Recovery of stilbenoids
A cis- or trans- stilbenoid of the general formula (1) in which each of R1, R2, R3, R4 and R5 is hydrogen or hydroxy, or a glycosylated or oligomeric form thereof, such as resveratrol or pinosylvin is produced by cultivating a microorganism such as a genetically engineered yeast to produce said stilbenoid in a culture medium in solid form, and is separated by filtration or settling.

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Metabolically engineered cells for the production of pinoylvin
A genetically engineered micro-organism having an operative metabolic pathway producing cinnamoyl-CoA and producing pinoylvin therefrom by the action of a stilbene synthase is used for pinoylvin production. Said cinnamic acid may be formed from L-phenylalanine by a L-phenylalanine ammonia lyase (PAL) which is one accepting phenylalanine as a substrate and producing cinammic acid therefrom, preferably such that if the PAL also accepts tyrosine as a substrate and forms coumaric acid therefrom, the ratio Km(phenylalanine)/Km(tyrosine) for said PAL is less than 1:1 and if said micro-organism produces a cinammate-4-hydroxylase enzyme (C4H), the ratio Kcat(PAL)/Kcat(C4H) is at least 2:1.

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Metabolically Engineered Fungal Cells With Increased Content Of Polysaturated Fatty Acids
This invention relates to the production of fatty acids and particularly to the production of the polysaturated fatty acids (PUFAs) arachidonic acid (ARA) and eicosapentaenoic acid (EPA) in genetically engineered fungal cells, in particular, to metabolically engineered Saccharomyces cerevisiae cells with increased content of ARA and EPA. The invention especially involves improvement of the PUFA content in the host organism through various over-expression of e.g.
cytochrome b5 and cytochrome b5 reductase involved in fatty acid desaturation, and heterologous expression of cytochrome b5 and cytochrome b5 reductase and expression of heterologous fatty acid synthases.

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**Metabolic network-driven analysis of genome-wide transcription data from Aspergillus nidulans.**

**General information**
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Organisations: Department of Systems Biology, Center for Microbial Biotechnology, Center for Biological Sequence Analysis
Contributors: David, H. S. M., Hofmann, G., Soberano de Oliveira, A. P., Jarmer, H. Ø., Nielsen, J.
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**CreA influences the metabolic fluxes of Aspergillus nidulans during growth on glucose and xylose.**

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Contributors: David, H. S. M., Krogh, A. M., Roca, C., Åkesson, M., Nielsen, J.
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Investigation of network topology and quantification of fluxes in central carbon metabolism of Aspergillus nidulans under different conditions of glucose repression

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Contributors: David, H., Åkesson, M., Nielsen, J.
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Towards a systems level understanding of cellular function in Aspergillus

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Reconstruction of the central carbon metabolism of Aspergillus niger

The topology of central carbon metabolism of Aspergillus niger was identified and the metabolic network reconstructed, by integrating genomic, biochemical and physiological information available for this microorganism and other related fungi. The reconstructed network may serve as a valuable database for annotation of genes identified in future genome sequencing projects on aspergillus. Based on the metabolic reconstruction, a stoichiometric model was set up that includes 284 metabolites and 335 reactions, of which 268 represent biochemical conversions and 67 represent transport processes between the different intracellular compartments and between the cell and the extracellular medium. The stoichiometry of the metabolic reactions was used in combination with biosynthetic requirements for growth and pseudo-steady state mass balances over intracellular metabolites for the quantification of metabolic fluxes using metabolite balancing. This framework was employed to perform an in silico characterisation of the phenotypic behaviour of A. niger grown on different carbon sources. The effects on growth of single reaction deletions were assessed and essential biochemical reactions were identified for different carbon sources. Furthermore, application of the stoichiometric model for assessing the metabolic capabilities of A. niger to produce metabolites was evaluated by using succinate production as a case study.

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