

### **Investigation of protein mutations associated with heart failure using bioinformatic tools**

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Cardiovascular disease (CVD) is an ever-growing burden both worldwide and in UK, and is one of the leading causes of death worldwide. Often, CVDs progress into heart failure, where the heart can no longer pump effectively. The progression of CVDs to heart failure has been linked with single-gene mutations, including MLP; a multi-function protein found within the cytosol and nucleus of myocytes. To investigate mutations within MLP, homology models including IntFOLD4 were utilized to ascertain the potential structure and relevance of individual mutations in terms of their side chains. A combination of online protein bioinformatics tools were then used to assess the impact of these mutations upon function. Classical molecular dynamics is then used to observe the stability and flexibility of the mutants versus the wild type. Using bioinformatic tools, it is possible to direct wet lab experiments, saving time and reagents. From this study, mutants can be categorized into structural or functional impact groups, thus determining whether a structural biology route, or cell culture based studies would be most telling in how the mutations cause heart failure. From this, therapeutic routes can be considered and tailored based upon the mutants' effect.

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### **Woody plants' promoters of secondary wall-associated NAC domain homologs drive GUS and GFP activities in vascular tissues of *Arabidopsis thaliana***

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The novel and promising biotechnological strategies to improve forest plants growth and wood quality involve building high-precision vector to precisely engineer cell wall biosynthesis in the complex phenomena such as wood formation in timber plants. In this study, a comparative functional and *in silico* analyses of four promoters from woody and *Arabidopsis thaliana* plants was performed. The promoter regions (1.1-2 kbp) of secondary cell wall-specific genes were successfully PCR amplified with gDNA extracted from *Arabidopsis thaliana* col-0, *Eucalyptus grandis* and *Populus* high-value hybrid (*P. alba* x *P. grandidentata*). GUS and GFP analyses showed that vectors constructed with *A. thaliana* derived promoters were highly and precisely interfascicular and xylary fiber-specific while those engineered with woody plants derived promoters were also vascular (xylem and phloem) specific. *In silico* analysis revealed the presence of specific *cis*-regulatory elements that may turn off woody plant' promoters activities in interfascicular fibers. Overall, our results in this study implicate woody plant EgrNAC61 and PWND1A promoters as genetic tools for driving gene expression in vascular tissues while AthSND1 promoter is fiber specific tool.

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