J Biochem Tech (2008) 1(1):30-37
ISSN: 0974-2328

Recent abstracts in biochemical technology

R R Siva Kiran, Brijesh

"Recent abstracts in biochemical technology" is a collection of interesting research articles published in "List of biochemical technology journals" (Table 1). The abstracts are most likely to report significant results in biochemical technology.

- Sylvain P, Alamgir Md, Green JR et al (2008) Computational Methods For Predicting Protein–Protein Interactions, Advances in Biochemical Engineering/Biotechnology

Protein–protein interactions (PPIs) play a critical role in many cellular functions. A number of experimental techniques have been applied to discover PPIs; however, these techniques are expensive in terms of time, money, and expertise. There are also large discrepancies between the PPI data collected by the same or different techniques in the same organism. We therefore turn to computational techniques for the prediction of PPIs. Computational techniques have been applied to the collection, indexing, validation, analysis, and extrapolation of PPI data. This chapter will focus on computational prediction of PPI, reviewing a number of techniques including PIPE, developed in our own laboratory. For comparison, the conventional large-scale approaches to predict PPIs are also briefly discussed. The chapter concludes with a discussion of the limitations of both experimental and computational methods of determining PPIs.

January 18, 2008, Advances in Biochemical Engineering/Biotechnology.

- Beutling U, Stading K, Stradal T, Frank R (2008) Large-Scale Analysis of Protein–Protein Interactions Using Cellulose-Bound Peptide Arrays. Advances in Biochemical Engineering/Biotechnology

Peptide arrays for screening large numbers of peptide fragments and probing with large numbers of samples is discussed.

R R Siva Kiran*

Department of Biotechnology, M S Ramaiah Institute of Technology, MSR Nagar, Bangalore – 560054, India

Brijesh
Department of Chemical Engineering, M S Ramaiah Institute of Technology, MSR Nagar, Bangalore – 560054, India

*Tel: 0091 80 23600822, Fax: 0091 80 23603124
E-mail: rrskiran@msrit.edu

April 17, 2008, Advances in Biochemical Engineering/Biotechnology.

- Takaaki I, Murayama Y, et al (2008) Probing force-induced unfolding intermediates of a single staphylococcal nuclease molecule and the effect of ligand binding, Biochemical and Biophysical Research Communications

Single-molecule manipulation techniques have given experimental access to unfolding intermediates of proteins that are inaccessible in conventional experiments. A detailed characterization of the intermediates is a challenging problem that provides new possibilities for directly probing the energy landscape of proteins. We investigated single-molecule mechanical unfolding of a small globular protein, staphylococcal nuclease (SNase), using atomic force microscopy. The unfolding trajectories of the protein displayed sub-molecular and stochastic behavior with typical lengths corresponding to the size of the unfolded substructures. Our results support the view that the single protein unfolds along multiple pathways as suggested in recent theoretical studies. Moreover, we found the drastic change, caused by the ligand and inhibitor bindings, in the mechanical unfolding dynamics.

August 26, 2008, Biochemical and Biophysical Research Communications

- Taru T, Tuulia T, et al. (2008) A multi-metabolite analysis of serum by 1H NMR spectroscopy: Early systemic signs of Alzheimer's disease. Biochemical and Biophysical Research Communications

A three-molecular-window approach for 1H NMR spectroscopy of serum is presented to obtain specific molecular data on lipoproteins, various low-molecular-weight metabolites, and individual lipid molecules together with their degree of (poly)(un)saturation. The multiple data were analysed with self-organising maps, illustrating the strength of the approach as a holistic metabonomics framework in solely data-driven metabolic phenotyping. We studied 180 serum samples of which 30% were related to mild cognitive impairment (MCI), a neuropsychological diagnosis with severely increased risk for Alzheimer's disease (AD). The results underline the association between MCI and the metabolic syndrome (MetS). Additionally, the low relative amount of ω-3 fatty acids appears more indicative of MCI than low serum ω-3 or polyunsaturated fatty acid concentration as such. The analyses also feature the role of elevated glycoproteins in the risk for AD, supporting the view that coexistence of inflammation and the MetS forms a high risk condition for cognitive decline.

Table1: List of Biochemical Technology Journals

Journal Name	Impact Factor	Journal Description	Website
ADVANCES IN BIOCHEMICAL ENGINEERING	3.253	Advances in Biochemical Engineering/Biotechnology reviews actual trends in modern biotechnology. Its aim is to cover all aspects of this interdisciplinary technology where knowledge, methods and expertise are required for chemistry, biochemistry, microbiology, genetics, chemical engineering and computer science.	http://www.springer.com/series/10
BIOCHEMICAL AND BIOPHYSICAL RESEARCH	2.749	Biochemical and Biophysical Research Communications is the premier international journal devoted to the very rapid dissemination of timely and significant experimental results in diverse fields of biological research.	http://www.sciencedirect.com/science/journal/0006291X
BIOCHEMICAL ENGINEERING JOURNAL	1.872	The Biochemical Engineering Journal aims to promote progress in the crucial chemical engineering aspects of the development of biological processes associated with everything from raw materials preparation to product recovery, relevant to industries as diverse as medical/healthcare, food and environmental protection.	http://www.sciencedirect.com/science/journal/1369703X
BIOCHEMICAL GENETICS	0.876[1]	Biochemical Genetics links the sciences of biology, chemistry and genetics by offering an interdisciplinary forum for the discussion of new developments.	http://www.springer.com/biomed/human+genetics/journal/10528
BIOCHEMICAL JOURNAL	4.100[2]	The coverage includes different knowledge environments: Cell, Disease, Energy, Gene, Plant, Signal, Structure	http://www.biochemj.org/bj/default.htm
BIOCHEMICAL PHARMACOLOGY	4.006	Biochemical Pharmacology is an international journal devoted to publishing original work on the interaction of drugs and nontherapeutic xenobiotics with biological systems.	http://www.sciencedirect.com/science/journal/00062952
BIOCHEMICAL SOCIETY SYMPOSIUM	3.300	Journal covers selected topic in the forefront of research in any aspect of the cellular and molecular life sciences.	http://symposia.biochemistry.org/
BIOCHEMICAL SOCIETY TRANSACTIONS	3.447	The journal captures the exciting science presented at the Biochemical Society Annual Symposium, Focused Meetings and Independent Meetings supported by the Society as a series of mini-reviews.	http://www.biochemsoctrans.org/
BIOCHEMICAL SYSTEMATICS AND ECOLOGY	1.048	The application of biochemistry to problems relating to systematic biology of organisms (biochemical systematics) & the role of biochemistry in interactions between organisms or between an organism and its environment (biochemical ecology).	http://www.sciencedirect.com/science/journal/03051978
CHEMICAL AND BIOCHEMICAL ENGINEERING QUARTERLY	0.632	The scope of the journal is wide and no limitation except relevance to chemical and biochemical engineering is required.	http://www.fkit.hr/cabeq/index.html
JOURNAL OF BIOCHEMICAL AND BIOPHYSICAL METHODS	1.403[3]	The development of new methods or the significant modification of existing techniques to solve theoretical and experimental problems in the field of life sciences, particularly biochemistry and biophysics.	http://www.sciencedirect.com/science/journal/0165022X
JOURNAL OF BIOCHEMICAL AND MOLECULAR TOXICOLOGY	1.410[4]	The scope includes effects on the organism at all stages of development, on organ systems, tissues, and cells as well as on enzymes, receptors, hormones, and genes.	http://as.wiley.com/WileyCDA/WileyTitle/productCd-JBT.html
JOURNAL OF BIOCHEMICAL TECHNOLOGY	N/A	Coverage includes enzymes and proteins; applied genetics and molecular biotechnology; computational biology, genomics and proteomics; metabolic & tissue engineering; medical, environmental, food and agro biotechnology; biodiversity, reactor design, modeling. The journal is a unique source for scientists interested in both engineering as well as basic biology research.	http://jbt.biodbs.info/
JOURNAL OF COMPARATIVE PHYSIOLOGY B-BIOCHEMICAL	2.209	The journal publishes topics related to comparative physiology of invertebrate and vertebrate animals. Special emphasis is placed on integrative studies that elucidate mechanisms at the whole-animal, organ, tissue, cellular and/or molecular levels.	http://www.springerlink.com/content/100425/
MOLECULAR AND BIOCHEMICAL PARASITOLOGY	2.896	The journal provides a medium for rapid publication of investigations of the molecular biology and biochemistry of parasitic protozoa and helminths, and their interactions with both the definitive and intermediate host.	http://www.sciencedirect.com/science/journal/01666851
PHYSIOLOGICAL AND BIOCHEMICAL ZOOLOGY	2.010[5]	The journal publishes the results of original investigations in animal physiology and biochemistry at all levels of organization, from the molecular to the organismic, focusing on adaptations to the environment.	http://www.journals.uchicago.edu/page/pbz/brief.html
TRENDS IN BIOCHEMICAL SCIENCES	13.90	TiBS covers discoveries in the fields of biophysics, biochemistry, genetics, microbiology, and cell biology.	http://www.sciencedirect.com/science/journal/09680004
CHEMBIOCHEM	3.446	ChemBioChem is a source for important primary and secondary information across the whole field of chemical biology, bio(in)organic chemistry, and biochemistry.	http://www3.interscience.wiley.com/journal/72510898/home

