

CHARACTERISATION OF STRESS-INDUCIBLE STI1 IN YEAST, MICE AND HUMANS

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Stress-induced phosphoprotein 1 (STI1) is a 60kDa protein found in eukaryotic cells. The role of StI1 has not been fully characterised and it seems that the protein has several functions within the cell. Functions identified to date include the role of StI1 in regulating the expression of certain heat shock proteins (Hsps) responsible for preventing the unfolding of cellular proteins during unfavourable environmental conditions. StI1 is also a transient member of the Hsp90/Hsp70-based heterocomplex responsible for the maturation of important steroid hormone receptors (SHR), such as the progesterone and glucocorticoid receptors. While the cDNA of *STI1* is available, the complete 3D structure of the STI1 protein has not been solved. Additionally, the gene boundaries have not been identified and genetic regulatory elements remain to be identified. The aim of this project is to develop a complete bioinformatic description of the genes encoding *STI1* in humans, mice and yeast. In particular, *STI1* gene structure will be predicted and the regulatory elements of *STI1* will be investigated. Gene structure will be predicted by aligning the full-length DNA with its corresponding cDNA, as well as by employing algorithms such as GenScan and HMMGene. Regulatory elements will be predicted using the prediction algorithms Promoter2.0, PromoterScan, CorePromoter and TSSW. Phylogenetic footprinting will be used to identify yeast regulatory sequences. This will be achieved by aligning the upstream regions of genes co-regulated with *STI1* in AlignACE. Understanding the regulation of *STI1* expression is a small step toward understanding the intricacies of the eukaryotic heat stress response and hormone signalling pathways.

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