



**CALIFORNIA STATE SCIENCE FAIR  
2016 PROJECT SUMMARY**

<b>Name(s)</b> <b>Ryan D. Kmet</b>	<b>Project Number</b> <b>S0519</b>
<b>Project Title</b> <b>A Pharmacologic Study Side Effect Prediction through Evaluation of Target and Nontarget Proteins</b>	
<p style="text-align: center;"><b>Abstract</b></p> <p><b>Objectives/Goals</b> The project hypothesizes that possible side effects of drugs can be predicted through identification of similarities in the amino-acid sequences of targeted and nontargeted proteins.</p> <p><b>Methods/Materials</b> Twenty random drugs with single-protein targets were selected from drugbank.com. The drug descriptions, indications, pharmacodynamics, mechanisms of action, and side effects were catalogued. Once the target proteins for each drug were identified, their specific functions were determined through the Kyoto Encyclopedia of Genes and Genomes (KEGG) Database and also catalogued. The National Center for Biotechnology Information (NCBI) Gene page was utilized to obtain the amino-acid sequences of the targeted proteins, and then the NCBI Basic Alignment Search Tool (BLAST) was employed to identify at least two more human proteins with highly similar amino-acid sequences. The processes of the targeted proteins and their related nontarget proteins were catalogued and compared to determine possible adverse disruption of biological processes.</p> <p><b>Results</b> The results validated that all but one of the target proteins shared at least one biologic process with one or both of the nontarget proteins. Additionally, side effect profiles of all 20 medications showed functional relationships to at least one of the two selected nontarget proteins.</p> <p><b>Conclusions/Discussion</b> Evaluation of target proteins and their related nontarget proteins prior to the initiation of clinical trials could help to properly anticipate potential adverse events by identifying cellular networks or pathways by these proteins from a genome-wide perspective.</p>	
<b>Summary Statement</b> The project hypothesizes that possible side effects of drugs can be predicted through identification of similarities in the amino-acid sequences of target and nontarget proteins	
<b>Help Received</b> Tami Johnson	