, 54:441-454.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-9-345.asp#Pfeil>

Marine and freshwater bacterioplankton transcriptomes

Analysis of microbial gene transcripts in environmental samples. Poretsky RS, Bano N, Buchan A, Lecleir G, Kleikemper J, Pickering M, Pate WM, Moran MA, Hollibaugh JT. *Appl Environ Microbiol* 2005, **71**:4121-4126.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-9-345.asp#Poretsky>

RNA secondary structure prediction

RNA secondary structure prediction by centroids in a Boltzmann weighted ensemble. Ding Y, Chan CY, Lawrence CE. *RNA* 2005, **11**:1157-1166.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-9-345.asp#Ding>

Unraveling the tissue origin of cancer samples

Interpreting expression profiles of cancers by genome-wide survey of breadth of expression in normal tissues. Ge X, Yamamoto S, Tsutsumi S, Midorikawa Y, Ihara S, Wang SM, Aburatani H. *Genomics* 2005, **86**:127-141.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-9-345.asp#Ge>