## Aqa Biol1 June 2014 Exam Paper Biology And Disease

Regulation and targeting of enzymes mediating Parkinson's disease pathogenesis: focus on Parkinson's disease Kinases, GTPases and ATPasesDiscoidin Domain Receptors in Health and DiseaseProtein engineering and other bio-synthetic routes for bio-based materials: Current uses and potential applicationsQuantitative Assessment and Validation of Network Inference Methods in BioinformaticsInformation-based methods for neuroimaging: analyzing structure, function and dynamicsQuantitative analysis of neuroanatomyThe Million Person Study of Low-Dose Radiation Health EffectsBibliography of AgricultureThe Journal of Cell BiologyQuarterly Cumulative Index to Current Medical Literature. V. 1–12; 1916–26Bibliography of Agriculture with Subject Index Jean-Marc Taymans Rafael Fridman Carissa M Soto Benjamin Haibe-Kains Jesus M. Cortés Julian M L Budd John D. Boice Jr

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understanding the molecular pathogenesis of parkinson s disease pd is a priority in biomedical

research and a pre requisite to improve early disease diagnosis and ultimately to developing disease modifying strategies in the past decade and a half geneticists have identified several genes that are involved in the molecular pathogenesis of pd they not only identified gene variants segregating with familial forms of pd but also genetic risk factors of sporadic pd via genome wide association studies gwas understanding how pd genes and their gene products function holds the promise of unraveling key pd pathogenic processes therefore the precise cellular role of pd proteins is currently the subject of intense investigation interestingly a number of pd proteins have enzymatic functions including kinase gtpase or atpase functions in the context of understanding disease pathogenesis or developing disease modifying therapies enzymes possess several useful features firstly enzymes are often key elements of cellular signaling networks acting as on off switches to determine signaling intensity for instance kinases mediate phosphorylation events which activate or inactivate their substrates while gtpases modulate activity of their effector proteins via direct interaction in a qdp qtp dependent manner atpases also control cellular processes through their involvement in cellular energy production and or in transmembrane transport secondly enzymes are attractive targets for therapeutics development this is exemplified by the growing number of kinase inhibitors approved for clinical use while compounds modulating gtpases or atpases have also been proposed as potential therapeutics finally as elements in cellular signaling networks enzymes are not generally constitutively active but subject to further regulation through additional signaling components knowledge of how pd kinases gtpases and atpases are activated or inactivated can aid in understanding how pd signaling networks are deregulated in disease and point to new possibilities in targeting pathological signaling processes the objective of this research topic is to provide an overview of current knowledge on the regulation of cellular signaling networks of pd kinases gtpases and atpases both upstream and downstream signaling events will be covered with a focus on molecular events that can readily be monitored relevance as disease biomarkers and have a potential to be modulated relevance as potential therapeutic target

the interactions of cells with their surrounding extracellular matrix ecm plays a pivotal role in driving normal cell behavior from development to tissue differentiation and function at the cellular level organ homeostasis depends on a productive communication between cells and ecm which eventually leads to the normal phenotypic repertoire that characterize each cell type in the organism a failure to establish these normal interactions and to interpret the cues emanating from the ecm is one of the major causes in abnormal development and the pathogenesis of multiple diseases to recognize and act upon the biophysical signals that are generated by the cross talk between cells and ecm the cells developed specific receptors among them a unique set of receptor tyrosine kinases rtks known as the discoidin domain receptors ddrs the ddrs are the only rtks that specifically bind to and are activated by collagen a major protein component of the ecm hence the ddrs are part of the signaling networks that translate information from the ecm and thus they are key regulators of cell matrix interactions under physiological conditions ddrs control cell and tissue homeostasis by acting on collagen sensors transducing signals that regulate cell polarity tissue morphogenesis cell differentiation and collagen deposition ddrs play a key role in diseases that are characterized by dysfunction of the stromal component which lead to abnormal collagen deposition and the resulting fibrotic response that disrupt normal organ function in disease of the cardiovascular system lungs and kidneys just to mention a few in cancer ddrs are hijacked by tumor and stromal cells to disrupt normal cell collagen communication and initiate pro oncogenic programs importantly several cancer types exhibit ddr mutations which are thought to alter receptor function and contribute to cancer progression therefore the strong causative association between altered rtk function and disease it is been translated today in the development of specific tyrosine kinase inhibitors targeting ddrs for various disease conditions in spite of the accumulating evidence highlighting the importance of ddrs in health and diseases there is still much to learn about these unique rtks as of today there is a lack in the medical literature of a book dedicated solely to ddrs this is the first comprehensive volume dedicated to ddrs which will fill a gap in the field and serve those interested in the scientific community to learn more about these important receptors in health and

disease

in the past 20 years protein engineering has been used for the production of proteins mostly for biological applications the incorporation of artificial amino acids and chemical handles into proteins had made possible the design and production of protein based materials like hybrid inorganic organic materials smart responsive materials monodisperse polymers and nanoscale assemblies in the current topic we cover current uses and envision future applications of materials generated using protein engineering and biosynthesis techniques i would like to acknowledge the u s office of naval research for financial support and dr cherise bernard for her contributions during the early stages of the research topic