[1]http://www.ovid.com/site/catalog/Journal/1447.jsp, [2]http://en.wikipedia.org/wiki/Biochemical_Journal, [3]http://www.speciation.net/Appl/Literature/Source/sources.html?id=1237
[4]http://www.genebee.msu.su/journals/if01j1.html, [5]http://www.genebee.msu.su/journals/if01p.html and impact factors of other journals are taken from corresponding journal website
N/A-Not Available

August 26, 2008, Biochemical and Biophysical Research Communications

- Yun X, Simon G et al (2008) Rapid detection and identification of a pathogen's DNA using Phi29 DNA polymerase. Biochemical and Biophysical Research Communications

Zoonotic pathogens including those transmitted by insect vectors are some of the most deadly of all infectious diseases known to mankind. A number of these agents have been further weaponized and are widely recognized as being potentially significant biothreat agents. We describe a novel method based on multiply-primed rolling circle in vitro amplification for profiling genomic DNAs to permit rapid, cultivation-free differential detection and identification of circular plasmids in infectious agents. Using Phi29 DNA polymerase and a two-step priming reaction we could reproducibly detect and characterize by DNA sequencing circular DNA from Borrelia burgdorferi B31 in DNA samples containing as little as 25 pg of Borrelia DNA amongst a vast excess of human DNA. This simple technology can ultimately be adapted as a sensitive method to detect specific DNA from both known and unknown pathogens in a wide variety of complex environments.

August 26, 2008, Biochemical and Biophysical Research Communications

- Xing Y, Lu X et al (2008) The effect of high intensity focused ultrasound treatment on metastases in a murine melanoma model.. Biochemical and Biophysical Research Communications

This study aims to assess the risk of high intensity focused ultrasound (HIFU) therapy on the incidence of distant metastases and to investigate its association with HIFU-elicited anti-tumor immunity in a murine melanoma (B16-F10) model. Tumor-bearing legs were amputated immediately after or 2 days following HIFU treatment to differentiate the contribution of the elicited anti-tumor immunity. In mice undergoing amputation immediately after mechanical, thermal, or no HIFU treatment, metastasis rates were comparable (18.8%, 13.3%, and 12.5%). In contrast, with a 2-day delay in amputation, the corresponding metastasis rates were 6.7%, 11.8%, and 40%, respectively. Animal survival rate was higher and CTL activity was enhanced in the HIFU treatment groups. Altogether, our results suggest that HIFU treatment does not increase the risk of distant metastasis. Instead, HIFU treatment can elicit an anti-tumor immune response that may be harnessed to improve the overall effectiveness and quality of cancer therapy.

August 24, 2008, Biochemical and Biophysical Research Communications

- Takahashi S, Sakakibara Y et al (2008) Molecular cloning, expression, and characterization of mouse amine N-sulfotransferases. Biochemical and Biophysical Research Communications

By searching the GenBank database, we recently identified a novel mouse cytosolic sulfotransferase (SULT) cDNA (IMAGE Clone ID 679629) and a novel mouse SULT gene (LOC 215895). Sequence analysis revealed that both mouse SULTs belong to the cytosolic SULT3 gene family. The recombinant form of these two newly identified SULTs, designated SULT3A1 and SULT3A2, were expressed using the pGEX-4T-1 glutathione S-transferase fusion system and purified from transformed BL21 Escherichia coli cells. Both purified SULT3A1 and SULT3A2 exhibited strong amine N-sulfonating activities toward 1-naphthylamine among a variety of endogenous and xenobiotic compounds tested as substrates. Kinetic constants of the sulfation of 1-naphthylamine and 1-naphthol by these two enzymes were determined. Collectively, these results imply that these two amine-sulfonating SULT3s may play essential roles in the metabolism and detoxification of aromatic amine compounds in the body.

August 24, 2008, Biochemical and Biophysical Research Communications

- Kenneth LS, Caleb BM et al. Thermodynamic analysis of the heterodimerization of leucine zippers of Jun and Fos transcription factors. Biochemical and Biophysical Research Communications

Jun and Fos are components of the AP1 family of transcription factors and bind to the promoters of a diverse multitude of genes involved in critical cellular responses such as cell growth and proliferation, cell cycle regulation, embryonic development and cancer. Here, using the powerful technique of isothermal titration calorimetry, we characterize the thermodynamics of heterodimerization of leucine zippers of Jun and Fos. Our data suggest that the heterodimerization of leucine zippers is driven by enthalpic forces with unfavorable entropy change at physiological temperatures. Furthermore, the basic regions appear to modulate the heterodimerization of leucine zippers and may undergo at least partial folding upon heterodimerization. Large negative heat capacity changes accompanying the heterodimerization of leucine zippers are consistent with the view that leucine zippers do not retain α-helical conformations in isolation and that the formation of the native coiled-coil α-helical dimer is attained through a coupled folding-dimerization mechanism.

