Volume 7, Issue 2 February, 2014

Bioinformatics up to Date

(Bioinformatics Infrastructure Facility, Biotechnology Division)
North-East Institute of Science & Technology
Jorhat - 785 006, Assam
(http://www.rrljorhat.res.in/biotechnology.html)

Inside…..

Protein Data Bank

As of Tuesday Feb 25, 2014 there are 98117 Biomolecular Structures

1st annual meeting and symposium of Society of Biological Chemists (India), North East Chapter

The 1st annual meeting and symposium of Society of Biological Chemists (India) organised by North East Chapter was held at CSIR- North East Institute of Science & Technology, Jorhat, Assam on 22nd February, 2014. The President of Society Biological Chemists (India) along with the renowned Professors and Scientists from all the 8 states of North East India attended the meeting. The topics related to metagenomics, Biomolecular aspects of cancer, Chronic Obstructive Pulmonary Disease (COPD), medicinal plants, Crop improvement through genetic engineering, DNA bar-coding, Implications of toxic heavy metals in health, Microbe and plant based bio molecules; Genomics in biodiversity from North East India, Developments of Tea Research etc. were discussed.

Dr R C Boruah, President of SBC (I), North East Chapter gave a brief review about the history of SBC (I) and designated the society as the longest surviving society of Biological chemists in India. He highlighted the symposium as a significant occasion for the institute because it brought leading scientific personals of North East India into an open forum. Dr B G Unni, Convenor of Society of Biological Chemists, SBC (India) NE chapter talked in brief about the history of the society's North East chapter and also mentioned how he sustained and strengthened the activities of the society with the help of members. Then Prof. D Chattopadhayay, President SBC (I) addressed the meeting stating that it was a historic moment for all as the meeting was held in the auditorium, which was built in the memory of the founder of SBC (I), North East Chapter and appreciated for the efforts taken by the chapter for having such scientific gathering at Jorhat. Dr D Ramaiah, Chairman of the Organizing Committee expressed his happiness for having such gathering from the states of NE India at CSIR NEIST, Jorhat.

Bioinfo. Carrier

1. **Ph.D. Programme in Computational Biology; The Institute of Mathematical Sciences (IMSc) Chennai, India; http://www.imsc.res.in/biology_imsc**
2. **Research Associate and SRF posts under a DBT sponsored project for novel anti-Diabetes drug discovery@ Tezpur University. http://www.tezu.ernet.in/ProjectWalkin/Advt-MKC-Feb14.pdf**

RNA CoMPASS: A Dual Approach for Pathogen and Host Transcriptome Analysis of RNA-Seq Datasets

High-throughput RNA sequencing (RNA-seq) has become an instrumental assay for the analysis of multiple aspects of an organism's transcriptome. Further, the analysis of a biological specimen's associated microbiome can also be performed using RNA-seq data and this application is gaining interest in the scientific community. RNA CoMPASS, a comprehensive RNA-seq analysis pipeline for the simultaneous analysis of transcriptomes and metatranscriptomes from diverse biological specimens. RNA CoMPASS leverages existing tools and parallel computing technology to facilitate the analysis of even very large datasets. RNA CoMPASS has a web-based graphical user interface with intrinsic queuing to control a distributed computational pipeline. Cluster analysis of the human transcriptome component of the RNA CoMPASS output clearly separated the BLs (which have a germinal center-like phenotype) from the LCLs (which have a blast-like phenotype) with evidence of activated MYC signaling and lower interferon and NF-kB signaling in the BLs. Together, this analysis illustrates the utility of RNA CoMPASS in the simultaneous analysis of transcriptome and metatranscriptome data. RNA CoMPASS is freely available at http://rnacompass.sourceforge.net/.

[http://www.citeulike.org/user/heathervincent/article/13074806]

Novel therapeutic targets for Huntington's disease discovered

A study led by researchers at Boston University School of Medicine (BUSM) provides novel insight into the impact that genes may have on Huntington's disease (HD). The study, published online in PLOS Genetics, identified specific small segments of RNA (called micro RNA or miRNA) encoded in DNA in the human genome that are highly expressed in HD. Micro RNAs are important because they regulate the expression of genes. The researchers showed that these miRNAs are present in higher quantities in patients with HD and may act as a mitigating factor in the neurologic decline associated with the disease, making them a possible therapeutic target. HD is an inherited and fatal neurological disorder that is usually diagnosed when a person is between 30 and 50 years old. Huntingtin, the single gene mutation responsible for the disease, was identified in 1993.

