The fifth industrial fluid properties simulation challenge

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A graphical unitary group approach-based hybrid density functional theory multireference configuration interaction method

The Chlamydomonas genome reveals the evolution of key animal and plant functions

RL-SAGE and microarray analysis of the rice transcriptome after Rhizoctonia solani infection

Magnaporthe grisea infection triggers RNA variation and antisense transcript expression in rice

Patient confidentiality in the research use of clinical medical databases

Use of robust-long serial analysis of gene expression to identify novel fungal and plant genes involved in host-pathogen interactions.

Deep and comparative analysis of the mycelium and appressorium transcriptomes of Magnaporthe grisea using MPSS, RL-SAGE, and oligoarray methods
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Hardware/software integration for FPGA-based all-pairs shortest-paths

Network analysis using transitive closure: New methods for exploring networks