Abstract

• Briefly summarize (approximately 150 words) - the problem, the method, the results, and the conclusions so that

– The reader can decide whether or not to read the whole article

• Together, the title and the abstract should stand on their own

• Many authors write the abstract last so that it accurately reflects the content of the paper See: The Structured Abstract: An Essential Tool for Research <http://research.mlanet.org/structured_abstract.html>

Results: Just say you found whatever things “Using this method I found this gene this gene this gene”

Describe your most interesting results.

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Oak ecosystems are vital to the health of ecosystems, serve as a valuable commodity in the hardwood industry. But as climates change due to industrialization, this may disrupt the oak ecosystem. To account for this, the Apollo genome-editing software was used to construct gene models from the reference genome of oak tree species in search of genes that allow the tree to adapt to climate change. Five constructed gene models were made. The peptide sequences were derived from the gene models, pasted to NCBI Protein Blast, and at least six extra peptide homologous sequences were found. The peptide sequences of the gene model, together with the homologous sequences were uploaded to Clustal Omega to construct a Multiple Sequence Alignment and Phylogenetic Tree, were both constructed to check the degree of sequence conservation between the homologous sequences found in BLAST versus the sequence of the Apollo gene model. Since all five peptide sequences derived from the gene model had excellent conservation with their homologous counterparts, this indicated a strong likelihood that the gene models were constructed correctly. Secondly, the peptide sequences of the constructed gene models were pasted to SWISS and InterProScan to make inferences on their functions. Peptide sequences derived from three of the gene models: a 1693, 1840, and finally a 322 amino acid peptide sequences were all found to be affiliated with protein binding using InterProScan. A protein with 402 residues was found to be affiliated with DNA and RNA binding. Lastly a 230 amino acid sequence was found to be affiliated with calcium ion binding.