



# CALIFORNIA SCIENCE & ENGINEERING FAIR 2018 PROJECT SUMMARY

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<b>Project Title</b> <b>Structure and Sequence Conservation of Rhodopsin across Ectothermic and Endothermic Vertebrates</b>	
<b>Objectives/Goals</b> The purpose of the study was to analyze the sequence and structure conservation and identity of the vision protein, rhodopsin, across multiple species of ectothermic and endothermic vertebrates. Analyzing sequence differences can provide insight towards how different species go through the process of visual phototransduction. Rhodopsin has been studied for use in gene therapy for restoring vision in humans. In addition, analyzing the differences in the sequence, and how they affect the structure can provide medical benefits when searching for rhodopsin from other species that could cure or prevent blindness in humans. <b>Abstract</b> <b>Methods/Materials</b> Obtained 8 vertebrate protein sequences from Uniprot.org, a protein database, and performed a multiple sequence alignment of all the sequences using the program, Clustal Omega. Clustal Omega was utilized to calculate percent conservation and identity of the amino acid sequences compared. Next, homology models of each protein were created using the program, SWISS-MODEL. These models were loaded into the program, UCSF Chimera, and superimposed. The superimposed structure was rendered by conservation to visualize the structural similarities and differences between the rhodopsin proteins compared. <b>Results</b> Through the multiple sequence alignment performed on Clustal Omega, it was found that the sequences have an identity of 63.842%. From the structural analysis of the rhodopsin sequences on Chimera, it was found that the intracellular region of the protein was poorly conserved across the species. The binding site of retinal in the protein appeared to be highly conserved across all species compared. <b>Conclusions/Discussion</b> The vertebrate rhodopsin sequences compared were found to have a 63.842% identity, implying that the sequence of rhodopsin has been conserved across all 8 species compared. Structural visualization and comparison revealed that the proteins were highly conserved in their extracellular and transmembrane region. The docking site of the retinal, which initiates the process of phototransduction, was also highly conserved, implying that all 8 vertebrate species have conserved the imitation of process of transduction through their evolution. The poor conservation of the intracellular regions of the protein suggests that the vertebrates continue the process of phototransduction differently.	
<b>Summary Statement</b> The study analyzed the structure and sequence conservation of the vision protein, rhodopsin, across vertebrate species.	
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