The investigators examined 21 autopsy brain samples: 12 with HD and nine without. Genetic sequencing analyses were performed on these brain tissues, including quantifying the amount of all the microRNAs present in the brain and their corresponding gene or messenger RNA (mRNA) counterparts. Based on this analysis, the investigators discovered increased amounts of four miRNAs were expressed in the brains of HD patients and that the amount of miRNA was highly correlated with disease status. An increased amount of miRNA in brain cells was correlated with a younger age at disease onset and an earlier age at death of the patients. "The genes which these miRNAs regulate also had increased levels, indicating that these gene expression, indicating that these gene products were likely targeted for storage and for possible future use within the brain cell, rather than for destruction. The authors conclude that these genes may represent new therapeutic targets for HD.

TCGA bladder cancer study reveals potential drug targets, similarities to several cancers

Investigators with The Cancer Genome Atlas (TCGA) Research Network have identified new potential therapeutic targets for a major form of bladder cancer, including important genes and pathways that are disrupted in the disease. They also discovered that, at the molecular level, some subtypes of bladder cancer - also known as urothelial carcinoma - resemble subtypes of breast, head and neck and lung cancers, suggesting similar routes of development.

The researchers' findings provide important insights into the mechanisms underlying bladder cancer, which is estimated to cause more than 15,000 deaths in the United States in 2014. TCGA is a collaboration jointly supported and managed by the National Cancer Institute (NCI) and the National Human Genome Research Institute (NHGRI), both parts of the National Institutes of Health.

In this study, published online Jan. 29, 2014 in Nature, investigators examined bladder cancer that invades the muscle of the bladder, the deadliest form of the disease. The current standard treatments for muscle-invasive bladder cancer include surgery and radiation combined with chemotherapy. There are no recognized second-line therapies - second choices for treatments when the initial therapy does not work - and no approved targeted agents for this type of bladder cancer. Approximately 72,000 new cases of bladder cancer will be diagnosed in the United States in 2014.

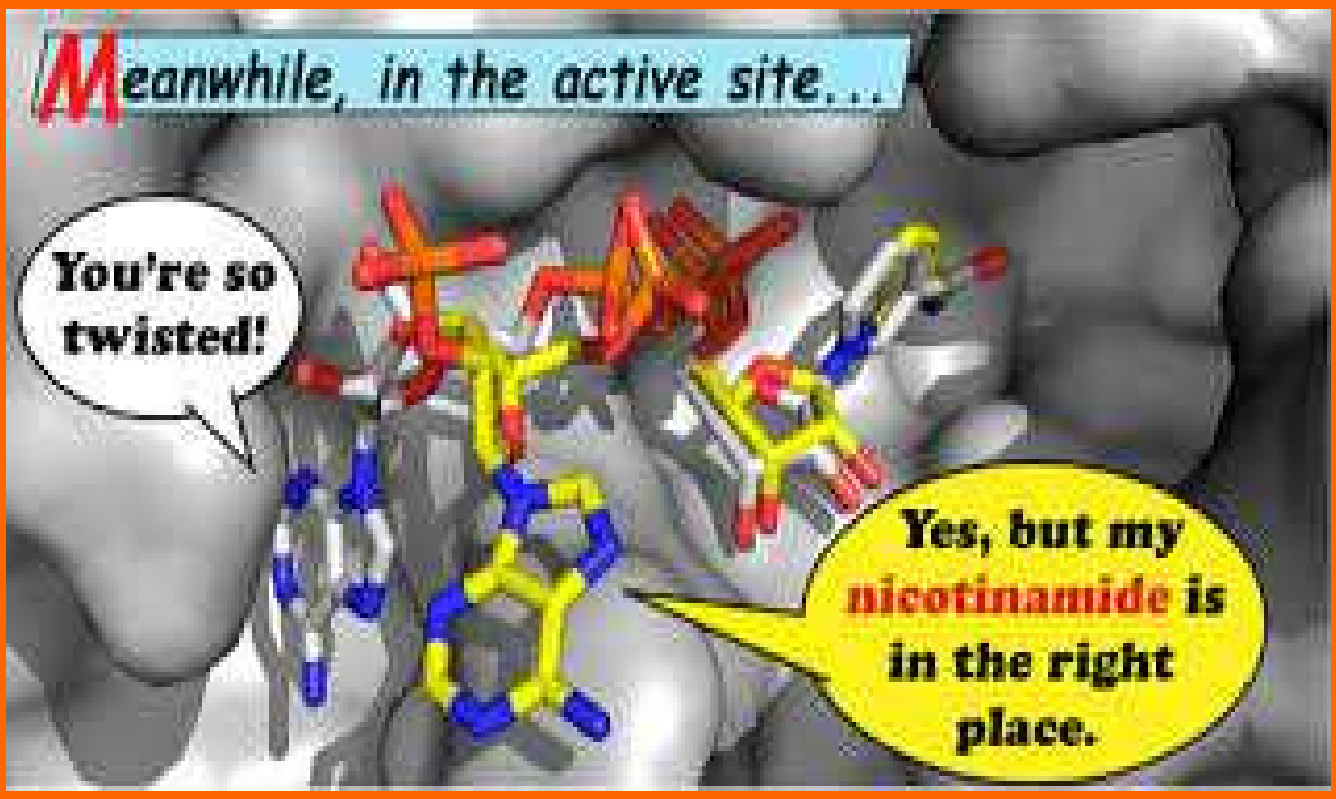
New Integrated Tool to Predict the Function of Non-Coding Variants

