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The b-Zip transcription factor AtfA plays a key role in regulating stress responses in the filamentous fungus *Aspergillus nidulans*. To identify the core regulons of AtfA, we examined genome-wide expression changes caused by various stresses in the presence/absence of AtfA using *A. nidulans* microarrays. We also intended to address the intriguing question regarding the existence of core ...

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Antagonistic co-evolution can drive rapid adaptation in pathogens and shape genome architecture. Comparative genome analyses of several fungal pathogens revealed highly variable genomes, for many species characterized by specific repeat-rich genome compartments with exceptionally high sequence variability. Dynamic genome structure may enable fast adaptation to host genetics.

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BioMed Central Page 1 of 11 (page number not for citation purposes) BMC Genomics Research article Open Access Discernment of possible mechanisms of hepatotoxicity via biological processes over-represented by co-expressed genes Jeff W Chou<sup>1,2</sup> and Pierre R Bushel\*<sup>1</sup>

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is a positive selection towards mutations leading to amino acid changes. CONCLUSIONS: Genomic variation within the core genome is useful for investigating molecular evolution and providing candidate genes for bacterial genome typing. Identification of genes with different degrees of variation is important especially in trend analysis.

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affecting children. The three core symptoms of autism spectrum disorders (ASD) are: 1) deficits in social interactions and understanding, 2) aberrant communication and/or language development, and 3) restricted interests and repetitive, stereotyped behaviors [1]. To date, there Published: 18 May 2006 BMC Genomics 2006, 7:118 doi:10.1186/1471 ...

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### **BMC Genomics BioMed Central**

Results. We generated a draft genome for *R. culicivox* and compared its gene content with that of

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*C. elegans*, a second nematode, the vertebrate parasite *Trichinella spiralis*, and a representative arthropod, *Tribolium castaneum*. This comparison revealed that *R. culicivora* has retained components of the conserved ecdysozoan developmental gene toolkit lost in *C. elegans*.

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