



ISOBC NEWSLETTER

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Techniques for Studying Protein Heterogeneity and Post-translational Modifications	2
The Interplay Between Structure and Function in Intrinsically Unstructured Proteins	2
The Mammalian Unfolded Protein Response	2
A global reorganization of the metabolome in <i>Arabidopsis</i> during cold acclimation is revealed by metabolic fingerprinting	3
New function for telomerase?	3
Nano Valve Created by UCLA Chemists	3
Agressive Formation	3
New Alzheimer's Drug	4
DNA- Based Molecular Nano-wires	4
Small Worm Yields Big Clue On Muscle Receptor Action	4
Host Can Help RNA Virus Evolve	4
Pear Protein Characterized in Study	4
Neurobiology: Glyceraldehyde 3-Phosphate Dehydrogenase	5
New Journal	5
A New Kind of Birdsong	5
Congresses & Ads	6
J. Iran. Chem. Soc.	6

300 million Rials Financial Support for Researchers

In the last week of its activity, the government of President Khatami approved a draft calling for financial aid for researchers. According to this draft which is now a law - as of Mordad 5, 1384 (July 20, 2005)- every year, the govern-

ment will donate 300,000,000 Rials to each of the outstanding scientists or researchers of the country, who will be chosen by the High Commission of Science, Research and Technology. In addition, these people will be treated like

high ranking government officials in having special (Tashrifat) ID cards. The government also vowed to help facilitate the traveling of foreign scientists to Iran.

Capture Knowledge By Writing It Down; Prophet Mohammed (p.b.u.h)

Cooperative Folding in a Multi-Domain Protein

Most protein domains are found in multi-domain proteins, yet most studies of protein folding have concentrated on small, single-domain proteins or on isolated domains from larger proteins. Spectrin domains are small (106 amino acid residues), independently folding domains consisting of three long alpha-helices. They are found in multi-domain proteins with a number of spectrin domains in tandem array. Structural studies have shown that in these

arrays the last helix of one domain forms a continuous helix with the first helix of the following domain. It has been demonstrated that a number of spectrin domains are stabilized by their neighbors. Here we investigate the molecular basis for cooperativity between adjacent spectrin domains 16 and 17 from chicken brain alpha-spectrin (R16 and R17). We show that whereas the proteins unfold as a single cooperative unit at 25 degrees C, cooperativity is lost at higher temperatures and in the

presence of stabilising salts. Mutations in the linker region also cause the cooperativity to be lost. However, the cooperativity does not rely on specific interactions in the linker region alone. Most mutations in the R17 domain cause a decrease in cooperativity, whereas proteins with mutations in the R16 domain still fold cooperatively. We propose a mechanism for this behaviour.

[Batey S, Randles LG, Steward A, Clarke J](#)
J Mol Biol. 2005 Jun 24;349 (5):1045-59.

The 8th ICB & First ICBMB was held in **Tarbiat Modarres University in Tehran**, September 11-15, 2005, with more than 600 participants mostly from around Iran, but also from around the globe. It was clear that the organizers had put their utmost effort into its programming and conduction as it was obviously different from previously held internal congresses. Each day of the congress started with three plenary lectures lasting 30 minutes each. Oral sessions started right after until noon and continued in the evening after a 4 hour poster presentation time break. The event was considered a new experience for Iranians as everyone tried to speak and present their work in English language, perhaps for the first time in our history. The next congress which will be two years from now, shall be held in either Meshed or Shiraz. We thank the organizers of the **8th ICB & First ICBMB** and wish well for those who are going to make the next one possible.

I don't know what your destiny will be, but one thing I know: the only ones among you who will be really happy are those who have sought and found how to serve.

Albert Schweitzer

From evil springs forth more evil. Therefore, evil is to be feared even more than fire.

To commit no wrong, even against one's enemies, Is said to be supreme wisdom.

-Tirukkural 21:202-203

There may be more to learn from climbing the same mountain a hundred times than by climbing a hundred different mountains.

