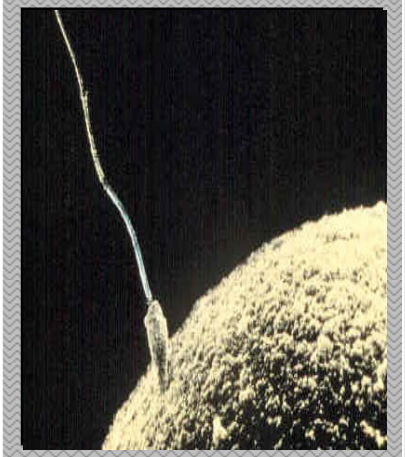

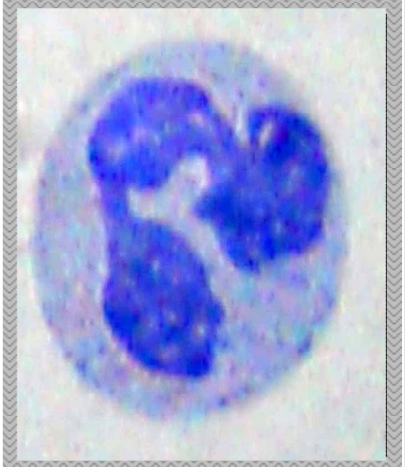

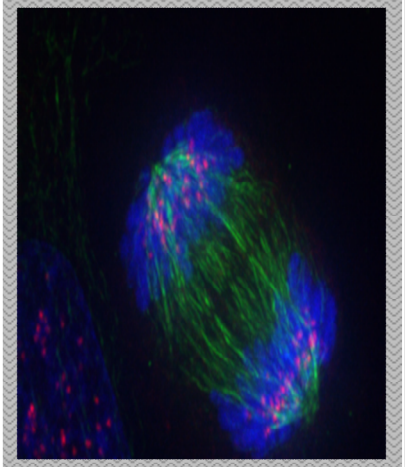

EMGEN Newsletter

Vol. 4, Issue 8, October, 2012

IN THIS ISSUE:

Eastern Mediterranean Health Genomics and Biotechnology Network (EMHGBN) was created in 2004 with collaboration of representatives of selected centres of excellence in (health related) molecular biology, biotechnology & genomics in the Eastern Mediterranean region by recommendations and efforts of WHO/EMRO.

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Article

HIV-malaria co-infection:

effects of malaria on the prevalence of HIV in East sub-Saharan Africa

*The paper entitled: "HIV-malaria co-infection: effects of malaria on the prevalence of HIV in East sub-Saharan Africa" which is published in the International Journal of Epidemiology (*2012. 41(3):891-2*) describes the association between malaria and HIV prevalence in East sub-Saharan Africa. This association is related to the role of malaria on the transmission of HIV. The study was carried out by Dr. Cuadros DF from the Infectious Disease Epidemiology Group, Weill Cornell Medical College - Doha- Qatar.*

Dr. Cuadros DF

Malaria is present throughout the tropical world, where it remains one of the most prevalent infectious diseases with an estimated 300 million cases per year. Approximately 90% of these cases occur in sub-Saharan Africa. This region has also experienced the greatest burden of HIV infection, with an estimated 25 million infected individuals over the past two decades. The fact that these diseases overlap geographically has generated much interest in their potential interactions. However, the causes and implications of this geographical overlap at the population level are still unclear. In the absence of adequate statistical adjustment the spatial distribution visual analysis for each infection may be an attractive option. Regardless of the broad geographic overlap of these two illnesses in sub-Saharan Africa, these diseases show some distinct characteristics: first, malaria is more common in rural areas, whereas HIV is more frequent in urban areas; second, malaria affects mainly pregnant women and young children, while HIV patients are mostly young adults.

We examined the association between malaria and HIV prevalence in East sub-Saharan Africa. This association is plausibly related to the effect of malaria on the transmission of HIV in dually infected individuals (malaria-HIV co-infection). Extensive biological evidence has suggested that co-infection with malaria in HIV infected individuals substantially increases the HIV viral load, which correlates with transmission efficiency of the virus. Several in vitro studies demonstrated that the presence of malaria antigens significantly enhanced

HIV replication. Additionally, population-based studies have shown that HIV-positive in individuals co-infected with malaria had a notably increased viral load and perhaps an increased infection transmission. Therefore, we hypothesized that HIV seropositive individuals who live in areas with high malaria transmission intensity are more likely to be co-infected with malaria, and consequently, to sustain an elevated viral load, increasing the likelihood of transmitting the virus. This raise in viral transmission could increase the number of HIV infections, reflected in notable variations in the HIV prevalence in areas with different malaria transmission intensities.