August 24, 2008, Biochemical and Biophysical Research Communications

- Jorge P, Romero F et al (2008) Some effects of the venom of the Chilean spider Latrodectus mactans on endogenous ion-currents of Xenopus laevis oocytes. Biochemical and Biophysical Research Communications

A study was made of the effects of the venom of the Chilean spider Latrodectus mactans on endogenous ion-currents of Xenopus laevis oocytes. 1 μg/ml of the venom made the resting plasma membrane potential more negative in cells voltage-clamped at −60 mV. The effect was potentially due to the closure of one or several conductances that were investigated further. Thus, we determined the effects of the venom on the following endogenous ionic-currents: (a) voltage-activated potassium currents, (b) voltage-activated chloride-currents, and (c) calcium-dependent chloride-currents (Tout). The results suggest that the venom exerts its action mainly on a transient outward potassium-current that is probably mediated by a Kv channel homologous to shaker. Consistent with the electrophysiological evidence we detected the expression of the mRNA coding for xKv1.1 in the oocytes.

August 24, 2008, Biochemical and Biophysical Research Communications

- Laura Barsanti, Coltelli P et al (2008) Low-resolution characterization of the 3D structure of the Euglena gracilis photoreceptor. Biochemical and Biophysical Research Communications

This paper deals with the first characterization of the structure of the photoreceptive organelle of the unicellular alga Euglena gracilis (Euglenophyta). This organelle has a three-dimensional organization consisting of up to 50 closely stacked membrane lamellae. Ionically induced unstacking of the photoreceptor lamellae revealed ordered arrays well suited to structural analysis by electron microscopy and image analysis, which ultimately yielded a low-resolution picture of the structure. Each lamella is formed by the photoreceptive membrane protein of the cell assembled within the membrane layer in a hexagonal lattice. The first order diffraction spots in the calculated Fourier transform reveals the presence of 6-fold symmetrized topography (better resolution about 90 Å). The 2D and 3D structural data are very similar with those recently published on proteorodopsin, a membrane protein used by marine bacterio-plankton as light-driven proton pump. In our

opinion these similarity indicate that a photoreceptive protein belonging to the same superfamily of proteorodopsin could form the Euglena photoreceptor.

August 21, 2008, Biochemical and Biophysical Research Communications

- John E McRory, Rehak R et al (2008) Syntaxin 1A is required for normal in utero development. Biochemical and Biophysical Research Communications

We have generated a syntaxin 1A knockout mouse by deletion of exons 3 through 6 and a concomitant insertion of a stop codon in exon 2. Heterozygous knockout animals were viable with no apparent phenotype. In contrast, the vast majority of homozygous animals died in utero, with embryos examined at day E15 showing a drastic reduction in body size and development when compared to WT and heterozygous littermates. Surprisingly, out of a total of 204 offspring from heterozygous breeding pairs only four homozygous animals were born alive and viable. These animals exhibited reduced body weight, but showed only mild behavioral deficiencies. Taken together, our data indicate that syntaxin 1A is an important regulator of normal in utero development, but may not be essential for normal brain function later in life.

August 14, 2008, Biochemical and Biophysical Research Communications

- Hidenori Nonaka, Watabe T et al (2008) Development of stabilin2^{+} endothelial cells from mouse embryonic stem cells by inhibition of TGFβ/activin signaling. Biochemical and Biophysical Research Communications

To understand the endothelial cell (EC) development, arterial, venous, and lymphatic EC (LEC) have been successfully induced from embryonic stem cells (ESC). However, tissue-specific EC, such as hepatic sinusoidal EC (HSEC), have never been generated from ESC. Based on the findings that TGFβ/activin signaling negatively regulates differentiation of both LEC and HSEC, and that HSEC and LEC are distinguishable by the expression of marker genes, we assessed the role of TGFβ/activin signaling in EC development from ESC. Here we show that the inhibition of TGFβ/activin signaling by a TGFβ receptor I (TGFβRI) kinase inhibitor increased the expression of Lyve1 and stabilin2 but not podoplanin in CD31+CD34+ EC derived from ESC. EC generated by the inhibition of TGFβRI signaling also exhibited stronger endocytic activity than control EC, indicating that their phenotype is similar to fetal HSEC. Our results reveal that TGFβ/activin signaling negatively regulates the early events of HSEC differentiation.

August 14, 2008, Biochemical and Biophysical Research Communications

- Xiaobing Han, Xi L et al (2008) The potassium ion channel opener NS1619 inhibits proliferation and induces apoptosis in A2780 ovarian cancer cells. Biochemical and Biophysical Research Communications

Diverse types of voltage-gated potassium (K^{+}) channels have been shown to be involved in regulation of cell proliferation. The maxi-conductance Ca^{2+}-activated K^{+} channels (BK channels) may play an important role in the progression of human cancer. To explore the role of BK channels in regulation of apoptosis in human ovarian cancer cells, the effects of the specific BK channel activator NS1619 on induction of apoptosis in A2780 cells were observed. Following treatment with NS1619, cell proliferation was measured by MTT assay. Apoptosis of A2780 cells pretreated with NS1619 was detected by agarose gel electrophoresis of cellular DNA and flow cytometry. Our data demonstrate that NS1619 inhibits the proliferation of A2780 cells in a dosage and time dependent manner IC_{50} = 31.1 μM, for 48 h pretreatment and induces apoptosis. Western blot analyses showed that the anti-proliferation effect of NS1619 was associated with increased expression of p53, p21, and Bax. These results indicate that BK channels play an important role in regulating proliferation of human ovarian cancer cells and may induce apoptosis through induction of $p21^{Cip1}$ expression in a p53-dependent manner.

August 13, 2008, Biochemical and Biophysical Research Communications

- Salvatore Patané, Pietrancosta N et al (2008) A new Met inhibitory-scaffold identified by a focused forward chemical biological screen. Biochemical and Biophysical Research Communications

The receptor tyrosine kinase Met is crucial for the genetic program causing cancer progression and metastasis. Its nodal function during aggressiveness and resistance acquisition poses Met inhibition as an obligatory step in anti-cancer targeted therapy. Here, we applied a "Met-focussed" forward chemical biological screen to discover new agents antagonizing Met-triggered biological functions. The identified new scaffold, JLK1360, has a dual mechanism of action towards Met: it impairs Met signalling and also prevents its restoration after degradation. Docking and molecular dynamics provide evidences on the interacting mode of JLK1360 within the Met ATP-binding pocket. Moreover, computational and biochemical studies also highlighted that JLK1360 has a good degree of selectivity towards Met than other RTKs tested. Altogether, these findings demonstrate that the approach we have applied is a powerful strategy to identify compounds with combined properties towards a chosen target. Our studies show how integration of chemistry, biology and computational analysis can provide robust strategies to identify new inhibitory scaffolds suitable for further development of anti-cancer targeted therapies.

August 12, 2008, Biochemical and Biophysical Research Communications

- Helena Mistry, Gibson L et al (2008) Interplay between Np95 and Eme1 in the DNA damage response. Biochemical and Biophysical Research Communications

Mus81 (methyl methansulfonate UV sensitive clone 81) and Eme1 (essential meiotic endonuclease 1, also known as MMS4) form a heterodimeric endonuclease that is critical for genomic stability and the response to DNA crosslink damage and replication blockade. However, relatively little is known as to how this endonuclease is regulated following DNA damage. Here, we report mammalian Eme1 interacts with Np95, an E3 ubiquitin ligase that participates in chromatin modification, replication-linked epigenetic maintenance and the DNA damage response. Np95 and Eme1 co-localize on nuclear chromatin following exposure of cells to camptothecin, an agent that promotes the collapse of replication forks. The observed co localization following DNA damage was found to be dependent on an intact RING finger, the structural motif that encodes the E3 ubiquitin ligase activity of Np95. Taken together, these findings link Mus81–Eme1 with the replication-associated chromatin modifier functions of Np95 in the cellular response to DNA damage.

