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Summary

A selection of evaluations from Faculty of **1000** covering the *Pseudomonas putida* genome, SAGE and microarray analysis of cell death, a screen for phosphopeptide binding domains and an engineered bacterium that uses a non-natural amino acid.

Pseudomonas putida genome

Complete genome sequence and comparative analysis of the metabolically versatile *Pseudomonas putida* KT2440. Nelson KE, Weinel C, Paulsen IT, Dodson RJ, Hilbert H, Martins dos Santos VA, Fouts DE, Gill SR, Pop M, Holmes M, *et al. Environ Microbiol* 2002, **4**:799-808

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-4-315.asp#Nelson>

SAGE analysis of cell death

A SAGE approach to discovery of genes involved in autophagic cell death. Gorski SM, Chittaranjan S, Pleasance ED, Freeman JD, Anderson CL, Varhol RJ, Coughlin SM, Zuyderduyn SD, Jones SJ, Marra MA. *Curr Biol* 2003, **13**:358-363.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-4-315.asp#Gorski>

Array analysis of apoptosis

Genome-wide analyses of steroid- and radiation-triggered programmed cell death in *Drosophila*. Lee CY, Clough EA, Yellon P, Teslovich TM, Stephan DA, Baehrecke EH. *Curr Biol* 2003, **13**:350-357.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-4-315.asp#Lee>

Screen for phosphopeptide binding domain

Proteomic screen finds pSer/pThr-binding domain localizing Plk1 to mitotic substrates. Elia AE, Cantley LC, Yaffe MB. *Science* 2003, **299**:1228-1231.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-4-315.asp#Elia>

Using non-natural amino acids

Generation of a bacterium with a 21 amino acid genetic code. Mehl RA, Anderson JC, Santoro SW, Wang L, Martin AB, King DS, Horn DM, Schultz PG. *J Am Chem Soc* 2003 **125**:935-939.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-4-315.asp#Mehl>