



**CALIFORNIA STATE SCIENCE FAIR
2010 PROJECT SUMMARY**

Name(s) Arjun B. Sharma	Project Number S0417
Project Title A Computational Analysis of Tissue Specific Transcription Factor Networks	
Abstract Objectives/Goals Last year my project involved taking a network of transcription factors, and testing if that network was scale-free. This year, what I did was take the expression values of each transcription factor in 34 different tissues. My goal was to then create 34 networks, one for each organ, and test if they were scale-free. Methods/Materials <ol style="list-style-type: none">1. Obtained data: transcription factor PPI data, and tissue expression data from Dr. Ravasi.2. Identify proteins that are expressed by 500 or more per tissue.3. Create 34 tissue-specific networks (one for each tissue), only proteins that are expressed by 500 or more.4. Found the k-value(number of links) for each protein.5. Found the respective P(k) values for each unique k-value and graphed it on a logarithmic scale for each tissue specific network.6. Compared each P(k) graph to the literature, and concluded the tissue-specific networks are scale-free.7. For Adipose and Adrenal_Gland found the five most expressed proteins. Using the PPI file created networks for each tissue, and visualized by using Cytoscape. Results My figures show that the tissue-specific networks are scale-free. The k- P(k) graphs on a logarithmic scale show a mostly linear downwards trend, signifying many nodes with a low k-value and few nodes with a high k-value, suggesting a scale-free network. Conclusions/Discussion The tissue-specific networks that I studied are all scale-free. When I graphed the k-value versus P(k) values on a logarithmic scale they fit the scale-free properties of having many nodes with a small k-value and few nodes with a high k-values, thus producing a network of many hubs and few nodes.	
Summary Statement I applied the concept of network analysis to tissue specific interactions among transcription factors	
Help Received Received Data for analysis from Dr. Timothy Ravasi of UCSD.	