-Richard Nelson

Techniques for Studying Protein Heterogeneity and Post-translational Modifications

Proteins often undergo several post-translational modification steps in parallel to protein folding. These modifications can be transient or of a more permanent nature. Most modifications are, however, susceptible to alteration during the lifespan of proteins. Post-translational modifications thus generate variability in proteins that are far beyond that provided by the genetic code. Co- and post-translational modifications can convert the 20 specific codon-encoded amino acids

into more than 100 variant amino acids with new properties. These, and a number of other modifications, can considerably increase the information content and functional repertoire of proteins, thus making their analysis of paramount importance for diagnostic and basic research purposes. Various methods used in proteomics, such as 2D gel electrophoresis, 2D liquid chromatography, mass spectrometry, affinity-based analytical methods, interaction analyses, ligand blotting tech-

niques, protein crystallography and structure-function predictions, are all applicable for the analysis of these numerous secondary modifications. In this review, examples of some of these techniques in studying the heterogeneity of proteins are highlighted. In the future, these methods will become increasingly useful in biomarker searches and in clinical diagnostics.

[Baumann M, Meri S](#)

Expert Rev Proteomics. 2004 Aug;1(2):207-17.

The Interplay Between Structure and Function in Intrinsically Unstructured Proteins

Intrinsically unstructured proteins (IUPs) are common in various proteomes and occupy a unique structural and functional niche in which function is directly linked to structural disorder. The evidence that these proteins exist without a well-defined folded structure in vitro is compelling, and justifies considering them a separate class within the pro-

tein world. In this paper, novel advances in the rapidly advancing field of IUPs are reviewed, with the major attention directed to the evidence of their unfolded character in vivo, the interplay of their residual structure and their various functional modes and the functional benefits their malleable structural state provides. Via all these details,

it is demonstrated that in only a couple of years after its conception, the idea of protein disorder has already come of age and transformed our basic concepts of protein structure and function.

[Tomba P](#)

FEBS Lett. 2005 Jun 13;579 (15):3346-54. Epub 2005 Apr 8.

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The Mammalian Unfolded Protein Response

In the endoplasmic reticulum (ER), secretory and transmembrane proteins fold into their native conformation and undergo posttranslational modifications important for their activity and structure. When protein folding in the ER is inhibited, signal transduction pathways, which increase the biosynthetic capacity and decrease the biosynthetic burden of the ER to maintain the homeostasis of this organelle, are activated. These pathways are called the unfolded protein response (UPR). In this review, we briefly summarize principles of protein folding and molecular chaperone

function important for a mechanistic understanding of UPR-signaling events. We then discuss mechanisms of signal transduction employed by the UPR in mammals and our current understanding of the remodeling of cellular processes by the UPR. Finally, we summarize data that demonstrate that UPR signaling feeds into decision making in other processes previously thought to be unrelated to ER function, e.g., eukaryotic starvation responses and differentiation programs.

[Schroder M, Kaufman RJ.](#)

Annu Rev Biochem. 2005 Jul 7;74:739-789.

A global reorganization of the metabolome in *Arabidopsis* during cold acclimation is revealed by metabolic fingerprinting

Many plants, including *Arabidopsis*, increase their freezing tolerance in response to low, non-freezing temperatures. This process is known as cold acclimation and involves many complex biochemical changes at the level of the metabolome. Our goal was to examine the effects of cold acclimation on the metabolome using a non-targeted metabolic fingerprinting approach. Multivariate data analyses indicate that, in *Arabidopsis*, a global reprogramming of metabolism occurs as a result of cold accli-

mation. By measuring an entire spectrum of putative metabolites based on mass-to-charge (m/z) ratios, vs. an individual or group of metabolite(s), a comprehensive, unbiased assessment of metabolic processes relative to cold acclimation was determined. Whereas leaves *shifted* to low temperature present metabolic profiles that are constantly changing, leaves *developed* at low temperature demonstrate a stable complement of components. Although it appears that some metabolic networks are modulated by the environment, others require

development under low-temperature conditions for adjustment. Understanding how metabolism as a whole is regulated allows the integration of cellular, physiological and ecological attributes in a biological system, a necessity if complex traits, such as freezing tolerance, are to be modified by breeding or genetic manipulation.