Our study is the first study to report malaria as a statistically significant risk factor for concurrent HIV infection at the population level. After adjusting for important socio-economic and biological co-variates we found that malaria prevalence is positively and monotonically correlated with HIV prevalence. According to the results, individuals who live in areas with high malaria prevalence (> 42%) run at least twice the risk of being HIV-positive, in contrast to individuals who live in areas with low PfPR malaria prevalence (<= 10%). We also estimated that malaria may account for ~27% of incidental HIV infections in areas with malaria prevalence higher than 10%.

Our results suggest one more independent explanatory variable for the high HIV prevalence in East sub-Saharan Africa. Malaria may be affecting the natural history of HIV and might be an additional important biological risk factor along with male circumcision and co-infection with sexually transmitted infections. Malaria infection may fuel and maintain differences in the HIV prevalence throughout different geographic areas that have similar socio-economical and biological characteristics to those observed in our study.

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1. Cuadros DF., Crowley PH, HIV–malaria co-infection: effects of malaria on the prevalence of HIV in East sub-Saharan Africa. *International Journal of Epidemiology*, 2011. 2011;40(4):931-939.
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Molecular Docking

Molecular docking is a computer simulation program that attempts to predict the best conformation of a complex of receptor-ligand, where usually a protein or a nucleic acid molecule (DNA or RNA) are the receptor and the ligand could be a small molecule or another protein. In other words, it is a simulation process where a ligand position is estimated in a predicted or non-predicted binding site.

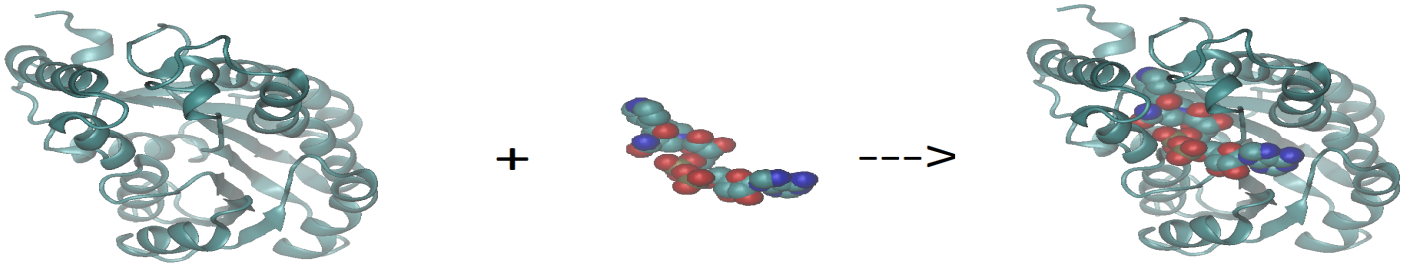


Diagram illustrating the docking of a small molecule ligand to a protein receptor to produce a complex

Molecule docking simulations could be used for reproducing experimental data by using docking validation algorithm; it means that protein-ligand or protein-protein conformations that are obtained *in silico* are compared to structures that are solved by X-ray crystallography or NMR (nuclear magnetic resonance). Moreover, virtual screening is the major docking application, where a library (ligands or proteins) is docked against a drug targets to find the best hit.

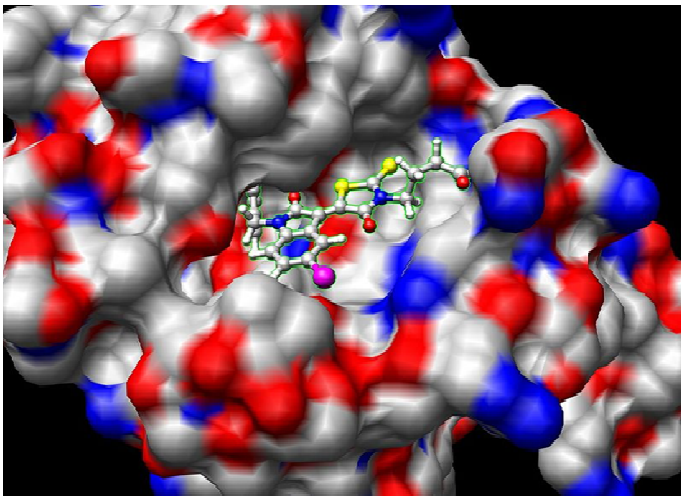
Bound docking is the simplest problem in docking. It is based on computational sachems that try to reconstruct a complex using the bond structures of the ligand and the receptor. A bound structure is derived from structures of molecules, usually a co-crystal of the ligand and the receptor. In contrast, the unbound problem is based on the computational schemes that aim to reconstruct a complex using the unbound structures of the ligand and the receptor. Native structure is one kind of unbound structure that is refers to the structure of a molecule while it is free in solution. An unbound structure may be in other forms such as pseudo-structure, ie. that is the structure when the complex with the molecule is different from the one is used for docking. Modeled structure is the final one and even more challenging task. First, practical docking came from Crick, and in the middle of the1980s docking was started. The Computational program for surface representation based on the Va Der Wals Forces was the first computational program. This program contrib-

uted to the development of algorithms for docking. Deposition of vast amounts of proteins in the PDB (protein data bank) was important too. The prior algorithms relied on geometric criteria, although some programs based on free energy were also developed. One of the first and widely used docking programs was DOCK.

