

BIOCHEMISTRY & MOLECULAR BIOLOGY TODAY



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Chair's Message

First of all, I want to congratulate Junji Iwahara, whose promotion to Associate Professor with tenure has been approved by the BMB and SOM APT Committees. Well deserved!

On March 9th we held our annual BMB faculty retreat. In addition to our faculty we had several guest faculty from both basic and clinical departments as a source of different perspectives on the topics addressed. Our format was different this year. After my brief review of implementation of the recommendations from the faculty retreat on 2011, we had a morning session devoted to four talks focused on new research opportunities for our faculty. The first two, by BMB professors Mark Emmett and Tom Wood, addressed new technology available now in the areas of "omics" and next generation DNA sequencing. This was followed by two talks by Larry Sower, professor and chair of the Pharmacology Department and Monte Pettitt, Director of the SCSBMB and BMB professor. They provided a new vision of the field of epigenetics and the organization and vision for the SCSBMB. In the afternoon we tackled issues relevant to departmental identity, graduate school education, APT perspectives in the new research environment, and approaches to pre-submission review. A summary of faculty recommendations will soon be distributed. One item of importance was the suggestion to put in place an in house "study section" no later than April of this year. I am happy to report that twelve colleagues have agreed to serve for one year in such a project, and that Jim Lee has agreed to act as chair of the BMB study section. Already several faculty interested in participating have volunteered to submit their proposals for review. This is a work in progress, and we will make evaluations with the help of the faculty as we proceed with

this important task. We will tackle implementation of other recommendations over the coming year with available resources. Our retreat topics reflect challenges that are very much on our minds, and we are not alone. The UTMB Research Executive Committee is also addressing the issue of pre-submission review and mechanisms to help faculty prepare grants. A recent visit from UT System Office of Health Affairs leadership confirmed that these same topics are being discussed at the system level in terms of impact on the individual component health science centers.

The Annual [Structural Biology Symposium](#) will take place on April 27th, and as always it will be an outstanding opportunity for all of us. The keynote presentation will be by Dr. Ada E. Yonath, Nobel Laureate and Director of the Helen & Milton A. Kimmelman Center for Biomolecular Structure & Assembly, Department of Structural Biology, Weizmann Institute Rehovot, Israel. Be sure to mark your calendars and register for the event. This year, there will be two student awards in biochemistry and molecular biology at the National Student Research Forum, which takes place on April 26 and 27. Yes, I know there is a conflict. Finally, the Commencement ceremonies for the graduate school will be on May 4th in the afternoon, and I hope to see many of you there.

Now that spring is here we'd best enjoy the temperate temperatures while we can.

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Special Items of Interest

- ✦ The Real Cost of Next Generation Sequencing (NGS) -Thomas G. Wood, Ph.D.

Awards and Announcements



Dr. Russ Carmical was the recipient of the ABRF Outstanding Scientist/Technologist Travel award at the Association of Biomolecular Resource Facilities meeting in Orlando, FL, March 17-20. **Dr. Carmical** was also appointed as co-Chair of Nucleic Acids Research Group (NARG) 2012-2014.

Dr. Muge Kuyumcu-Martinez received the March of Dimes Basil O'Connor Starter Scholar Grant in February 2012, at the Keystone Symposia for Cardiovascular Development and Regeneration January 22-27, 2012.

Dr. Poluri Maruthi Krishna Mohan, a research scientist in Dr. Rajarathnam's lab, recently had a [book chapter](#) published in Protein-Protein Interactions - Computational and Experimental Tools, ISBN 978-953-51-0397-4.

SCSB Structural Biology Symposium

April 27, 2012

Hotel Galvez

[CLICK FOR ONLINE REGISTRATION](#)

Faculty on the Road

Dr. Russ Carmical traveled to Orlando, FL, March 17-20 to speak at the Association of Biomolecular Resource Facilities where he had two speaking engagements:

- ✦ The Path from Instrument to Insight: Eric Rappaport discusses Ingenuity iReport and the advantages it can bring to a core lab setting.
- ✦ Biorepositories: Considerations for Sample Acquisition, Storage and QC



Dr. Kizhake Soman attended the Third PI Meeting of NHLBI Proteomics Centers in San Antonio, TX, February 14-15, 2012 to present abstract entitled "Comparison of Multiple Proteomic Platforms for the Analysis of Protein and Peptide Expression in COPD."

Dr. Konrad Pazdrak attended the Annual Meeting of American Academy of Allergy, Asthma and Clinical Immunology held in Orlando, FL on March 5-7, 2012.

On February 15, 2012, **A. Kurosky, K. Pazdrak, J. Wiktorowicz, and K. Soman** attended the 3rd NHLBI Proteomics Centers Meeting in San Antonio, TX. Dr. Kurosky chaired session "Using Proteomics to Understand Inflammation".

Dr. Andrzej Kudlicki gave a talk titled "The just-in-time expression of yeast ribosomal proteins" at the International Society for Computational Biology conference in Santiago, March 2012.

The Real Cost of Next Generation Sequencing (NGS)

UTMB acquired an Illumina HiSeq 1000 in September 2011. Since that time we have sequenced over 90 libraries representing a variety of technical applications. One question that has repeatedly come up in discussions of next generation sequencing (NGS) is the cost. To accurately address this question there are a couple of things that you first need to understand. NGS is performed using a flow cell that has eight (8) separate lanes, each lane can be used to sequence a different sample. NGS will generate 150-185 million reads from each lane of the flow cell. For a single 50 base read that translates into 7.5-9.2 Gb of sequence per lane. This is the power of NGS.



