



**CALIFORNIA STATE SCIENCE FAIR
2006 PROJECT SUMMARY**

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Project Title Bionformatics-based Prediction of Novel Caspase Substrates	
Abstract Objectives/Goals Many diseases have been linked to apoptosis, but the advance of new treatments is halted due to the limited knowledge of it. An identification of proteins involved in the process will provide insights on the relationship between caspases, the executors of the apoptosis, their targets, and cell's ultimate death. The objectives of this project are to build a model for the prediction of proteins cleaved by caspases, and provide the results to be tested in laboratory. Methods/Materials A mathematical model of amino acid sequence (pattern) has been created using the combination of the caspase cleavage motif and the nuclear localization signal sequence. The protein databases have been scanned in order to obtain results containing the pattern. The results have been sorted and proteins with most potential to be cleaved by caspases have been selected. Results Four families of proteins containing monopartite nuclear localization signals and twenty-seven families of proteins with bipartite nuclear localization signals have been determined to be potential caspase targets. The next step in the research is the actual experimentation with the proposed proteins that will validate the results of this work. Conclusions/Discussion Currently the rather accidental and rare cases of discovering the proteins cleaved by caspases provide new insights on the cell's regulatory processes and its death. New potential caspase substrates are identified methodologically in this project. If tested positive, they will help to obtain more knowledge of the core participants of the apoptotic process.	
Summary Statement This project utilizes bioinformatics methods of manipulating available data and creates a model for the prediction of potential proteins cleaved by caspases during apoptosis.	
Help Received Mr. Kevin Karplus gave advice on using bioinformatics software;	