



# SMART Teams 2013-2014

## Research and Design Phase

### Brookfield Central High School SMART Team

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### Now You See It: The Role of Ocular Albinism 1 in Foveal Development

**PDB:** OA1.pdb

**Primary Citation:** Ghosh, A., Sonavane, U., Andhirka, S.K., Aradhyam, G. K., Joshi, R. (2012). Structural insights into human GPCR protein OA1: a computational perspective. *Journal of Molecular Modeling* 18: 2117-2133

**Format:** Alpha carbon backbone

**RP:** Zcorp with plaster

#### Description:

One in every 60,000 children is born with ocular albinism type 1<sup>[1]</sup>. Ocular albinism is a genetic disease in which pigmentation is lost in the eye, in the retinal pigment epithelium (RPE) located just below the photoreceptors in the retina. This reduced pigmentation affects the development of the fovea (an area of the retina responsible for 99% of vision) and leads to poor visual acuity (the capacity to see fine detail). The mutation causing ocular albinism occurs in the gene *Oa1*, which encodes a G-protein coupled receptor called Ocular albinism type 1 (OA1). OA1 is found in RPE cells, which normally absorb scattered light with melanin, allowing the eye to generate a high-contrast image. While its exact function is unknown, OA1 is known to be central to melanin biosynthesis and foveal development in the retina. Under normal conditions, the highly-selective ligand L-DOPA binds to OA1, which triggers tyrosinase to increase melanin synthesis. Simultaneously, tyrosinase also triggers L-DOPA to further bind with OA1, which activates a positive feedback loop. However, in many cases of albinism, this pathway is disrupted and tyrosinase is not fully efficient. To counter this, scientists are researching the possibility of bypassing the enzyme and flooding the cells with L-DOPA. Further understanding of OA1 and its function could lead to more effective treatments for albinism. The Brookfield Central High School SMART (Students Modeling A Research Topic) Team created a physical model of OA1 using 3-D modeling printing technology to better understand its structure-function relationship.



### Specific Model Information:

- Alpha helices are colored deep pink.
- The day motif is highlighted in navy.
- The toggle switch is highlighted in gold.
- Missense mutations sites abolishing binding to the G-protein are highlighted in peru.
- The missense mutation causing ocular albinism is highlighted in dodger blue.
- The alpha carbon backbone for each of the following conserved residues is highlighted in lawn green and includes Asp 140, Ala 141, Tyr 142, Trp 162, Cys 184, Pro 210, Cys 256 and Trp 257.
- Active site residues are displayed in ball and stick and colored dark green include Asn 268, Glu 264, Tyr 127, Met 198 and Phe293.
- Structural supports are colored papaya whip.

<http://cbm.msoe.edu/smartTeams/>

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