scientists today have access to an unprecedented arsenal of high tech tools that can be used to thoroughly characterize biological systems of interest high throughput omics technologies enable to generate enormous quantities of data at the dna rna epigenetic and proteomic levels one of the major challenges of the post genomic era is to extract functional information by integrating such heterogeneous high throughput genomic data this is not a trivial task as we are increasingly coming to understand that it is not individual genes but rather biological pathways and networks that drive an organism s response to environmental factors and the development of its particular phenotype in order to fully understand the way in which these networks interact or fail to do so in specific states disease for instance we must learn both the structure of the underlying networks and the rules that govern their behavior in recent years there has been an increasing interest in methods that aim to infer biological networks these methods enable the opportunity for better understanding the interactions between genomic features and the overall structure and behavior of the underlying networks so far such network models have been mainly used to identify and validate new interactions between genes of interest but ultimately one could use these networks to predict large scale effects of perturbations such as treatment by multiple targeted drugs however currently we are still at an early stage of comprehending methods and

approaches providing a robust statistical framework to quantitatively assess the quality of network inference and its predictive potential the scope of this research topic in bioinformatics and computational biology aims at addressing these issues by investigating the various complementary approaches to quantify the quality of network models these validation techniques could focus on assessing quality of specific interactions global and local structures and predictive ability of network models these methods could rely exclusively on in silico evaluation procedures or they could be coupled with novel experimental designs to generate the biological data necessary to properly validate inferred networks

the aim of this research topic is to discuss the state of the art on the use of information based methods in the analysis of neuroimaging data information based methods typically built as extensions of the shannon entropy are at the basis of model free approaches which being based on probability distributions rather than on specific expectations can account for all possible non linearities present in the data in a model independent fashion mutual information like methods can also be applied on interacting dynamical variables described by time series thus addressing the uncertainty reduction or information in one variable by conditioning on another set of variables in the last years different information based methods have been shown to be flexible and powerful tools to analyze neuroimaging data with a wide range of different methodologies including formulations based on bivariate vs multivariate representations frequency vs time domains etc apart from methodological issues the information bit as a common unit represents a convenient way to open the road for comparison and integration between different measurements of neuroimaging data in three complementary contexts structural connectivity dynamical functional and effective connectivity and modelling of brain activity applications are ubiquitous starting from resting state in healthy subjects to modulations of consciousness and other aspects of pathophysiology mutual information based methods have provided new insights about common principles in brain organization showing the existence of an active default network when the brain is at rest it is not clear however how this default network is generated the different modules are intra interacting or disappearing in the presence of stimulation some of these open questions at the functional level might find their mechanisms on their structural correlates a key question is the link between structure and function and the use of structural priors for the understanding of the functional connectivity measures as effective connectivity is concerned recently a common framework has been proposed for transfer entropy and granger causality a well established methodology originally based on autoregressive models this framework can open the way to new theories and applications this research topic brings together contributions from researchers from different backgrounds which are either developing new approaches or applying existing methodologies to new data and we hope it will set the basis for discussing the development and validation of new information based methodologies for the understanding of brain structure function and dynamics

the true revolution in the age of digital neuroanatomy is the ability to extensively quantify anatomical structures and thus investigate structure function relationships in great detail large scale projects were recently launched with the aim of providing infrastructure for brain simulations these projects will increase the need for a precise understanding of brain structure e g through statistical analysis and models from articles in this research topic we identify three main themes that clearly illustrate how new quantitative approaches are helping advance our understanding of neural structure and function first new approaches to reconstruct neurons and circuits from empirical data are aiding neuroanatomical mapping second methods are introduced to improve understanding of the underlying principles of organization third by combining existing knowledge from lower levels of organization models can be used to make testable predictions about a higher level organization where knowledge is absent or poor this latter approach is useful for examining statistical properties of specific network connectivity when current experimental methods have not yet been able to fully reconstruct whole circuits of more than a few hundred neurons

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this book presents original research findings of the million person study of low dose radiation health effects mps the largest and most comprehensive epidemiologic study of its kind to investigate the health effects of low level chronic radiation exposure on american workers and veterans throughout the 20th century since the early 1900s epidemiologists have studied the consequences of radiation exposures yet the health effects of low levels received gradually over time remain unresolved this uncertainty comes at a time when the public and workers are experiencing ever increasing levels of radiation exposure from advances in medical radiation imaging techniques e g ct scans frequent flying at high altitudes and environmental and occupational exposures the mps is providing answers by studying 30 radiation exposed u s populations including workers at nuclear power plants radiologists workers at former manhattan project sites nuclear submariners nuclear weapons test participants atomic veterans industrial radiographers and radium dial painters ongoing for more than 20 years and coordinated by the national council on radiation protection and measurements vanderbilt university medical center and memorial sloan kettering cancer center the mps is a national effort supported by the department of energy national aeronautics and space administration u s navy defense threat reduction agency nuclear regulatory commission centers for disease control and prevention and the environmental protection agency unparalleled in scope and quality the mps provides an understanding of low dose health effects that is desperately needed for decision makers and the radiation protection community as society continues to increase the uses of radiation technologies individual chapters were originally published in the international journal of radiation biology

no 2 pt 2 of november issue each year from v 19 1963 47 1970 and v 55 1972 contain the abstracts of papers presented at the annual meeting of the american society for cell biology 3d 1963 10th 1970 and 12th 1972

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