Showcase Session A1: Health, Wellbeing and Related Areas.
Session Chair, Professor Sandra MacRury
Room: Sports hall

Presentation **1 - Genetics & Immunity**	
Ruth Whelan, Division of Biomedical Sciences	
Abstract	Aims: To determine the effect of schizophrenia related autoantigens on B-lymphocytes. Methods: A genome wide association study identified 108 genetic loci, which confer risk of schizophrenia, of these this lab selected fifteen for further study based on a number of selection criteria [1]. The reference sequences of all target proteins has been retrieved from the NCBI protein database and the linear peptide antigens were designed based on the computational prediction of HLA-II epitopes, which were synthesised for used in the in-house ELISA, which tests natural IgG antibodies. B-lymphocytes were cultured and incubated for a period of 48 hours with each antigen at physiologically relevant concentrations. Following incubation, cell viability, and expression of a number of cell markers were measured using flow cytometry, to ascertain whether there was any differences between cells incubated with the different concentrations of antigen and between each antigen. Results: Nine of the selected antigens demonstrated a significant change in autoantibody levels in those with schizophrenia in comparison to healthy controls. It has been identified that exposure to these antigens cause statistically significant reduction in cell viability & an increase in a number of cell markers. Conclusions: When treated with the antigens, the B-lymphocytes demonstrate a statistically significant increase the marker CD83, which suggests an increase in B-cell activation. This work suggests there may be a genetic basis to autoimmunity in schizophrenia.
References	1. Schizophrenia Working Group of the Psychiatric Genomics Consortium (2014) Biological insights from 108 schizophrenia-associated genetic loci, Nature, 511, 421–42.
Presentation **2 - *Does a genomic deletion upstream of CDKN2A lead to melanoma predisposition?***	
Dr Antonia Pritchard, Division of Biomedical Sciences	
Abstract	Background: Variants in the *CDKN2A* gene that affect function of the p16INK4a transcript are the most common cause of familial melanoma. These variants act in an autosomal dominant manner, with penetrance affected by UV radiation (UVR) exposure. Approximately 50% of familial melanoma does not have an attributed genetic cause, despite evident Mendelian inheritance of disease.

	Methods: A total of 529 individuals from 267 families with cutaneous or uveal melanoma have been either whole exome or whole genome sequenced. The identified variants were assessed for segregation within sequenced family members. Results: A 234kb deletion was identified approximately 240kb upstream of the CDKN2A gene in 20/23 affected individuals in a large cutaneous melanoma family. This variant was also present in a second Australian family, in all 5 affected members. Screening of melanoma families worldwide identified a further 10 families harbouring this deletion, but it was not present in a cohort of 61,869 controls. A haplotype linked rare coding SNV in neighbouring gene *DMRTA1*, which can be detected by exome sequencing, was found in 9 individuals in the gnoMAD aggregated cohort (VAF=0.00008). Functional assessment of how this deletion is modifying risk to cutaneous melanoma development is on-going. Conclusion: The deletion upstream of *CDKN2A* is the most common single mutation to have been found in cutaneous melanoma families. This finding is of further significance due to the distance of this deletion from CDKN2A and the fact it would not be detected using traditional exome screening techniques.
Presentation **3 - Investigation the Mechanisms of Inflammation**	
Nicole Brace, Division of Biomedical Sciences	
Abstract	Inflammation is a response to infection or injury that is triggered through the modulation of many signalling pathways in various cell types. Problems with these pathways can result in disruption to the level of inflammation. This can lead to tissue damage and the formation of inflammatory diseases including asthma, atherosclerosis and diabetes. The onset and maintenance of inflammation is driven by many mediators, these include signalling lipid molecules known as eicosanoids. Eicosanoids include prostaglandins, leukotrienes and hydroxyeicosatraenoic acids (HETEs) and have been associated with many physiological roles. Furthermore, they have been associated with various inflammatory disease and many therapeutic agents such as aspirin and ibuprofen target these pathways. The biosynthetic pathways of eicosanoid production is complex and not yet fully understood. Therefore, this project is employing lipidomic and proteomic strategies to investigate the dynamics of eicosanoid production. The work aims to provide further insights into the regulation of eicosanoid metabolism and the role it plays in inflammatory disorders.
Presentation **4 - Novel biomarkers of inflammatory disease**	
Mary Doherty, Division of Biomedical Sciences	

	Inflammation is a natural biological process but aberrant inflammation can lead to a wide range of disease states. Identifying biomarkers for early detection and prognostic evaluation is critical. Damage Associated Molecular Pathogens (DAMPs) describes mitochondrial derived molecules that are believed to drive inflammatory processes harmful to the body. We have identified a family of mitochondrial specific peptides that have the potential to act as biomarkers of a range of disease states. We have shown that specific panels of these peptides are altered in different disease states including inflammatory bowel disease and acute respiratory distress syndrome. We will discuss the role of these peptides in IBD and ARDS and also the potential provide early detection of neurodegenerative disease such as Parkinson's.
References	Boyapati RK, Dorward DA, Tambrowska A, Kalla R, Ventham NT, Duffin R, Doherty MK, Whitfield PD, Gray M, Loane J, Rossi AG, Satsangi J, Ho GT. Mitochondrial DNA is a damage-associated molecular pattern (DAMP) released during active IBD promoting TLR9-mediated inflammation. *Inflamm. Bowel Dis*. 2018; *in press*. Dorward DA, Lucas CD, Doherty MK, Chapman G, Scholefield EJ, Conway Morris A, Felton JM, Kipari T, Humphries DC, Robb CT, Simpson AJ, Whitfield PD, Haslett C, Dhaliwal K, Rossi AG. Novel role for endogenous mitochondrial formylated peptide-driven formyl peptide receptor 1 signalling in acute respiratory distress syndrome. *Thorax* 2017; 72: 928-936.