



# CALIFORNIA STATE SCIENCE FAIR 2011 PROJECT SUMMARY

<b>Name(s)</b> Alice R. Zhai	<b>Project Number</b> 31840
<b>Project Title</b> Bad for One, or Bad for All? A Cancer Genome Anatomy Project	
<b>Objectives/Goals</b> My project aims to identify highly over-expressed genes in one type of cancer and examine how over-expressed these genes are in other types of cancer.	<b>Abstract</b>
<b>Methods/Materials</b> Using the web-based software and bioinformatics tools from the Cancer Genome Anatomy Project (CGAP) developed by the National Cancer Institute (NCI), I identified 10 over-expressed genes in lung cancerous tissues. Then I searched for the expression frequency of these 10 genes in the normal and cancerous tissues of 17 human organs, and assigned each expression frequency a number between 1 and 10. I subtracted the number assigned to normal tissue from the number assigned to cancerous tissue to indicate the level of over-expression of each gene. Next, I added up the over-expression index of each gene for all 17 types of cancer and observed the patterns and trends. I repeated my analysis using genes from pancreatic cancer.  I used my laptop with high-speed Internet to access the online database. I also used Microsoft Excel to make tables and graphs. I used Microsoft Word to type up my report. Besides my computer, I used a printer to print out the charts, a glue-stick and a stapler to attach the print-outs to my lab notebook.	
<b>Results</b> I found that the highest over-expressed gene in either lung or pancreatic cancer is not the highest over-expressed gene for all 17 types of cancer together. Instead, the 4th (3rd) gene in lung (pancreatic) cancer ranks the highest for all 17 types of cancer together.	
<b>Conclusions/Discussion</b> I concluded that that some genes are unique to certain cancers, and some genes are universal for most types of cancer. The moderately-expressed genes in one type of cancer can be the highest over-expressed in all types of cancer. If sciences can identify these genes, they may be able to find a universal cure for all cancer. If I am to repeat the experiment, I would use the actual counts instead of the coarse color coding to indicate the expression frequency of each gene. I would also conduct the analysis using genes from other types of cancer and compare the results from lung and pancreatic cancer.	
<b>Summary Statement</b> My project is to find out if over-expressed genes in one type of cancer are over-expressed in other types of cancer.	
<b>Help Received</b> After an experience in the kitchen with a skillet, I wanted to test four common metals and their resistance to a change in temperatures. My hypothesis is that the cast iron would cool the slowest due to my experience in the kitchen and the aluminum would cool the fastest.	