The three key parts in the docking include:

1. Representation of the system
2. Conformational space search
3. Ranking of potential solutions

The first question is how to determine a protein surface, because docking simulates the interaction of the protein surfaces. The surface can be defined by mathematical models or by a grid; it can involve treatment as a protein frame, e.g. rigid or flexible. Solving of the docking problem involves two components: an effective search procedure and a good scoring function. Speed and effectiveness are the two critical elements in a search procedure. Moreover, the scoring function must be fast enough to allow application of a vast number of potential solutions and to discriminate effectively between native and non-native dock conformations effectively. The best matching algorithms and scoring functions should be combined to ideally solve the docking problem.



Small molecule docked to a protein.

The three aspects of the docking are interrelated: the types of conformational search algorithms depend on the choice of the system representation, and the ways to rank potential solutions.

Representation of the system

Surface representation by mathematical models

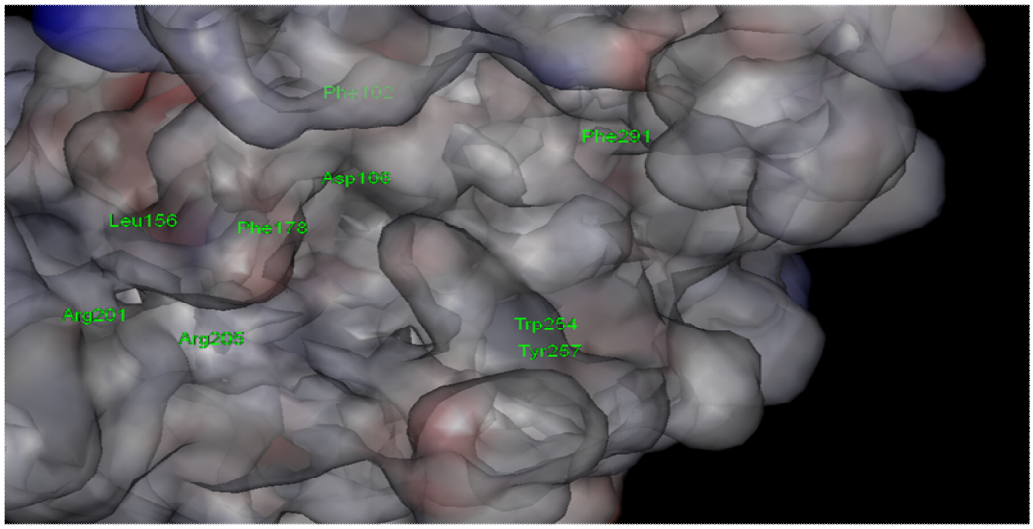
The simplest description of receptor and ligand surface is the atomic representation of exposed residues. This kind of representation is used when the ranking is dependent on real potential energy function. But mostly, the surface is defined by its geometric features such as a Connolly surface. It was indicated that small changes in the ligand representation could cause drastic changes in the docking output.

Types of conformational changes between the bound and unbound: Rigid to Flexible

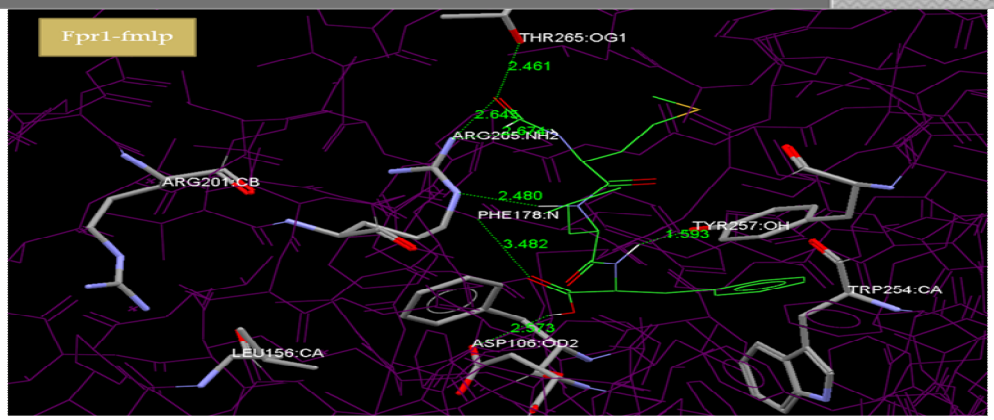
The computational procedures can be classified in to three levels based on their degree of approximation:

- Rigid body docking: it is the simplest models when two proteins are two rigid solid bodies. It would be helpful to tested ligands with their experimentally detected conformation.
- Semi-flexible docking: this model is asymmetric so that one of the molecules, usually the receptor is defined as rigid and the smaller molecule (ligand) is considered flexible.
- Flexible docking: both molecules are considered flexible.

