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Sorghum genome sequencing

A selection of evaluations from Faculty of 1000 covering sorghum genome sequencing, carbohydrate microarrays, metabolite profiling in fungi, *in silico* fate mapping and investigating cri du chat syndrome using array CGH.

Sorghum genome sequencing by methylation filtration. Bedell JA, Budiman MA, Nunberg A, Citek RW, Robbins D, Jones J, Flick E, Rholfing T, Fries J, Bradford K, *et al.* *PLoS Biol* 2005, **3**:e13.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-3-313.asp#Bedell>

Carbohydrate microarrays

The use of carbohydrate microarrays to study carbohydrate-cell interactions and to detect pathogens. Disney MD, Seeberger PH. *Chem Biol* 2004, **11**:1701-1707.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-3-313.asp#Disney>

Metabolite profiling in fungi

Metabolite profiling of fungi and yeast: from phenotype to metabolome by MS and informatics. Smedsgaard J, Nielsen J. *J Exp Bot* 2005, **56**:273-286.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-3-313.asp#Smedsgaard>

In silico fate mapping

A gene regulatory network model for cell-fate determination during *Arabidopsis thaliana* flower development that is robust and recovers experimental gene expression profiles. Espinosa-Soto C, Padilla-Longoria P, Alvarez-Buylla ER. *Plant Cell* 2004, **16**:2923-2939.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-3-313.asp#Espinosa-Soto>

Investigating cri du chat syndrome using array CGH

High-resolution mapping of genotype-phenotype relationships in cri du chat syndrome using array comparative genomic hybridization. Zhang X, Snijders A, Seagraves R, Zhang X, Niebuhr A, Albertson D, Yang H, Gray J, Niebuhr E, Bolund L, Pinkel D. *Am J Hum Genet* 2005, **76**:312-326.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-3-313.asp#Zhang>