Researchers at the Wellcome Trust Sanger Institute and the EMBL-European Bioinformatics Institute have developed software that predicts the likelihood of variants in non-coding regions - relatively unknown regions of DNA that make up 98 per cent of genome - having a functional role. The software, called GWAVA, integrates an enormous amount of information about the way genes are regulated, and prioritises non-coding variants in the human genome. This helps researchers focus their research on the most promising candidates, potentially saving considerable time and resources.

The team investigated if a combination of information related to genes, genetic regions associated with regulation and genome-wide properties can be used to identify the most likely variants that contribute to disease in the non-coding part of the genome. "GWAVA uses a classifier to discriminate apparently harmless non-coding variants from those that are likely to be involved in disease," said Graham Ritchie, first author from EMBL-EBI and the Sanger Institute. "We tested it out using several scenarios and found that it consistently prioritises the regions known to be associated with disease. This could be really useful for people who need to decide which mutations to look at as cancer drivers, for example." The authors hope that using GWAVA predictions for non-coding variants in disease association studies will substantially improve the chances of finding genetic variants that are involved in human disease.

[http://www.nature.com/nmeth/journal/vaop/ncurrent/full/nmeth.2832.html]

Bioinfo. Animation



Patent News

Peptides with antiproliferative properties

United States Patent 6,660,830

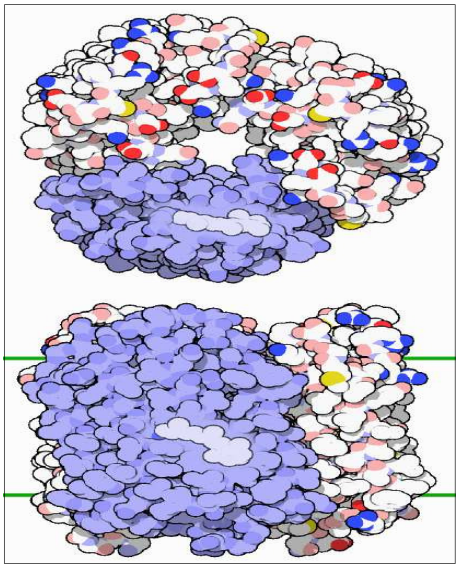
December 9, 2003

Inventors: Radulescu; Razvan T

Abstract

The present invention relates to antiproliferative peptides which are derived from a tumor suppressor protein and bind to growth factor segments or growth factor receptor segments. The invention also relates to nucleic acids (DNAs/RNAs) which code for these peptides and structurally homologous peptide nucleic acids and pharmaceutical compositions containing such peptides. The invention can be used in biotechnology, molecular biology, bioinformatics and in the diagnosis and therapy of hyper proliferative disorders, in particular cancer and atherosclerosis.

Bacteriorhodopsin



Bacteriorhodopsin is a compact molecular machine that pumps protons across a membrane powered by green sunlight. It is built by halophilic (salt loving) bacteria, found in high-temperature brine pools. They use sunlight to pump protons outwards across their cell membranes, making the inside 10,000-fold more alkaline than the outside. These protons are then allowed to flow back inwards through another protein, ATP synthase, building much of the ATP that powers the cell.Bacteriorhodopsin, shown here from PDB entry 1fbb, is composed of three protein chains. It is found embedded in dense arrays in the membranes of the bacteria. The area spanning the membrane is shown in the lower picture between the two green lines. At the heart of each protein chain is a molecule of retinal, which is bound deep inside the protein and connected through a lysine amino acid. In these pictures, one of the three protein chains is shown in blue and the retinal molecule, which is buried inside, is shown in white. Retinal contains a string of carbons that strongly absorb light. When a photon is absorbed, it causes a change in the conformation of the molecule.

Upcoming Events

International Conference on Advances in Bio-Informatics, Bio-Technology and Environmental Engineering - ABBE 2014

1st to 2nd June 2014

London, United Kingdom

Website: http://abbe.theired.org

2014 2nd Journal Conference on Bioscience, Biochemistry and Bioinformatics (JCBBB 2014 2nd)

9th to 10th June 2014

Bangkok, Thailand

Website: http://www.ijbbb.org/jcbbb/2nd/

Kindly send us your feedback to

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