Flexible docking is more accurate. On of the other hand, rigid docking has the advantage of speed.



Surface representation of FPR1



Active site represented by sticks fMLP

Overview of search procedures and matching algorithms

Computational approach to the search approaches

There are many ways to put two molecules together; hence docking calculations can be computationally difficult. The number of possibilities depends on the size of the components and this proves to be more profound in those cases when proteins are considered flexible. A candidate solution search is addressed to two essentially different approaches in docking problems:

1. a full solution space search that scans the whole solution space and 2. a gradual guided progression through solution space; its approaches including MC (Monte Carlo), MD (molecular dynamics), GA (genetic algorithms) and Tabu search.

The search stage for molecular docking of ligands to proteins can be separated into two distinct procedures depending on their binding site. Mostly, the binding sites can be detected by using experimental data or by computational predictions so that some docking efforts concentrate on this method. In the second one the binding site is considered unknown.

Approaches to scoring schemes

A search program leads to a large number of possible orientations (poses) of a ligand in the protein binding site make it unmanageable for any analysis. Scoring functions are used to optimize and rank results, finding the best orientation after the docking. Speed and effectiveness are the two critical elements in a search procedure, covering the relevant conformational space. Moreover, the scoring function needs to be fast enough to calculate a large number of potential solutions. Ideally, the best matching algorithms and

scoring schemes need to be combined, that depending on the algorithms matching and scoring, this may be costly in computational time.

Existing tools

There is a large number of molecular docking programs but no single program has been recognized as a standard, but some programs are preferred by researchers. Docking programs are not easy to use and need some deep understanding of their computational principle, so people are inclined to use the program they are familiar with.

AutoDock

AutoDock uses Monte Carlo simulate annealing and Lamarckin genetic algorithm to make a set of conformations. The AutoDock web page has a wider range than others because it has a free academic license. autodock.scripps.edu/

Dock

Dock is the oldest and one of the best known programs for ligand protein docking. The initial version was used for rigid ligands; flexibility was added to the program later. Dock handle polar binding site better and is useful for fast docking.

FlexX

FlexX is another fragment base method that can make use of flexible ligands and rigid proteins. MIMUMBA torsion angle is used for the creation of conformers. For scoring the Boehm function is used. FelexE is used for flexible receptors showing better results and significantly lower running time.

Gold

Its good results in impartial tests has made it more popular in recent years. Genetic algorithms as used in Gold to provide docking of flexible ligands and proteins with the flexible hydroxyl groups, makes it a good choice when the binding site contains amino acids that form hydrogen bond to the ligands. Gold scoring is based on the favorable conformation as found in the Cambridge Structural Database and on empirical results in weak chemical interactions.

http://www.ccdc.cam.ac.uk/products/life_sciences/gold/

Applications

1. Drug Discovery (lead optimization): it is used to predict the best orientation of the ligand receptor complex. And it could be use to design a ligand. A binding interaction between an enzyme molecule (enzyme) and small molecule (ligand) can inhibit (antagonist) or activate (agonist) the enzyme. Docking is one of the important tools for drug design.
2. Virtual screening (hit Identification): docking alongside a scoring function can be used to screen large databases containing potential drugs *in silico* to find the best hit.
3. Prediction of KA (biological activity)
4. Binding site identification (blind docking)
5. Structure-function studies
6. Enzyme reaction mechanisms
7. Protein engineering
8. Protein-protein or protein-nucleic acid interactions

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1. http://www.eco-itn.eu/sites/eco-itn.eu/files/reports/Rapport%20Jacques%20Ehret.pdf
2. http://en.wikipedia.org/wiki/Docking_(molecular)
3. http://www.dockingserver.com/web
4. autodock.scripps.edu/
5. http://www.ccdc.cam.ac.uk/products/life_sciences/gold/

Metabolomics

What is Metabolomics?

Metabolomics is a subject that deals with small molecule metabolites in the metabolome. The metabolome is defined as the collection of all small molecule metabolites that are found in a biological cell, tissue, organ or organism. These products are the final results of cellular processes in living organisms. In the field of Metabolomics a metabolite is defined as any molecule with a size less than 1 KDa, but there are some exceptions such as albumin which is more than 1KDa in size. In plants Metabolomics refers to primary and secondary metabolites. On the other hand, in humans Metabolomics refers to endogenous or exogenous and foreign substances metabolites such as drugs called xenometabolites.