Gordon R. Gray and Doug Heath

Physiologia Plantarum
Volume 124 Issue 2 Page

New function for telomerase?

Telomerase promotes proliferation of resting stem cells through a mechanism that does not involve the extension of chromosomal telomeres, researchers [report](#) in *Nature* this week.

"This is a completely new function for telomerase that gives us new insight into stem cells and cancer," [Steven Artandi](#) of Stanford University, the study's senior author, told *The Scientist*.

It had generally been thought that the only function of telomerase was to promote telomere extension, but in recent years evidence has started to accumulate suggesting that the enzyme promotes the development of [cancer](#), and that it might have roles other than synthesizing telomere repeats. In spite of this, some [researchers have remained skeptical](#).

> www.the-scientist.com/2005/2/28/18/1

Agressome Formation

Bulk protein degradation in the cell is catalyzed by the ubiquitin-proteasome system (UPS). At the heart of the UPS is the proteasome, a large multisubunit tightly-regulated protease. The UPS performs key functions in protein quality control by monitoring and eliminating potentially toxic misfolded or damaged proteins. When the capacity of this protease system is exceeded, mis-

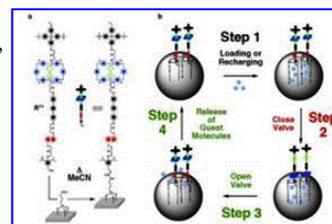
folded protein substrates aggregate and are assembled through an active and regulated process to form an aggresome. Aggresomes are dynamic structures, formed as a general response to an overload of improperly folded proteins. Assembly of aggresomes occurs at the centrosome, a perinuclear structure that also serves as a site for the recruitment and concentration of components of the

UPS, including the proteasome, its regulators, and other proteins typically involved in protein quality control. Thus, in addition to other cellular activities, the centrosome may play a central role in protein quality control, sitting at the crossroads of protein folding, degradation, and aggregation.

[Corboy MJ](#), [Thomas PJ](#), [Wigley WC](#)

Nano Valve Created by UCLA Chemists

UCLA chemists have created the first nano valve that can be opened and closed at will to trap and release molecules. A nano valve potentially could be used as a drug delivery system. > [full story](#) (July 21, 2005)



Basic research is like shooting an arrow into the air and, where it lands, painting a target.

--- Homer Adkins

The spiritual path ruins the body, but subsequently restores it to health. It ruins the house to reveal the treasure, and with that treasure it builds better than before.

-Rumi, "Mathnawi"

I am only one, but still I am one. I cannot do everything, but still I can do something. I will not refuse to do the something I can do.

Helen Keller

Do not strut proudly on account of your good deeds.

Do not let pride waylay you.

When you deem yourself holier than others, know that you have fallen into grave error because in your pride you believed yourself equal to God.

-Sheikh Abdul Qadir Jillani, "Futhul Ghaib"

New Alzheimer's Drug

A team of scientists has discovered three molecules -- from a search of 58,000 compounds -- that appear to inhibit a key perpetrator of Alzheimer's disease. Each of the three molecules protects the protein called "tau," which becomes hopelessly tangled in the brains of patients with Alzheimer's. The finding is promising news for the development of drugs for the disease. > [full story](#)

DNA- Based Molecular Nano-wires

An international consortium of 7 universities and research centres are seeking an alternative to silicon-based microelectronics in using molecules of DNA, which could enable a reduction in size of the current systems by a thou-

Small Worm Yields Big Clue On Muscle Receptor Action

Biological researchers report the identity of a previously elusive subunit of a neurotransmitter in *C. elegans*. The finding may have applicability to research on the human nervous system. > [full story](#)

The big jumps ahead are taken by people who disregard the conventional wisdom and do something unexpected. –

Freeman Dyson

Host Can Help RNA Virus Evolve

RNA viruses, or viruses with RNA genomes, evolve rapidly, and, due to recombination with their hosts, can contribute to disease outbreaks by rendering vaccines ineffective. RNA recombination may have contributed to recent outbreaks of dengue, SARS, and influenza. The Tombusvirus that infects plants is no stranger to recombination either, and its damaging effect on plants is something scientists have long sought to curtail, or remove altogether.

