How the human genome precisely regulates the immense task of coordinating the on and off switch for almost twenty thousand genes at the correct time as well as at the correct place is a fundamental and enduring question for researchers. With the advent of molecular techniques and the application of disease models to study gene regulating epigenetic changes we have the ability to characterize gene expression and expand our fundamental understanding of the genome in normal development and human disease.

Research Brief
When, in 2009, the Epigenetics group expanded its research capacity with Australia’s inaugural Profiling Facility, the significance of epigenome wide characterization was probably under-appreciated. However, in this short time the field has move rapidly and under the tutelage of Dr El-Osta, his group have made critical insight to characterizing specific extracellular stimuli regulating crosstalk between signalling pathways that confer specific epigenomic changes that are important in human disease.

Methodologies
- Primary culture of human aortic endothelial cells as well as mouse derived vascular cells to examine role of epigenetic changes conferring metabolic memory
- Conditional and constitutive knockout of the Set7 enzyme to assess the role of epigenetic persistence and diabetic induced vascular complications
- Chromatin fractionation studies as well as genomic methylation and histone modification to understand their role in vascular gene expression
- Gene regulation experiments examining transcription and epigenetic changes conferring heart disease
- Development of epigenome wide bioinformatics approaches and computational tools that integrate large datasets to the study of gene-environment interactions to understand cardiovascular disease, diabetes and its complications

Selected Publications
- Redox mediating epigenetic changes confer metabolic memories. El-Osta A. Circulation Research. 2012 111:262-4
Glucose Induced Epigenetic Changes

The advent of massive parallel sequencing means specialized tools are required for genome wide integration of massive databases, and the project will include the development and analysis of ChIP approaches and strategies to the broad application of determining epigenomic signatures in small animal models of cardiovascular disease, diabetes and its complications as well as human clinical samples.

Effects of Acute & Chronic Hyperglycaemia on Gene Activity & Epigenetic Change

Gene regulating epigenetic changes mediates changes in cytokine and chemokines and can be assayed also in vivo using small animal models.