Where mRNA gene expression data and proteomics analysis don't tell the whole story of what is going on in a cell, Metabolomics can give a snapshot of the cell physiology. Metabolomics is referred to by some other names as well, such as metabonomics and metabolic profiling. Metabolomics like other "omics" such as genomics and proteomics is the result of recent technologies. These technologies could be categorized in three groups:

1) Identification systems such as mass spectrometry (MS) and nuclear magnetic resonance (NMR).
2) Separation systems like Gas chromatography, Capillary electrophoresis and HPLC systems.
3) Creation of software tools to increase the rate of speed for analyzing data.

With these innovations (software and hardware) scientists are able to identify and qualify more than one small molecule at a time; specifically, hundreds or more of these small molecules in as little as a few minutes.

This field and its progress has served as an aid to many potential applications covering a large number of areas. Beverage testing, general plant biology, functional genomics, drug toxicology and testing, genetic disease testing and organ transplant monitoring are some of these areas.

Replica of an early mass spectrometer

Metabolomics applications:

1. Metabolomics in organ transplantation

The success of any organ depends on the ability to monitor patients, and change their medications. Transplant organ monitoring is still dependent on the old technologies such as serum creatine levels, urine output, blood pressure, etc. These old technologies are insufficient, insensitive and inaccurate. Hence, the tools of Metabolomics, genomics and proteomics are being used to overcome these difficulties. Organ transplant monitoring has been a part of Metabolomics for more than 40 years. Since 1999 reports have shown the use of Metabolomics methods such as NMR, LC-MS, spectral pattern analysis, etc., to monitor organ functions. Metabolite measurements have been used to monitor two aspects of organ physiology:

- organ function and
- organ reperfusion injury

2. Plant Metabolomics

Plants react to any change in their environment, for example if a bird perches on a leaf, the leaf should adjust its photosynthetic pathway to cope with darkness. These kinds of changes in a plant can be followed by looking at the changes in the low molecular weight chemicals. Single nucleotide changes in the genome can result in small changes in its protein and consequently small changes in its metabolite. Therefore, changes in the genotype will be affected by changes in metabolome. Linking these differences to the genetic differences that cause them is the aim of plant Metabolomics. Plant Metabolomics is trying to link genome, proteome to the metabolome. First and foremost, the challenge is how to measure all these chemicals and

secondly, how to analyze these vast amounts of measurements.

Plant Metabolomics is not still not fully comprehended. Metabolomics helps to characterize and differentiate genotypes and phenotypes on their metabolite levels. Some possible applications of plant Metabolomics could be summarized thus:

- Characterization of metabolism
- Measurements of metabolites in order to comprehend the response of plants to environmental and physiological changes.
- Identification of regulated key sites in networks
- For elucidating the important regulatory mechanisms within a network where systematic investigation of metabolites that involved
- Investigation of gene function
- Role of genes and their expression levels could be determined by metabolic analysis

Drug discovery and development

Metabolomics became a new powerful method for drug discovery. Metabolomics is a means to measure biochemical changes and the mapping of these changes. Metabolomics provide data which are more precise, less complex, more relevant and more quantitative than genomics, proteomics or transcriptomics. Using this technology, makes it easier now to obtain an understanding of certain diseases and new treatments faster and more accurate compared to the old technologies.

Metabolomics has a vast range of applications in the field of drug discovery and drug development. Some of these applications are:

- Target identification and validation
- Lead prioritization and optimization
- Preclinical studies
- Clinical trials
- Marketing studies
- Diagnostics.

Metabolomics computational approaches

Identification and quantification are not the only goals of Metabolomics, but like other 'omics' Metabolomics generates vast amounts of data. Handling, processing and analyzing of these data is a challenge for researchers for which statistical, mathematical and bioinformatic tools are necessary.

Creating a database is necessary, considering the extensive and multi-dimentional data derived from Metabolomics. Metabolomics needs bioinformatics in certain areas for further progress. These areas comprise: data and information management, raw analytical data processing, Metabolomics standards and ontology, statistical analysis and data mining, data integration and mathematical modeling of metabolic networks from system biology.

The most challenging step in data analysis is the Metabolomics raw data processing. AMDIS (automated mass spectral deconvolution and identification system) software is useful in processing the GC - MS. CONDA (component detection algorithm) and WMSM (windowed mass selection method) are used to process ESI-LC-MS data. Metabolomics used two algorithms to analyze the data which are: unsupervised and supervised algorithms. PCA (principal component analysis) is an example of unsupervised algorithm and PLS (Partial least squares) for supervised algorithm. Metadata, raw and processed experiment data are required to be stored in databases. In short, a Metabolomics database should be comprehensive, flexible enough and easy to retrieve. Some of these databases are: KEGG, MtaCyc, AraCyc, MapMan, KaPPA-View, ArMet, MetNet, and DOME. Metabolomics as a research area needs a standard, but there are not any agreed standards for this area. A Metabolomics society has been created recently. It is focused on developing such standards