In "Genome-wide screen identifies host genes affecting viral RNA recombination," Elena Serviene and colleagues

of the University of Kentucky use yeast cells and Tombusvirus to show that host genomes can actually spur RNA virus evolution. Their findings are published in the latest issue of the Proceedings of the National Academy of Sciences online.

Using a high-throughput screen of a single-gene deletion library composed of 80% of yeast genes, as well as the tomato bushy stunt virus, researchers found 11 host genes that significantly affected viral recombination. A single deletion of the identified genes had three types of effects: five genes increased

viral recombination, four decreased the accumulation of recombinants, and two changed the profile of recombinants.

Four of the five genes had a role in RNA degradation, which could suggest that such a phenomenon could play a role in viral RNA recombination. Researchers also found that one of the genes has similarities with those found in rice and *Arabidopsis*, suggesting that the gene may increase viral recombination in plants as well.

Find out more at <http://www.pnas.org/cgi/doi/10.1073/>

Science is organized knowledge. Wisdom is organized life.

Immanuel Kant

Pear Protein Characterized in Study

In "Isolation, Characterization, and Cloning of α -L-Arabinofuranosidase Expressed during Fruit Ripening of Japanese Pear," Akira Tateishi and colleagues from Nagoya University purify a protein involved in fruit ripening. Their findings are published in the latest issue of Plant Physiology.

The action of enzymes on the cell wall of fruits, mainly by removing side chains from

sugars in the cell matrix, contributes to fruit softening, and thus affects fruit shape and quality. In the case of this study's Japanese pear, the enzyme, α -L-Arabinofuranosidase (α -L-arafase), was extracted and purified from the cell walls, and its gene coding sequence isolated. Researchers did not detect the enzyme in the fruit's buds, leaves, roots, or shoots; they also found the

same enzyme may be implicated in ripening in other fruits such as peaches, apples, avocados, and persimmons.

Information on the enzyme's protein sequence also allowed researchers to predict its behavior, or how it folded, and how it was transported out of the cell. Read more in this month's Plant Physiology at <http://www.plantphysiol.org>. The article appears on pp. 1653-1664 of the journal.

New Name: Chemical Biology and Drug Design

From January 2006, *Journal of Peptide Research* will be re-launched under the new title [Chemical Biology and Drug Design](#).

Building on the long standing success of *Journal of Peptide Research*, the newly launched *Chemical Biology and Drug Design* will be dedicated to the

advancement of innovative science, technology and medicine with a broader focus on cutting-edge research integrating chemical biology and drug design.

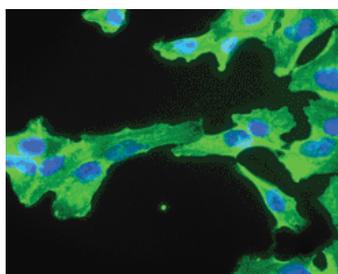
Neurobiology: Glyceraldehyde 3-Phosphate Dehydrogenase

The metabolic enzyme GAPDH (glyceraldehyde-3 phosphate dehydrogenase) is commonly referred to as a "housekeeping" protein because of its ubiquitous and readily detectable expression in most every cell and tissue type. This led to the widespread use of GAPDH antibodies as "Loading Controls" in Western blots to normalize protein levels to GAPDH. Other commonly used loading control antibodies include [B-actin](#) and [Histone H2B](#).