August 8, 2008, Biochemical and Biophysical Research Communications

- Soumen Mukherjee, Das P et al (2008) Enhanced production of biosurfactant by a marine bacterium on statistical screening of nutritional parameters. Biochemical Engineering Journal

Marine microorganisms can serve as rich sources for novel biosurfactants with diverse biological activities. In the present investigation, the nutritional requirement for the growth and biosurfactant production by a marine bacterium was determined using a

Plackett–Burman-based statistical screening procedure. Six out of the eleven factors of a reported production medium were found to be critically affecting the biosurfactant metabolism. Glucose, the carbon substrate of the medium was the most influential factor with an effect contribution of 78.13% and a very low *p*-value of <0.001. Glucose, NH_4NO_3 and $FeSO_4{\cdot}7H_2O$ had a direct proportional correlation with biosurfactant production while, K_2HPO_4, KH_2PO_4 and $MgSO_4{\cdot}7H_2O$ showed inversely proportional relationship with biosurfactant production in the selected experimental range. A simpler modified medium (MM) was formulated based on the statistical screening results. Modified medium combination (MM-1) having the following composition in g l^{-1}: glucose 30; NH_4NO_3 6.0; K_2HPO_4 1.1; $MgSO_4{\cdot}7H_2O$ 0.3; KH_2PO_4 2.8×10^{-2} and $FeSO_4$. $7H_2O$ 6×10^{-2} showed 84.7% increase in biosurfactant yield over the reported medium (SM). Fourier transform infrared spectroscopy and thin layer chromatography studies showed that the biosurfactants produced in the modified medium (MM) were similar to those produced in the reported medium (SM).

July 15, 2008, Biochemical Engineering Journal

- Lianghua Wang, Shen S et al (2008) Adsorption and elution behaviors of bovine serum albumin in metal-chelated affinity cryogel beds. Biochemical Engineering Journal

Metal-chelated supermacroporous cryogels are effective supports for affinity chromatographic separation of biomolecules in downstream processes. In this work, polyacrylamide cryogel beds were prepared in glass columns (16 mm inner diameter) and coupled with iminodiacetic acid (IDA). These cryogels were loaded with Zn^{2+} and Ni^{2+} and the so-called Zn^{2+}-IDA-cryogels and Ni^{2+}-IDA-cryogels were obtained. Permeabilities and height equivalent to theoretical plates (HETPs) of these cryogel beds were measured and the cryogel structure was analyzed using scanning electron microscopy (SEM). Bovine serum albumin (BSA) was employed as a model protein to elucidate the adsorption and elution behaviors of these cryogels under various conditions, such as different flow rate, solution pH, and composition of the eluents. The results showed that the Zn^{2+}-IDA-cryogels and Ni^{2+}-IDA-cryogels in this study had interconnected supermacropores and high water permeabilities ($\sim 10^{-11}$ m^2). The loading flow velocity had a weak influence on the breakthrough curves and binding capacities for BSA, while the solution pH had an evident effect on the binding capacities for BSA in these cryogels. Maximum binding capacity for BSA was observed near the isoelectric point of BSA. The bound BSA can be eluted effectively using an imidazole solution. A low-eluting flow rate was found to be beneficial to the elution process. Possible mechanisms were proposed and discussed.

July 15, 2008, Biochemical Engineering Journal

- Teresa Lopes da Silva, Reis A et al (2008) Physiological effects of the addition of n-dodecane as an oxygen vector during steady-state Bacillus licheniformis thermophillic fermentations perturbed by a starvation period or a glucose pulse. Biochemical Engineering Journal

The effect of the presence of n-dodecane as a potential oxygen vector during oxygen-limited continuous cultures of a Bacillus strain was studied, under extreme nutrient supply conditions: glucose excess, limitation and starvation. The addition of n-dodecane to the aqueous phase of a mechanically agitated and aerated fermentation increased the kLa by up to 35%. The n-dodecane additions to Bacillus licheniformis cells during starvation (oxygen limitation with concomitant glucose starvation) caused a severe detrimental progressive change in cell physiological state with respect to cytoplasmic membrane polarisation and permeability which was mitigated against by alleviating either the oxygen limitation (by increasing the mean energy dissipation rate or by the addition of n-dodecane as an oxygen vector) or by alleviating the carbon limitation (by resuming the carbon feed or by the addition of a glucose pulse). Further that during periods of excess glucose (glucose pulse) a much higher kLa was required to prevent the onset of anaerobic mixed acid fermentation than could be provided by the addition of n-dodecane alone. n-Dodecane can be used to increase the kLa when added in sufficient quantities to the aqueous phase of a mechanically agitated and aerated bioreactor but the magnitude of this increase is process and vessel geometry specific.

July 9 2008, Biochemical Engineering Journal

- Syed Asif Nizam, Shimizu K (2008) Effects of arcA and arcB genes knockout on the metabolism in Escherichia coli under anaerobic and icroaerobic conditions. Biochemical Engineering Journal

The Arc system is a two-component regulatory system composed of ArcA and ArcB in Escherichia coli. In the present study, the effects of arcA and arcB genes knockout on the TCA cycle activation in E. coli were investigated for the anaerobic and microaerobic conditions. Under anaerobic condition, the TCA cycle was up-regulated along with high lactate production, together with up-regulation of LDH for arcB mutant as compared with the parent strain. Due to down-regulation of aceE, aceF and lpdA genes which code for PDHc and low activity of Pfl in arcB mutant, the glycolysis as well as oxidative pentose phosphate pathway was down-regulated under anaerobic condition. The TCA cycle enzymes were further up-regulated when nitrate was added by modifying the redox state along with lower lactate production for arcB mutant. Different from the case of anaerobic condition, the glycolysis was activated under microaerobic condition, which may be partly due to the increased activity of PDHc encoded by aceE, F and lpdA genes. Under microaerobic condition, the TCA cycle genes together with their corresponding enzymes were up-regulated for arcB mutant as compared with the parent strain. These characteristics were further enhanced in arcA mutant as compared with the case of arcB mutant. The up-regulation of the TCA cycle together with down-regulation of cydB gene expression caused higher redox state in the arcA/B mutants, which in turn repressed the TCA cycle. Then the TCA cycle could be further increased by the addition of nicotinic acid (NA).

July 3, 2008, Biochemical Engineering Journal

- Serpil Ozmihci, Kargi F (2008) Ethanol production from cheese whey powder solution in a packed column bioreactor at different hydraulic residence times. Biochemical Engineering Journal

Cheese whey powder (CWP) solution containing 50 g L^{-1} total sugar was fermented to ethanol in a continuously operated packed column bioreactor (PCBR) using olive pits as support particles for cell attachment. Pure culture of *Kluyveromyces marxianus* (DSMZ 7239) was used in the PCBR for ethanol formation from lactose content of CWP solution. Sugar utilization and ethanol formation were investigated as function of the hydraulic residence time (HRT) between 17.6 and 64.4 h. Sugar concentration decreased with increasing ethanol concentration along the height of the column. Percent sugar utilization increased while effluent sugar concentration was decreasing with HRT between 17.6 and 50 h. Similarly, effluent ethanol concentration increased while ethanol productivity was decreasing with increasing HRT up to 50 h. Further increases in HRT above 50 h resulted in decreases in effluent ethanol concentration. The ethanol yield coefficient also increased with increasing HRT and reached the highest level of 0.54 gE g^{-1}S at an HRT of 50 h. Due to cell settling to the bottom of the column, high fermentation rates were obtained in the lower section of the system. Therefore, the system can be operated with a height of 36 cm from the inlet to obtain high ethanol contents in the effluent with an HRT of 18 h.