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New Method to Find Novel Connections from Gene to Gene, Drug to Drug and Between Scientists

Researchers from Mount Sinai School of Medicine and Ma'ayan laboratory have developed a new computational method to help scientists to identify and prioritize genes, drug targets, and strategies for repositioning drugs that are already on the market. Researchers will be able to better understand gene-gene, protein-protein, and drug/side-effect interactions, simply and efficiently. This new algorithm will also help scientists to identify fellow researchers with whom they can collaborate. To build networks from data will become easier and simpler with the use of this algorithm. Converting data to the network will enable us to better understand the data and to discover new and significant relationships to better focus on the important features of the data. One million medical records of patients were analyzed to build a network that connects commonly co-prescribed drugs, commonly co-occurring side effects, and the relationships between side effects and combinations of drugs. They showed that side effects may not be caused by the drugs, but they may be caused by the condition of the patient, which in itself may be unrelated to the drugs.

Reference: Dannenfelser R., NR Clark, A Ma'ayan. Genes2FANs: connecting genes through functional association networks. *BMC Bioinformatics*, 2012; 13 (1): 156 DOI: 10.1186/1471-2105-13-156.

Is There Such a Thing as Eating Too Many Fruits and Vegetables?

Loyola University Health System registered dietitian, Brooke Schantz, has revealed that it is possible to overeat healthy foods.

According to research by Schantz, fruits, although nutritious, can still lead to weight gain. Control as to portion sizes of the food consumed should be kept in mind. Schantz's report shows that overeating healthy foods easily occurs. However, the same rules for junk food should apply to healthy food as well. Weight fluctuates are governed by the basic concept that if your total caloric intake is higher than the energy you burn off in a day, you will gain weight. On the other hand, if it is lower, you will lose weight. Most of Schantz's patients wonder why they don't lose weight, since they reportedly eat fruit all day long. They were shocked by his advice to watch the quantity of food they eat, even if it is healthy. Schantz poses that foods carrying these health claims may still have high sugar and calories contents.

Reference: http://www.sciencedaily.com/releases/2012/07/120724144423.htm

New Strategy That Repairs Mitochondrial Mutations

Researchers have identified a new genetic approach to correct mutations in DNA of human mitochondria by targeting corrective RNAs. Human mitochondrial genome mutations are connected with neuromuscular diseases, aging, and metabolic defects. According to the Dr. Michael Teitell's study there are no methods to effectively repair these mutations. The Dr. Teitell research group have been looking for such methods for a long time. They revealed the role of an essential protein that shuttles RNA into the mitochondria. The introduction of nucleus-encoded small RNAs into mitochondria is necessary for the replication, transcription, and translation of the mitochondrial genome, but the mechanisms for delivering RNA into mitochondria is poorly understood.

This study defines a new role for polynucleotide phosphorylase (PNPASE) in regulating the RNA into mitochondria. Decreasing the expression of this protein reduced RNA import, which indicated the processing of mitochondrial genome-encoded RNAs. Translation of proteins required for maintaining the mitochondrial electron transport chain was inhibited because of the reduction of RNA processing. Unprocessed mitochondrial-encoded RNAs accumulate because of the reduction of PNASE and consequently protein translation was inhibited and energy production was compromised, leading to a stop of cell growth.

According to Dr. Kohler this finding opens up new ways to understand and develop therapies for diseases related to mitochondria. Gene therapy has been used to express proteins that are threats to the causes of various diseases. In this study researchers developed a strategy to import specific RNA molecules encoded in the nucleus into the mitochondria to express protein necessary to repair mitochondrial gene mutations. First, reparative RNA that was moved out of the nucleus had to be stabilized and then targeted to the mitochondrial membrane. This was completed by correcting an export sequence to direct the RNA to the mitochondrion. When RNA was on the mitochondrial surface, the next transport sequence was necessary to direct the RNA into the targeted organelle. By performing these two modifications, a wide range of RNAs were targeted to be imported into the mitochondria, to repair mutations in mitochondria.

Reference: Wang G., E Shimada, J Zhang, JS Hong, GM Smith, MA Teitell, M Koehler. Correcting human mitochondrial mutations with targeted RNA import. *Proceedings of the National Academy of Sciences*, March 12, 2012 DOI:10.1073/pnas.1116792109

Bioactive Compounds: Types, Biological Activities and Health Effects

Study of the types, biological activities and health effects of bioactive compounds is the goal of this book. Editors have tried to discuss topics including: calcium orthophosphate bioceramics in biomedical applications; the biological and toxicological effects of naphthoquinones; probiotics, bioactive compounds and vaccines used in bovine mastitis; supercritical fluid extraction of bioactive compounds and microalgae as a promising source of bioactive compound and flavonoid compounds and their antioxidant activity.