There is increasing realization that [GAPDH](#) has important functions beyond its integral role in glycolysis, where it

catalyzes the reversible oxidative phosphorylation of glyceraldehyde in the cytoplasm. For example, GAPDH interacts with proteins implicated in neurodegenerative disease, including beta-amyloid precursor protein (*Alzheimer's*), and proteins containing polyglutamine repeats such as [huntingtin](#) (*Huntington's*). GAPDH translocates from the cytoplasm to the nucleus during [apoptosis](#) and nuclear GAPDH is also associated with transcriptional activation. Elucidating the role of GAPDH in apoptosis, transcription and disease processes is critical for understanding GAPDH

etiology in neurodegeneration.



Fluorescence microscopy of glyceraldehyde 3-phosphate dehydrogenase (GAPDH) Using [IMG-5019A](#) in human neuroblastoma Sh-SY5Y cells, cells were stained with GAPDH followed by a FITC labeled second step antibody (green) and counterstained with Hoechst dye (blue).

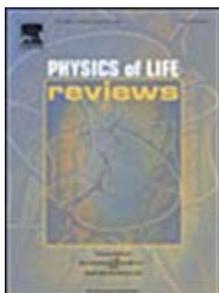
The purpose of science is to create opportunities for unpredictable things to happen. --- Freeman Dyson

Science without religion is lame, religion without science is blind.

Albert Einstein

New Journal

Physics of Life Reviews is an international journal appearing quarterly, that publishes review articles on physics of living systems, complex phenomena in biological systems, and related fields of artificial life, robotics, mathematical bio-semiotics, and artificial intelligent systems.



A New Kind of Birdsong

Richard Prum, a Yale ornithologist, was hiking through an Ecuadorian forest 18 years ago when he had one of the strangest experiences an ornithologist can have. He watched a bird sing with its wings. The manakin produced a loud, clear tone that sounded as if it came from a violin.

The club-winged manakin is the only bird known to sing with its feathers. The bird uses a club-shaped feather as a pick to rake the ridges of another feather. It does this by raising its wings over its back, and shaking them back and forth more than 100 times a second so that one feather rubs the other like a spoon moving across a washboard. [NY times](#).



Science and art belong to the whole world, and before them vanish the barriers of nationality.

Goethe

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Deadline to Participate in
Razi festival
is
Mehr 14, 1384
(Oct 6, 2005).

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International workshop on protein characterizations,
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2nd INTERNATIONAL SYMPOSIUM ON CALORIMETRY AND CHEMICAL THERMO- DYNAMICS

April 9-13, 2006

Deadline for submission of abstracts:
Dec 15, 2005

<http://www.calorimetry.iqm.unicamp.br/>

The 10th National Iranian Chemical Engineering Congress
(**ICHEC10**), Zahedan, 15-17 November 2005. August 22nd:
Deadline for submission of papers. The details of the meeting
are available at

<http://www.ichec10.com>.



Journal of the Iranian Chemical Society (**JICS**)

welcomes high quality original papers in English dealing with experimental, theoretical and applied research related to all branches of chemistry. These includes the fields of analytical, inorganic, organic and physical chemistry as well as the chemical biology area. Review articles discussing specific areas of chemistry of current chemical or biological importance are also published. Journal of the Iranian Chemical Society ensures visibility of your research results to a worldwide audience in science. You are kindly invited to submit your manuscript to the Editor-in-Chief or your Regional Editor. All contributions in the form of original papers or short communications will be peer reviewed and published free of charge after acceptance.

Vol. 2 No. 3 [Sept 2005]

Abbreviation: "J. Iran. Chem. Soc."

Qualified Faculty Member Recruitment

Institute of Biochemistry and Biophysics (IBB), University of Tehran, is now embarking upon a major reallocation of faculty positions to better accomplish its mission. IBB seeks for qualified Iranian scholars and researchers, experienced professors, and those who embrace the challenges and opportunities for higher education in the 21st century.

The following research fields vacancies are notified by administration of IBB:

- Molecular and Cell Biology
- Plant Biochemistry
- Enzymology & Biotechnology
- Structural Biology
- Protein Crystallography & X-ray
- Protein NMR
- Radiation Biology
- Bioinformatics

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