July 1, 2008, Biochemical Engineering Journal

- Xiaojuan Yang, Zhang X et al (2008) The leaching of pentlandite by Acidithiobacillus ferrooxidans with a biological–chemical process.

Biochemical Engineering Journal

The Fe^{3+} leaching solution which was produced by *Acidithiobacillus ferrooxidas* was used to leach pentlandite. The effects of several kinetic parameters including temperature, Fe^{3+} concentration and Cl^- on Ni recovery were investigated in a container independently. The results showed that the leaching rate of Ni was favored by the rise of temperature, the increase of Fe^{3+} concentration and the partial replacement of SO_4^{2-} by Cl^-, all of which could prove the indirect mechanism for sulfides leaching. Then a bioleaching process comprising biooxidation and chemical leaching is proposed. In the biooxidation process, *A. ferrooxidans* was used to produce Fe^{3+} at 30 °C, which was then fed to the chemical process to oxidize pentlandite at 50 °C. This biological–chemical leaching process features the continuous production of Fe^{3+} in the bioreactor and the high temperature leaching of pentlandite in the chemical reactor. By using this process, Ni leaching rate of 83.8% was obtained at 5 days. According to the results, the present heap leaching process could be improved by the results obtained by this biological–chemical leaching process.

July 28 2008, Biochemical Engineering Journal

- Jean-Marc Engasser, Chamouleau F et al (2008) Kinetic modeling of glucose and fructose dissolution in 2-methyl 2-butanol. Biochemical Engineering Journal

With the objective of developing simulation models for sugar bioconversion processes in non-aqueous media, the present study investigated the dissolution kinetics of glucose and fructose in 2-methyl 2-butanol at temperatures between 20 °C and 80 °C. For both sugars a two-phase dissolution process was observed, characterized by an initially fast dissolution lasting a few minutes, followed by a much slower dissolution phase extending up to 24 h. The experimental results are described by a combined sugar dissolution and mutarotation kinetic model that considers the dissolution of the sugar anomeric form present in the solid particles, namely α-d-glucopyranose and ß-d-fructopyranose, and its subsequent mutarotation in solution. The initial dissolution step is assumed limited by the solute transport from the surface to the bulk solution, and the corresponding sugar transport coefficient evaluated from established mass transport correlations. The second slower dissolution phase is solely controlled by the sugar mutarotation rate, and modeled as a first-order reversible reaction. The determined values of the mutarotation rate and equilibrium constants can be related to the solution temperature by an Arrhenius and Van't Hoff relationship, respectively.

July 27 2008, Biochemical Engineering Journal

- Dumont E, Andrès Y et al (2008) Evaluation of a new packing material for H2S removed by biofiltration. Biochemical Engineering Journal

This study aims to evaluate the feasibility of using a new packing material (UP20) in treating H_2S. Three identical laboratory-scale biofilters, filled with, respectively, UP20 alone, pine bark, and a configuration made of two layers of pozzolan/UP20 (80/20, v/v), were used for critical comparison. Various concentrations of H_2S (up to 100 ppmv) were used to determine the optimum biofilter performances. The superficial velocity of the polluted gas on each biofilter was 65 m h^{-1} (0.018 m s^{-1}; gas flow rate 0.5 N m^3 h^{-1}) corresponding to an empty bed residence time of 57 s. Changes in elimination capacity, removal efficiency, moisture content, temperature and pH were tracked during 95 days. The pressure drops along each biofilter were also measured by varying the gas flow rate from 0.5 to 4 N m^3 h^{-1}. After 63 days of operation, the loading rate was significantly increased to 10 g m^{-3} h^{-1} and the UP20 biofilter retained a removal efficiency of more than 93%, indicating a strong ability to stimulate microbial activity (compared to 69% for the pine bark biofilter and 74% for the biofilter filled with a configuration of two layers of pozzolan/UP20). A Michaelis–Menten type equation was applied and the maximum removal rate (V_m) and saturation constant (K_s) were calculated. V_m was evaluated at 35gH_2S $m^{-3}_{biofilter}h^{-1}$ for UP20 (14 and 15gH_2S $m^{-3}_{biofilter}h^{-1}$ for pine bark and pozzolan/UP20, respectively). The saturation constant K_s was 70 ppmv for UP20 (18 ppmv for pine bark and 20 ppmv for pozzolan/UP20) indicating that the new packing material will be effective in treating large pollutant concentrations. At low concentrations of pollutant, the results suggest that a biofilter with a configuration of two layers of pozzolan/UP20 is the most suitable choice for treating H_2S.

July 22 2008, Biochemical Engineering Journal

- Haifeng Pan, Xie Z et al (2008) Optimization of culture conditions to enhance cis-epoxysuccinate hydrolase production in Escherichia coli by response surface methodology. Biochemical Engineering Journal

The effect of culture conditions on the *cis*-epoxysuccinate hydrolase (CESH) production in recombinant *Escherichia coli* BL21 was investigated using response surface methodology (RSM), which was based on rotatable central composite design. The optimization of seed conditions consisted of a total of 13 experiments involving 4 star points and 5 replicates at the central points, while the optimization of induction conditions consisted of a total of 31 experiments involving 8 star points and 7 replicates at the central points. The optimum predicted culture conditions for maximum expression of recombinant CESH were found to be comprised of 11.75 h seed age, 4.13% (v/v) inoculation level, OD_{600} 0.2 induction-starting time, 2.53% (w/v) lactose, 24.29 °C post-induction temperature and 27.56 h post-induction time, with a predicted CESH activity of 40,460 U/g, which was very close to the experimental CESH activity of 40,129 U/g resulting in 4.6-fold increment after optimization.

July 20 2008, Biochemical Engineering Journal

- Fernando GF, Bartacek J et al (2008) Supplementation of cobalt to UASB reactors by pulse dosing: $CoCl_2$ versus $CoEDTA^{2-}$ pulses. Biochemical Engineering Journal

The effect of chelation on the dosing strategy of cobalt to restore the performance of a cobalt limited methanol-fed bioreactor was investigated. Three upflow anaerobic sludge bed (UASB) reactors (30 °C, pH 7.0) were operated with methanol as the substrate at an organic loading rate of 8.5 g COD L^{-1} d^{-1}. One UASB reactor was supplied with several pulses of cobalt bound to EDTA, and its operation was compared to that of another UASB reactor to which several pulses of $CoCl_2$ were given. The addition of cobalt (5 μmoles cobalt per litre of reactor volume) in the form of $CoCl_2$ creates a pool of cobalt in the granular sludge matrix due to the high cobalt retention (around 90%). The methanogens present in the granular sludge are able to use that cobalt pool for stable methane formation from methanol during the subsequent 15 days. When added as Co-$EDTA^{2-}$, only around 8% of the cobalt added is retained. The small amount of retained cobalt in case of Co-$EDTA^{2-}$ addition supports methylotrophic methanogenesis only a few operational days. Furthermore, the side-effects EDTA has on the granule matrix or microbial cells make EDTA an unsuitable ligand for cobalt dosage in full-scale applications.