Editors: Ahmed Bitterlich and Sahar Fischl

Publisher: Nova Science Publishers (March 30, 2012) **ISBN:** 978-1-61324-865-2

Bioinformatics Research: New Developments

The current book presents new developments in the field of bioinformatics research. In this book the authors present and discuss various topics including: natural selection, molecular recombination structure and evolutionary historical relationships in bioinformatics; gene-gene and gene-environment causal interactions from different types of genomic data using bioinformatics; bioinformatics analysis of gene networks involved in genomic stability and cancer and protein bioinformatics for drug discovery.

Editors: Chiheb Battik and Khalil Belhassine

Publisher: Nova Science Publishers (June 8, 2012) **ISBN:** 978-1-61942-363-3

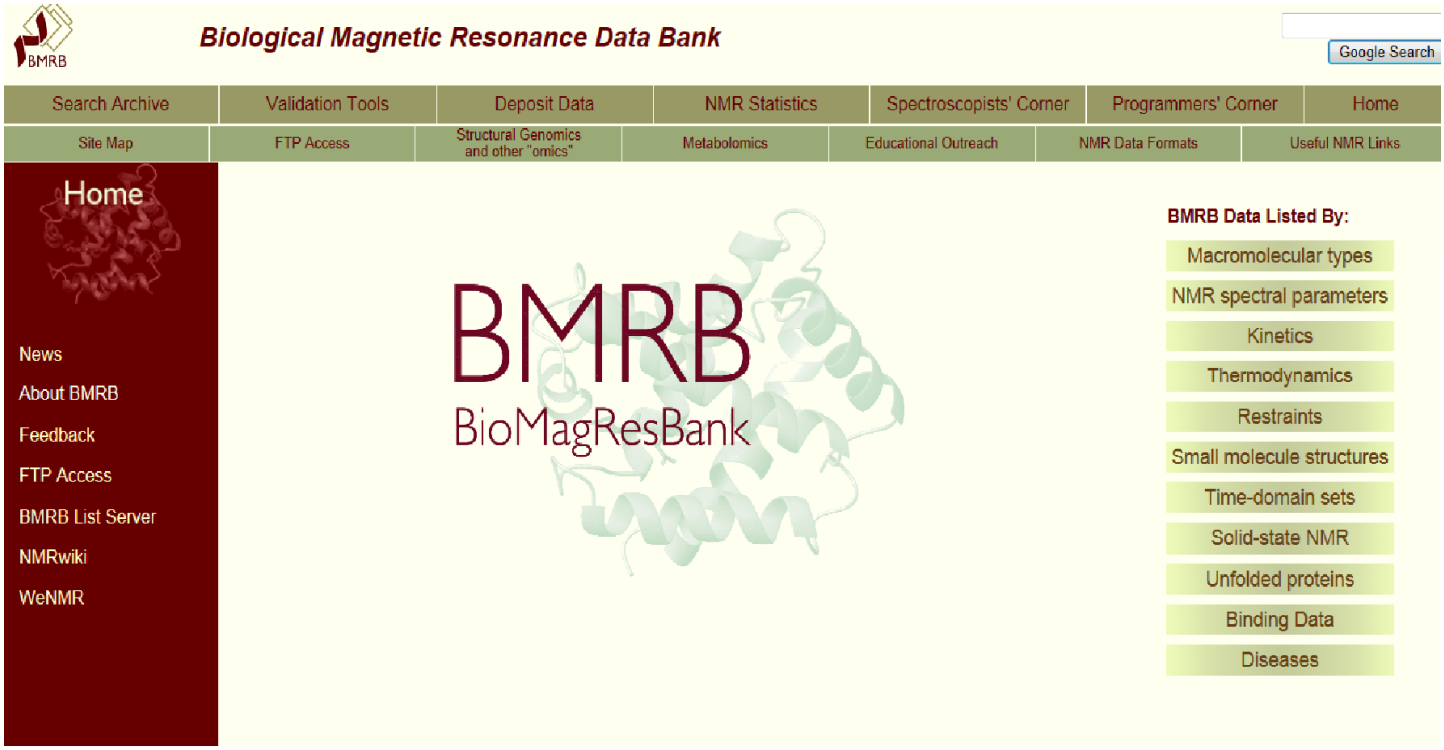
Cancer Metastasis Research: Pathological Insight

Behavior of tumor cells in metastasis can be observed by electron microscopy and molecular biology helped the identification of the molecular base of the metastasis. Cellular diversity of metastatic tumor cells and host cells are important to understanding the behavior of malignant tumor cells and elucidating why such populations may display different responses to treatment. This book could help people in the research and medical field.

