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The core-genome of the genus Lactobacillus contains 266 genes and the pan-genome 20 800 genes. Clustering of the Lactobacillus pan- and core-genome resulted in two highly similar trees. This shows that evolutionary history is traceable in the core-genome and that clustering of the core-genome is sufficient to explore relationships.

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BMC Genomics 2010, 11(1):1 – 17. 42. Chen JH, Jiang H-W, Hsieh E-J, Chen H-Y, Chien C-T, Hsieh H-L, Lin T-P. Drought and salt stress tolerance of an Arabidopsis Glutathione S-Transferase U17 knockout mutant are attributed to the combined effect of glutathione and abscisic acid.

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The core collection comprises three different subpopulations. Genotypes in subpopulation 1 are the most diverse genotypes and could be used in future breeding programs if they have desired traits. The distribution of LD hotspots across the genome was investigated which provides useful information on the genomic regions that includes interesting genes.

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This resulted in the identification of a set of core functionalities necessary for a bacterium to survive and reproduce, as a universal minimal gene set represented in all living systems . In order to explore the efficacy of genome-resolved metagenomics in providing comprehensive biological information on the uncultured members of the human microbiome, here we wondered if UMGS, which now remain bioinformatic entities, possesses the minimal set of core genes necessary – even if not ...

Do the human gut metagenomic species possess the minimal ...

RNA interference (RNAi) is a highly conserved, sequence-specific gene silencing mechanism present in Eukaryotes. Three RNAi pathways are known, namely micro-RNA (miRNA), piwi-interacting RNA (piRNA) and short interfering RNA (siRNA). However, little knowledge exists about the proteins involved in these pathways in Acari. Moreover, variable successes has been obtained in gene knockdown via ...

A genome-wide screening for RNAi pathway proteins in Acari ...

BMC Genomics BioMed Central Open Access Research article Muscle regeneration in dystrophin-deficient mdx mice studied by gene expression profiling R Turk1,3, E Sterrenburg1, EJ de Meijer1, G-JB van Ommen1, JT den Dunnen1,2 and PAC 't Hoen*1 Address: 1Center for Human and Clinical Genetics, Leiden University Medical Center, Wassenaarseweg 72, 2333 AL Leiden, Nederland, 2Leiden Genome Technology ...

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BMC Genomics BioMed Central Open Access Research article Uncovering rate variation of lateral gene transfer during bacterial genome evolution Weilong Hao and G Brian Golding* Address: Department of Biology, McMaster University, Hamilton, Ontario L8S 4K1, Canada Email: Weilong Hao - ; G Brian Golding* - * Corresponding author

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BMC Genomics BioMed Central Open Access Research article Autocorrelation analysis reveals widespread spatial biases in microarray experiments Amnon Koren1, Itay Tirosh1 and Naama Barkai*1,2 Address: 1Department of Molecular Genetics, Weizmann Institute of Science, Rehovot 76100, Israel and 2Department of Physics of Complex Systems, Weizmann Institute of Science, Rehovot 76100, Israel Email ...

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