July 17 2008, Biochemical Engineering Journal

- Ka F Luk, Ko MK, Ng KM (2008) Separation and purification of (−)schisandrin B from schisandrin B stereoisomers. Biochemical Engineering Journal

Schisandrin B (Sch B), consisting of a mixture of its stereoisomers, namely (−)Sch B and (±)γ-schisandrin, is the most abundant and biologically active dibenzocyclooctadiene lignan present in *Fructus*

Schisandrae (FS). The objective of this study is to develop a process for large-scale separation and purification of a single stereoisomer of Sch B, (−)Sch B, which offers the highest desirable bioactivities. To this end, a crystallization-based separation and purification process has been conceptualized. Bench-scale crystallization experiments guided by experimental solid–liquid equilibrium phase diagrams were performed to verify process feasibility. A (−)Sch B product with a purity of 98.5 wt% and a (±)γ-schisandrin-enriched product with a purity of 65.0 wt% were obtained. The (−)Sch B product caused a 32% increase in cellular glutathione level and the (±)γ-schisandrin-enriched product a 26% increase, indicating a potentially more efficacious pharmaceutical preparation.

July 5 2008, Biochemical Engineering Journal

- Karunakaran S, Umapathy NS et al (2008) Interaction of tryptophan derivatives with SLC6A14 ($ATB^{0,+}$) reveals the potential of the transporter as a drug target for cancer chemotherapy. Biochemical Journal 414: 343-355

$ATB^{0,+}$ [SLC6A14 (solute carrier family 6 member 14)] is an Na^+/Cl^--coupled amino acid transporter whose expression is upregulated in cancer. 1-Methyltryptophan is an inducer of immune surveillance against tumour cells through its ability to inhibit indoleamine dioxygenase. In the present study, we investigated the role of $ATB^{0,+}$ in the uptake of 1-methyltryptophan as a potential mechanism for entry of this putative anticancer drug into tumour cells. These studies show that 1-methyltryptophan is a transportable substrate for $ATB^{0,+}$. The transport process is Na^+/Cl^--dependent with an Na^+/Cl^-/1-methyltryptophan stoichiometry of 2:1:1. Evaluation of other derivatives of tryptophan has led to identification of α-methyltryptophan as a blocker, not a transportable substrate, for $ATB^{0,+}$. $ATB^{0,+}$ can transport 18 of the 20 proteinogenic amino acids. α-Methyltryptophan blocks the transport function of $ATB^{0,+}$ with an IC_{50} value of ~250 μM under conditions simulating normal plasma concentrations of all these 18 amino acids. These results suggest that α-methyltryptophan may induce amino acid deprivation in cells which depend on the transporter for their amino acid nutrition. Screening of several mammary epithelial cell lines shows that $ATB^{0,+}$ is expressed robustly in some cancer cell lines, but not in all; in contrast, non-malignant cell lines do not express the transporter. Treatment of $ATB^{0,+}$-positive tumour cells with α-methyltryptophan leads to suppression of their colony-forming ability, whereas $ATB^{0,+}$-negative cell lines are not affected. The blockade of $ATB^{0,+}$ in these cells with α-methyltryptophan is associated with cell cycle arrest. These studies reveal the potential of $ATB^{0,+}$ as a drug target for cancer chemotherapy.

June 3 2008, Biochemical Journal

- Alphey MS, Janine K et al (2008) Structural and mechanistic insights into type II trypanosomatid tryparedoxin-dependent peroxidases. Biochemical Journal 414: 375-381

*Tb*TDPX (*Trypanosoma brucei* tryparedoxin-dependent peroxidase) is a genetically validated drug target in the fight against African sleeping sickness. Despite its similarity to members of the GPX (glutathione peroxidase) family, *Tb*TDPX2 is functional as a monomer, lacks a selenocysteine residue and relies instead on peroxidatic and resolving cysteine residues for catalysis and uses tryparedoxin rather than glutathione as electron donor. Kinetic studies indicate a saturable Ping Pong mechanism, unlike selenium-dependent GPXs, which display infinite K_m and V_{max} values. The structure of the reduced enzyme at 2.1 Å (0.21 nm) resolution reveals that the catalytic thiol groups are widely separated [19 Å (0.19 nm)] and thus unable to form a disulphide bond without a large conformational change in the secondary-structure architecture, as reported for certain plant GPXs. A model of the oxidized enzyme structure is presented and the implications for small-molecule inhibition are discussed.

June 3 2008, Biochemical Journal

- Lue X, Lin F et al (2008) Characterization of the topology and functional domains of RKTG. Biochemical Journal 414: 399-406

RKTG (Raf kinase trapping to Golgi) is exclusively localized at the Golgi apparatus and functions as a spatial regulator of Raf-1 kinase by sequestrating Raf-1 to the Golgi. Based on the structural similarity with adiponectin receptors, RKTG was predicted to be a seven-transmembrane protein with a cytosolic N-terminus, distinct from classical GPCRs (G-protein-coupled receptors). We analysed in detail the topology and functional domains of RKTG in this study. We determined that the N-terminus of RKTG is localized on the cytosolicside. Two short stretches of amino acid sequences at the membrane Proxximal to the N- and C-termini (amino acids 61–71 and 299–303 respectively) were indispensable for Golgi localization of RKTG, but were not required for the interaction with Raf-1. The three loops facing the cytosol between the transmembrane domains had different roles in Golgi localization and Raf-1 interaction. While the first cytosolic loop was only important for Golgi localization, the third cytosolic loop was necessary for both Golgi localization and Raf-1 sequestration. Taken together, these findings suggest that RKTG is a type III membrane protein with its N-terminus facing the cytosol and multiple sequences are responsible for its localization at the Golgi apparatus and Raf-1 interaction. As RKTG is the first discovered Golgi protein with seven transmembrane domains, the knowledge derived from this study would not only provide structural information about the protein, but also pave the way for future characterization of the unique functions of RKTG in the regulation of cell signalling.

June 11 2008, Biochemical Journal

- Ilhan A, Gartner W et al (2008) Localization and characterization of the novel protein encoded by C20orf3. Biochemical Journal 414: 485-495

In the present study, we characterized the gene product of open reading frame 3 encoded at human chromosome 20 (C20orf3), which represents a member of the lactonohydrolase super family. Multiple-tissue Northern blot analysis showed ubiquitous expression of the 2.4 kb transcript coding for 416 amino acids, with highest levels in human liver, placenta and kidney. After recombinant production of protein variants in Escherichia coli and insect cells, antibodies directed against different epitopes within the C20orf3 gene product were generated. Using these immunoreagents, protein expression was demonstrated in the liver, and glomerular and tubular structures of the kidney, as well as in endothelial cells and arterial wall. Positive staining was also observed at the pancreatic islets of Langerhans. Using immunoblotting, we identified three size variants. In line with the results of in silico analysis demonstrating a single transmembrane sequence (amino acids 40–61) at the N-terminus of the full-length protein, FACS cell-surface staining confirmed a mainly extracellular localization of the full-length protein. Sucrose density gradient cell fractionation revealed membrane association of the dominant 50 kDa variant in HepG2 and Rin-5F cells. The finding of a strong arylesterase activity with β-naphthyl acetate and phenyl acetate of the C20orf3 protein-containing fractions suggests potential involvement of this protein in enzymatic processes. C20orf3 promoter-driven reporter assays, which were verified by gene-specific RT-qPCR (real-time quantitative PCR) showed a strong inhibitory effect of human serum on transcription using the HEK-293 human embryonic kidney cell line. In conclusion, we characterized the structure and expression pattern of the C20orf3 gene product. According to a series of analogies with PON (paraoxonase) family members, we speculate that the C20orf3 gene product represents a new member of this important protein family present at the cellular level.

