

Summary, Year 1

WP2 Integrative bioinformatics for functional genomics and proteomics

The following activities have been carried out in order to achieve the final goal of this WP.

Tissue sampling, categorisation of samples in terms of pathologies, and descriptions of pre-operative pharmacological treatments were carried out. Experimental conditions to be studied in mRNA and protein expression analyses have been defined, as well as cell lines and protocols for the preparation of protein samples. Data resources, methods and tools necessary to meet the data analysis requirements of this WP have been identified and evaluated. Evaluations have been implemented on publicly-available microarray datasets relevant to the study of atherosclerosis and heart failure in humans. A list of significant genes potentially associated with atherosclerosis and its evolution has been generated. This was obtained through the extraction of information from microarray data, external databases and large-scale mining of published papers. Another list of putative targets was generated and annotated using more specialised pharmacological literature. Relevant databases for supporting the inference of biochemical networks have been identified and are being integrated into a Web-based software tool for retrieving and aligning networks. Mass spectrometry analyses of key proteins (myoglobin, albumin and trypsinogen) have been performed.