



**CALIFORNIA STATE SCIENCE FAIR  
2007 PROJECT SUMMARY**

<b>Name(s)</b> <b>Asimina S. Courelli</b>	<b>Project Number</b> <b>J0404</b>
<b>Project Title</b> <b>Exploring Protein Similarities with Bioinformatics Tools to Establish Reasonable Animal Models for Disease Research</b>	
<p style="text-align: center;"><b>Abstract</b></p> <p><b>Methods/Materials</b> A web browser enabled personal computer with internet access via a residential DSL line was used to access publicly available bioinformatics databases and tools. The OMIM (On line Mendelian Library) was used to find proteins associated with specific diseases, the NCBI protein/gene bank/database was used to find the amino-acid sequence of the selected protein, NCBI's BLAST tool was used to search for homologs in other species, ClustalW, a sequence alignment tool, was used to compare results of BLAST in greater detail, and the Pfam database was used to analyze conserved protein domains.</p> <p><b>Results</b> The proposed procedure was employed to investigate candidate animal models for two diseases: Long QT Syndrome (LQTS) and Parkinson's disease. The protein associated with the most prevalent LQT gene (LQT1) was chosen for LQTS and alpha-synuclein was chosen for Parkinson's disease. Analysis of LQT1 revealed three significant domains associated with ion channels that were conserved across several species even in the fruit fly. Analysis of alpha-synuclein revealed one domain conserved across several species as well. However, the domain was not conserved in evolutionary lower species to the extent that LQT1 was.</p> <p><b>Conclusions/Discussion</b> Several diseases have been linked to the production of defective proteins at the cellular level that can be found in humans and other evolutionarily lower species. Exploration of protein similarities and identification of conserved domains across the evolutionary tree can assist in understanding the evolution of a disease across species and in establishing reasonable animal models for researching a disease. This science project introduced a procedure and a set of publicly available bioinformatics tools to achieve this, employing the power of existing knowledge as it has been coded and stored in national and international resources which are available practically to anybody with access to the public internet. The proposed procedure is presented as a complement to experimental procedures in improving the quality and expediting the timeframe of the research process. It is worth noting that as the tools and the algorithms evolve, and as the databanks increase in content and improve in accuracy, the results of such electronic searching and result processing will become more thorough, more significant, and more important.</p>	
<b>Summary Statement</b> The objective is to establish reasonable animal models for disease research using publicly available bioinformatics databases and tools.	
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