May 30 2008, Biochemical Journal

- Ercisli S, Orhan1 E et al (2008) Genetic Diversity in Grapevine Germplasm Resources in the Coruh Valley Revealed by RAPD Markers. Biochemical Genetics

Random amplified polymorphic DNA analysis was carried out in 35 autochthonous table grapevine cultivars grown in Coruh valley. Fifty five oligonucleotide primers were screened on cultivars, and among them, 12 primers showed clear polymorphic patterns. PCR amplification with 12 primers generated a total of 157 polymorphic bands. There was genetic variation among the cultivars with values of genetic diversity ranging from 0.19 to 0.72 using the Jaccard coefficient. UPGMA analysis of the distance matrix resulted in a dendrogram with two main clusters. The first cluster included 28 cultivars and the second 7 cultivars. The greatest genetic similarity was observed between cultivars Gah and Kolik, while the greatest dissimilarity was observed between cultivars Gah and Siyah Kus Uzumu. The dendrogram revealed that the cultivars present in Coruh valley can be distinguished to a relatively high degree.

May 30 2008, Biochemical Genetics

- Sha L, Yang R et al (2008) Phylogenetic Analysis of Leymus (Poaceae: Triticeae) Inferred from Nuclear rDNA ITS Sequences. Biochemical Genetics

To investigate the phylogenetic relationships of polyploid *Leymus* (Poaceae: Triticeae), sequences of the nuclear rDNA internal transcribed spacer region (ITS) were analyzed for 34 *Leymus* accessions representing 25 species, together with three *Psathyrostachys* species (Ns genome), two *Pseudoroegneria* (St genome) species, *Lophopyrum elongatum* (E^e genome), and *Thinopyrum bessarabicum* (E^b genome). The phylogenetic analyses (maximum likelihood and Bayesian inference) supported two major clades, one including 21 *Leymus* species and three *Psathyrostachys* species, the other with nine *Leymus* species and four diploid species. The ITS RNA secondary structure of the *Leymus* species was compared with that of their putative diploid donor. It is suggested that (1) the species from the same areas or neighboring geographic regions are closely related to each other; (2) *L. coreanus*, *L. duthiei*, *L. duthiei* var. *longearistatus*, and *L. komarovii* are closely related to other *Leymus* species, and it is reasonable to transfer these species from the genus *Hystrix* to *Leymus*; (3) the ITS sequences of *Leymus* are evolutionarily distinct; (4) the different *Leymus* species and different distribution of a species derived their Ns genome from different *Psathyrostachys* species; and (5) there is a close relationship among *Leymus*, *Pseudoroegneria*, *Lophopyrum*, and *Thinopyrum*, but it is difficult to presume that the St, E^e, and E^b genome may be the Xm genome donor of the *Leymus* species.

August 15 2008, Biochemical Genetics

- Arora R, Bhatia S et al (2008) Genetic Polymorphism of Type 1 Intermediate Filament Wool Keratin Gene in Native Indian Sheep Breeds. Biochemical Genetics

Information is presented on the genetic polymorphism of the Type 1 intermediate filament wool keratin gene in 15 native Indian sheep breeds belonging to different agro-ecological regions of India. The study analyzed random blood samples of the 638 sheep by the PCR-RFLP technique. Restriction digestion analysis of a 480 bp PCR fragment of the first exon region with MspI revealed two allelic variants (M = 0.748 and N = 0.252) and three genotypes (MM = 0.543, MN = 0.410, and NN = 0.047) across the 15 sheep breeds. The allelic frequency differences for both alleles across the Indian breeds, irrespective of their geographic distribution, color pattern, and utility traits, were observed to be statistically insignificant by a chi-square test ($P > 0.05$). According to the pattern of occurrence of allelic variants (M > N), the Indian breeds exhibited similarity to some of the reported European sheep breeds. The average heterozygosity was 0.420, and none of the breeds deviated from Hardy-Weinberg equilibrium. The predominance of the M over the N allele supported its ancestry in Indian sheep too.

May 30 2008, Biochemical Genetics

- Zhu H, Wu H et al (2008) Role of MicroRNA miR-27a and miR-451 in the regulation of MDR1/P-glycoprotein expression in human cancer cells. Biochemical Pharmacology 76(5):582-588.

MicroRNAs are short non-coding RNA molecules able to affect stability and/or translation of mRNA, thereby regulating the expression of genes involved in many biological processes. We report here that microRNAs miR-27a and miR-451 are involved in activating the expression of P-glycoprotein, the MDR1 gene product that confers cancer cell resistance to a broad range of chemotherapeutics. We showed that expressions of miR-27a and miR-451 were up-regulated in multidrug resistant (MDR) cancer cell lines A2780DX5 and KB-V1, as compared with their parental lines A2780 and KB-3-1. Treatment of A2780DX5 cells with the antagomirs of miR-27a or miR-451 decreased the expression of P-glycoprotein and MDR1 mRNA. In contrast, the mimics of miR-27a and miR-451 increased MDR1 expression in the parental cells A2780. The sensitivity to and intracellular accumulation of cytotoxic drugs that are transported by P-glycoprotein were enhanced by the treatment with the antagomirs of miR-27a or miR-451. Our results demonstrate for the first time the roles of microRNAs in the regulation of drug resistance mediated by MDR1/P-glycoprotein, and suggest the potential for targeting miR-27a and miR-451 as a therapeutic strategy for modulating MDR in cancer cells.

September 1 2008, Biochemical Pharmacology

- Hollenbach M, Hintersdorf A et al (2008) Ethyl pyruvate and ethyl lactate down-regulate the production of pro-inflammatory cytokines and modulate expression of immune receptors. Biochemical Pharmacology 76(5):631-644

Esters of α-oxo-carbonic acids such as ethyl pyruvate (EP) have been demonstrated to exert inhibitory effects on the production of anti-inflammatory cytokines. So far, there is no information about effects, if any, of ethyl lactate (EL), an obviously inactive analogue of EP, on inflammatory immune responses. In the present study, we provide evidence that the anti-inflammatory action of α-oxo-carbonic acid esters is mediated by inhibition of glyoxalases (Glo), cytosolic enzymes that catalyse the conversion of α-oxo-aldehydes such as methylglyoxal (MGO) into the corresponding α-hydroxy acids using glutathione as a cofactor. In vitro enzyme activity measurements revealed the inhibition of human Glo1 by α-oxo-carbonic acid esters, whilst α-hydroxy-carbonic acid esters such as EL were not inhibitory. In contrast, both EP and EL were shown to suppress the Lipopolysaccharide (LPS)-induced production of pro-inflammatory cytokines such as tumor necrosis factor-α, interleukin (IL)-1β, IL-6 and IL-8 from human immunocompetent cells, and modulated the expression of the immune receptors HLA-DR, CD14 and CD91 on human monocytes. Here, we show a crossing link between glyoxalases and the immune system. The results described herein introduce glyoxalases as a possible target for therapeutic approaches of immune suppression.