Editors: Takanori Kawaguchi

Publisher: Nova Science Publishers (September,2012) **ISBN:** 978-1-61942-863-8

Biological Magnetic Resonance Data Bank (BMRB)



BioMagResBank (PMRB):

BMRB is a repository database responsible for data that come from spectroscopy on proteins, peptides, nucleic acids and other biomolecules and it also contains related tools for storing and analyzing data existing in the databases.

BMRB was created to help scientists in their analysis of the structure, dynamics and chemistry of macromolecules (peptide, protein and nucleic acid) recognized by the International Society of Magnetic Resonance and by the IUPAC-IUBMB-IUPAB Inter-Union Task Group on the Standardization of DataBase of Protein and Nucleic Acid Structure Determined by NMR Spectroscopy, and also to support further development in the NMR spectroscopy field. BMRB has tried to collect, annotate, archive and disseminate the spectral and quantitative data derived from NMR spectroscopy of biological macromolecules and metabolites. BMRB is collaborating with Protein Data Bank (PDB, Rutgers University) and Nucleic Acid Data Bank (NDB, Rutgers University) in order to develop the structural NMR data in proteins and nucleic acids collection sites.

A relatively good overview of the tools and databases that can be accessed through PMRB is provided in the list along the top of the page. Click on the link entitled **Search Archive** would lead you to the very strong search engine which provides fast availability to the entire BMRB data library. The PMRB database can be searched using several features of molecule such as BMRB ascension number and PDB ID.

Validation Tools is the second parameter on the top of the page that summarized the list of available tools to validate new data before uploading to the BMRB database. Consequently a user need to know how to prepare and deposit new entries that could be found in the **Deposit Data section**. ADIT-NMR and SMSDep are tools that allow you to deposit at both PDB and BMRB.

Statistic analysis such as Histogram representation of NMR data, Chemical shift statics and chemical shift outline are provided in the **NMR Statistics** part of the website.

Spectroscopists corner part of website is trying to represent some useful programs in the Metabolomics area for depositing at BMRB that are directed as following:

STAR Data Table Generators, Nomenclature and Defined Standards, Experimentally Determined Standards, Software and NMR Experiments and Pulse Programs. **Spectroscopists corner** represented useful software codes for manipulating NMR data files, data and developing NMR experiments.

The website also provides some other useful information such as:

- Structural genomics and other omics
- Metabolomics
- Educational outreach
- NMR data format
- Useful NMR links

Access to PMRB data is free and possible through its websites:

http://www.bmrb.wisc.edu

Reference:

http://www.bmrb.wisc.edu/bmrb/about/policies.html

Announcement

http://selectbiosciences.com/conferences/index.aspx?conf=SBE2012

http://www.keystonesymposia.org/index.cfm?e=Web.Meeting.Flyer&MeetingID=1224

http://www.icccb.org/

Announcement

http://www.icesb.org/

http://selectbiosciences.com/conferences/index.aspx?conf=GRA2012

http://www.advbiotech.org/

Title: Sperm

The word sperm originates etymologically from Latin sperma (seed) which derives from the Greek (σπέρμα) sperma (a form of the verb "to sow"). It denotes the male reproductive cell. As regards the types of anisogamy (sexual reproduction) and oogamy, there is a notable difference in the size of the gametes, the smaller ones being termed the "male" or sperm cell. A uniflagellar sperm cell referred to as a spermatozoon is motile , whereas a non-motile sperm cell is referred to as a spermatium. Sperm cells cannot reproduce and have a limited life span. During fertilization and after fusion with an egg cell, a new organism starts to develop, beginning as a pluripotent zygote. The human sperm cell is haploid, meaning it has 23 chromosomes forming a diploid cell by joining the 23 chromosomes of the female egg cell.

Reference: http://en.wikipedia.org/wiki/Sperm

Title: Nutrophil granulocytes

Neutrophil granulocytes are a type of white blood cell, abundant in mammals. They form an essential part of the immune system. Neutrophils are located in the blood stream. Neutrophils are the first responders to migrate towards: the site of inflammation resulting from bacterial infection, environmental exposure and some cancers. These cells are attracted by chemical signals, so-called chemotaxis. They are recruited to the site of injury within minutes, causing a whitish/yellow substance to appear at the site.

Reference: http://en.wikipedia.org/wiki/Neutrophil_granulocyte

Title: Mitosis

In the eukaryotic cell, mitosis is defined as a process when chromosomes separate into two identical sets, forming two separate nuclei immediately followed by cytokinesis. In this process nuclei, cytoplasm, organelles and cell membrane are divided into two cells. The mitotic phase of the cell cycle is defined as mitosis and cytokinesis occurring in direct sequence. Mitosis divides the mother cells into two distinct daughter cells that are genetically identical to each other. This stage of the cell cycle accounts for 10 per cent of the total cell cycle.

Reference: http://en.wikipedia.org/wiki/Mitoses