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Fluorescent tagging of *Arabidopsis* proteins

A selection of evaluations from Faculty of 1000 covering the fluorescent tagging of proteins in *Arabidopsis*; a chromosome-wide transcription-factor binding scan; the *Wolbachia* genome; the HNF 1 β transcriptional network; the proteome of the last universal common ancestor.

High-throughput fluorescent tagging of full-length *Arabidopsis* gene products *in planta*. Tian GW, Mohanty A, Chary SN, Li S, Paap B, Drakakaki G, Kopec CD, Li J, Ehrhardt D, Jackson D, Rhee SY, Raikhel NV, Citovsky V. *Plant Physiol* 2004, April 23.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-6-329.asp#Tian>

Chromosome-wide transcription-factor binding scan

CREB binds to multiple loci on human chromosome 22. Euskirchen G, Royce TE, Bertone P, Martone R, Rinn JL, Nelson FK, Sayward F, Luscombe NM, Miller P, Gerstein M, Weissman S, Snyder M. *Mol Cell Biol* 2004, **24**:3804-3814.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-6-329.asp#Euskirchen>

Wolbachia genome

Phylogenomics of the reproductive parasite *Wolbachia pipientis* w Mel: a streamlined genome overrun by mobile genetic elements. Wu M, Sun LV, Vamathevan J, Riegler M, Deboy R, Brownlie JC, McGraw EA, Martin W, Esser C, Ahmadinejad N, Wiegand C, Madupu R, Beanan MJ, Brinkac LM, Daugherty SC, Durkin AS, Kolonay JF, Nelson WC, Mohamoud Y, Lee P, Berry K, Young MB,

Utterback T, Weidman J, Nierman WC, Paulsen IT, Nelson KE, Tettelin H, O'Neill SL, Eisen JA. *PLoS Biol* 2004, **2**:E69.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-6-329.asp#Wu>

HNF 1 β transcriptional network

A transcriptional network in polycystic kidney disease. Gresh L, Fischer E, Reimann A, Tanguy M, Garbay S, Shao X, Hiesberger T, Fiette L, Igarashi P, Yaniv M, Pontoglio M. *EMBO J* 2004, **23**:1657-1668.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-6-329.asp#Gresh>

The proteome of the last universal common ancestor

A novel method for estimating ancestral amino acid composition and its application to proteins of the last universal ancestor. Brooks DJ, Fresco JR, Singh M. *Bioinformatics* 2004, April 8.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2004-5-6-329.asp#Brooks>