September 1 2008, Biochemical Pharmacology

- Cui X, Thomas A et al (2008) Application and interpretation of hPXR screening data: Validation of reporter signal requirements for prediction of clinically relevant CYP3A4 inducers. Biochemical Pharmacology 76(5):680-689

A human pregnane X receptor (PXR) reporter-gene assay was established and validated using 19 therapeutic agents known to be clinical CYP3A4 inducers, 5 clinical non-inducers, and 6 known inducers in human hepatocytes. The extent of CYP3A4 induction

(measured as RIF ratio in comparison to rifampicin) and EC50 was obtained from the dose–response curve. All of the clinical inducers (19/19) and human hepatocyte inducers (6/6) showed positive responses in the PXR assay. One out of five clinical non-inducers, pioglitazone, also showed a positive response. An additional series of 18 commonly used drugs with no reports of clinical induction was also evaluated as putative negative controls. Sixteen of these were negative (89%), whereas two of these, flutamide and haloperidol showed 16-fold (RIF ratio 0.79) and 10-fold (RIF ratio 0.48) maximal induction, respectively in the reporter-gene system. Flutamide and haloperidol were further demonstrated to cause CYP3A4 induction in human cryopreserved hepatocytes based on testosterone 6β-hydroxylation activity. The induction potential index calculated based on the maximum RIF ratio, EC50, and in vivo maximum plasma concentration was used to predict the likelihood of CYP3A4 induction in humans. When the induction potential index is greater than 0.08, the compound is likely to cause induction in humans. A high-throughput screening strategy was develop -ed based on the validation results at 1 μM and 10 μM for the same set of drugs. A RIF ratio of 0.4 was set as more practical screening cut-off to minimize the possibility of generating false positives. Thus, a tiered approach was implemented to use the human PXR reporter-gene assay from early lead optimization to late lead characterization in drug discovery.

September 1 2008, Biochemical Pharmacology

- Sheng MY, Chen QF, Yang QX (2008) Variation in icariin and flavonoid contents of barrenwort accessions native to Guizhou, China. Biochemical Systematics and Ecology

Flavonoid and icariin contents of 87 samples drawn from 21 accessions of seven species native to Guizhou, China, of the genus Epimedium were determined by means of ultraviolet and high-performance liquid chromatography. The contents differed significantly among the species and accessions. E. acuminatum, E. yinjiangense, E. myrianthum, E. wushanense, and E. simplicifloum had greater amounts of flavonoids and icariin than E. letorrhizum and E. luodianense.

July 23 2008, Biochemical Systematics and Ecology

- Onifade AK, Fatope MO et al (2008) Nematicidal activity of Haplophyllum tuberculatum and Plectranthus cylindraceus oils against Meloidogyne javanica. Biochemical Systematics and Ecology

The potentials of *Haplophyllum tuberculatum* and *Plectranthus cylindraceus* oils to control *Meloidogyne javanica* were investigated *in vitro* and in a greenhouse. A mixture of *Haplophyllum* and *Plectranthus* oils (1:1) was highly toxic to *M. javanica in vitro*, as it killed all nematode juveniles and inhibited hatching of eggs at 12.5 μg/ml concentration after 24 h exposure time, as did carbofuran at the same concentration. In the green-house, tomatoes grown in soil treated with a combination (1:1) of the two oils developed fewer root galls than those grown in soil treated with higher doses of either oil. The oil mixture, at 2.5 and 5.0 μg/ml of soil, was not phytotoxic to tomato plants as evident from the appearance and height of plants after 12 weeks exposure time, compared to treatment over the same period at lower effective doses. The nematicidal activity of the combined essential oils was suggested by the presence of C_{10} dienes, C_{10} trienes and C_{10} phenol.

July 1 2008, Biochemical Systematics and Ecology

- Gordiyenko Y, Robinson CV (2008) The emerging role of MS in structure elucidation of protein–nucleic acid complexes. Biochemical Society Transactions 36:723-731

Developments in MS enable us to apply this technique to non-covalent complexes, defining their stoichiometry, subunit interactions and architectural organization. We illustrate the application of this non-covalent MS approach to uncovering the overall topological arrangements of subunits and interactions within RNA–protein complexes studied in our laboratory over the last 5 years. These studies exemplify the emerging role and potential of MS as a complementary structural biology methodology and demonstrate its unique niche in investigations of dynamic or heterogeneous protein–nucleic acid complexes, which are not accessible to classical high-resolution structural biology techniques.

April 6 2008, Biochemical Society Transactions

- Curticapean C, Muntean D et al (2008) Optimized HPLC method for tramadol and O-desmethyl tramadol determination in human plasma. Journal of Biochemical and Biophysical Methods 70(6):1304-1312

The optimized method for HPLC determination of tramadol and its metabolite *O*-desmethyl tramadol in human plasma using sotalol as internal standard has been developed and validated by a new approach. The determination by fluorescence detection was performed on re-eluted solution, obtained after liquid–liquid extraction with ethyl acetate of the three analytes from plasma. The chromatographic separation of tramadol under a gradient elution was achieved at a temperature of 15 °C with a RP-18 column, guarded by a C18 precolumn. The mobile phase was a mixed aqueous solution containing ortho-phosphoric acid, triethylamine, acetonitrile and methanol in a complex gradient mode. The quantitative determination of tramadol was performed at different successive pairs of excitation/emission wavelengths (200/300 nm, 200/295 nm, 212/305 nm) with lower limits of quantification: LLOQ = 4.078 ng/ml for tramadol, respectively LLOQ = 3.271 ng/ml for *O*-desmethyl tramadol. For the LLOQ limits, were calculated the values of the coefficient of variation and difference between mean and the nominal concentration. For tramadol analyte they were CV% = 5.147% and bias% = − 7.273% in the intra-days and CV% = 4.894% and bias% = 0.836% in the between-days assay, respectively for the metabolite *O*-desmethyl tramadol they were CV% = 11.517% and bias% = 0.337% in the intra-days and CV% = 6.41% and bias% = 3.259% in the between-days assay.

In addition, the stabilities of the analytes were verified in different conditions. Both, tramadol and its metabolite proved to be stable in plasma for four weeks, frozen at − 20 °C, but also for 48 h at 15 °C in the re-eluted solution after liquid–liquid extraction.

February 9 2008, Journal of Biochemical and Biophysical Methods

- Fenton AW (2008) Allostery: an illustrated definition for the 'second secret of life'. Trends in Biochemical Sciences

Although allosteric regulation is the 'second secret of life', the molecular mechanisms that give rise to allostery currently elude understanding. In my opinion, experimental progress is hampered by a commonly used but misleading definition of allostery as protein structural changes that are elicited by the binding of a single ligand. Allostery is more strictly defined in functional terms as a comparison of how one ligand binds in the absence, versus the presence, of a second ligand. Therefore, as each of the two binding events involves two protein complexes, a study of allostery must consider four complexes and not just two. Such a comparison can distinguish allosteric from non-allosteric protein changes, the importance of which is frequently overlooked. When a study of all four complexes is not feasible, an alternative, albeit limited, strategy can identify subsets of allosteric-specific changes.

August 15 2008, Trends in Biochemical Sciences