Library construction costs \$150.00 per sample (DNA or RNA). For most applications, the data capacity (150-185 million reads) per lane is in excess of what is required for a single library. Current technology allows us the option of sequencing up to 12 libraries on the same lane. This is accomplished by tagging (indexing) each library with a six base identification code. During analysis, we use the index to separate the respective reads for each library into the correct data set for that sample.

The post-library construction cost for NGS is priced per lane on the flow cell and depends upon two choices; the read length (50 or 100 bases) and the decision to sequence one or both ends of each template in the library. As an example; a 50 base single end NGS costs \$865.00 per lane. However, the actual cost of sequencing depends upon the number of libraries that are sequenced on the lane. Ten libraries results in a sequencing cost of \$86.50 per library and would provide 15-18 million reads of 50 bases per read for each sample. A paired end 50 base read analysis costs \$147.00 per sample for ten "indexed" libraries. You may often hear that NGS is too expensive, as Paul Harvey was fond of saying, you've now heard "the rest of the story".

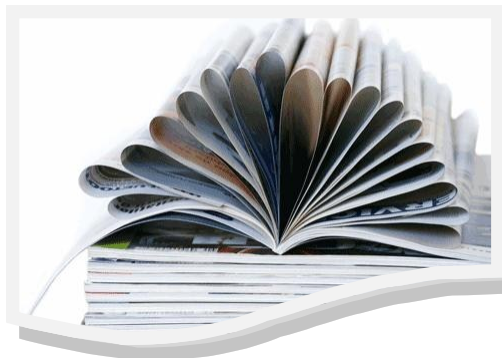
Graduate Program News



Congratulations to Aditya Hindupur (MBET) for a successful final defense. Dr. Hindupur will be continuing in Dr. Robert Fox's lab at the University of Houston as a postdoc.

Congratulations to Abhisek Mukherjee (BMB) for a successful final defense. Dr. Mukherjee will continue in Dr. Claudio Soto's lab at UT Health Science Center as a postdoc.

Publications



Oezguen, N., Power, T.D., Urvil, P., Feng, H., Pothoulakis, C., Stamler, J.S., **Braun, W.**, Savidge, T.C. "Clostridial toxins: Sensing a target in a hostile gut environment" *Gut Microbes*, 2012 Jan 1;3(1) [Epub ahead of print].

Singh, T.S., Kruger, H.G., Bisetty, K. and **Power, T.D.** "Theoretical study on the formation of a pentacyclo-undecane cage lactam" *Comp. Theor. Chem. (in press)*, 2012.

Lu, W., Negi, S.S., Oberhauser, A.F. and **Braun, W.** Engineering proteins with enhanced mechanical stability by force-specific sequence motifs. *Proteins*, 2012 Jan. 9, doi: 10.1002/prot.24027. [Epub ahead of print]

Allan R Brasier, Josefina Garcia, **John E. Wiktorowicz**, Heidi M. Spratt, Guillermo Comach, Hyunsu Ju, Adrian Recinos III, **Kizhake V. Soman**, Brett M. Forshey, Eric S. Halsey, Patrick J. Blair, Claudio Rocha, Isabel Bazan, Sundar S Victor, Zheng Wu, Susan Stafford, Douglas Watts, Amy C. Morrison, Thomas W. Scott, Tadeusz J. Kochel, and the Venezuelan Dengue Fever Working Group, *Discovery Proteomics And Nonparametric Modeling Pipeline In The Development Of A Candidate Biomarker Panel For Dengue Hemorrhagic Fever*; Clinical and Translational Science, 5, 8-20 (2012).

Improved Mass Defect Model for Theoretical Tryptic Peptides, *Analytical Chemistry, in press*, I. Mitra; A. Nefedov; A. Brasier; **R.G. Sadygov**.

Proteome Dynamics: Analysis of Lipoproteins and Acute Phase Response Proteins with $^2\text{H}_2\text{O}$ -Metabolic Labeling, *Molecular and Cellular Proteomics, in press*. L. Li, B. Willard, N. Rachdaoui, J. P. Kirwan, **R. G. Sadygov**, W. C. Stanley, S. Previs, A. J. McCullough and T. Kasumov.

3. Generalized Linear and Mixed Models for Label-Free Shotgun Proteomics, *Statistics and Its Interface, 2012, 5, 89-98*, M. C. Leitch, I. Mitra, **R.G. Sadygov**.

Kudlicki A (2012) The Optimal Exponent Base for emPAI Is 6.5. PLoS ONE 7(3): e32339. doi:10.1371/journal.pone.0032339.

Featured Abstract by BMB Faculty

The Optimal Exponent Base for emPAI Is 6.5.

[PLoS One](#). 2012;7(3):e32339. Epub 2012 Mar 5.

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Exponentially Modified Protein Abundance Index (emPAI) is an established method of estimating protein abundances from peptide counts in a single LC-MS/MS experiment. EmPAI is defined as $10(\text{PAI})$ minus one, where PAI (Protein Abundance Index) denotes the ratio of observed to observable peptides. EmPAI was first proposed by Ishihama et al [1] who found that PAI is approximately proportional to the logarithm of absolute protein concentration. I define $\text{emPAI}_{6.5} = 6.5(\text{PAI}) - 1$ and show that it performs significantly better than emPAI, while it is equally easy to compute. The higher accuracy of $\text{emPAI}_{6.5}$ is demonstrated by analyzing three data sets, including the one used in the original study [1]. I conclude that $\text{emPAI}_{6.5}$ ought to be used instead of the original emPAI for protein quantitation.

