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Plant comparative mitochondrial genomics

A selection of evaluations from Faculty of 1000 covering plant comparative mitochondrial genomics; open source proteomics database; identifying disease-associated enzymes; predicting microRNA targets; genome annotation using polymorphisms.

The complete nucleotide sequence and multipartite organization of the tobacco mitochondrial genome: comparative analysis of mitochondrial genomes in higher plants. Sugiyama Y, Watase Y, Nagase M, Makita N, Yagura S, Hirai A, Sugiura M. *Mol Genet Genomics* 2004, December 3.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-2-309.asp#Sugiyama>

Open source proteomics database

Open source system for analyzing, validating, and storing protein identification data. Craig R, Cortens JP, Beavis RC. *J Proteome Res* 2004, 3:1234-1242.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-2-309.asp#Craig>

Identifying disease-associated enzymes

Discovering disease-associated enzymes by proteome reactivity profiling. Barglow KT, Cravatt BF. *Chem Biol* 2004, 11:1523-1531.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-2-309.asp#Barglow>

Predicting micrRNA targets

Fast and effective prediction of microRNA/target duplexes. Rehmsmeier M, Steffen P, Hochsmann M, Giegerich R. *RNA* 2004, **10**:1507-1517.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-2-309.asp#Rehmsmeier>

Genome annotation using polymorphisms

Intraspecies sequence comparisons for annotating genomes. Boffelli D, Weer CV, Weng L, Lewis KD, Shoukry MI, Pachter L, Keys DN, Rubin EM. *Genome Res* 2004, **14**:2406-2411.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2005-6-2-309.asp#Boffelli>