

Fig. S1. Experimental setup for chemotaxis and phototaxis trials. **(A)** Chemotaxis test chamber showing the construction the modified, sterile, petri dish, dialysis membrane, and sterile glass tubing. Zoospore suspension is added to the base of the assembled chemotaxis test chamber and treatment solution is added to the glass tubing, resulting in a gradient within the chamber. **(B)** Phototaxis test chamber showing the whole chamber exposed to directional light and the subsequent sub-chambers (1-4) created for sampling after exposure.

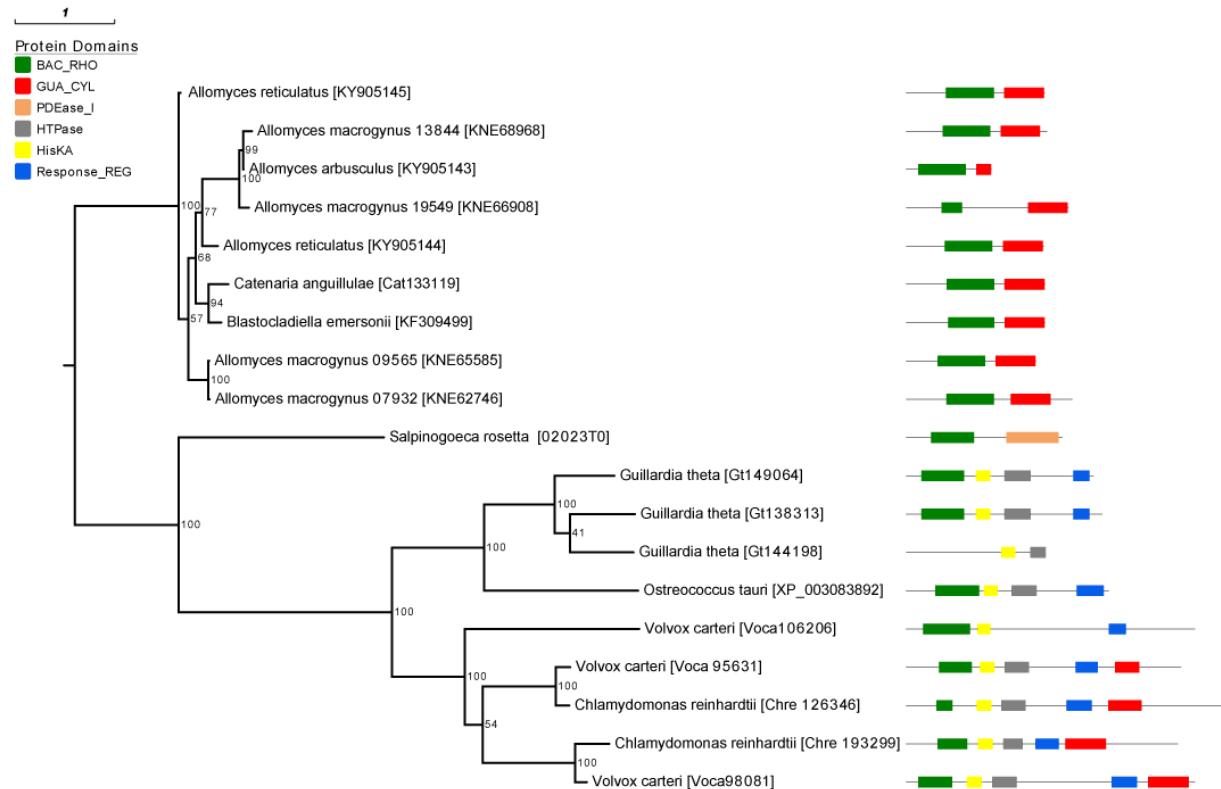


Fig. S2. Maximum likelihood phylogeny of Cyclops-like proteins and predicted protein domain architecture. Bootstrap support values from RAxML (1000 bootstraps) are shown at internal nodes. Domain architecture predictions are from Pfam. All *Allomyces* sequenced possessed putative genes for the bacteriorhodopsin (green) guanylate-cyclase (red) fusion.

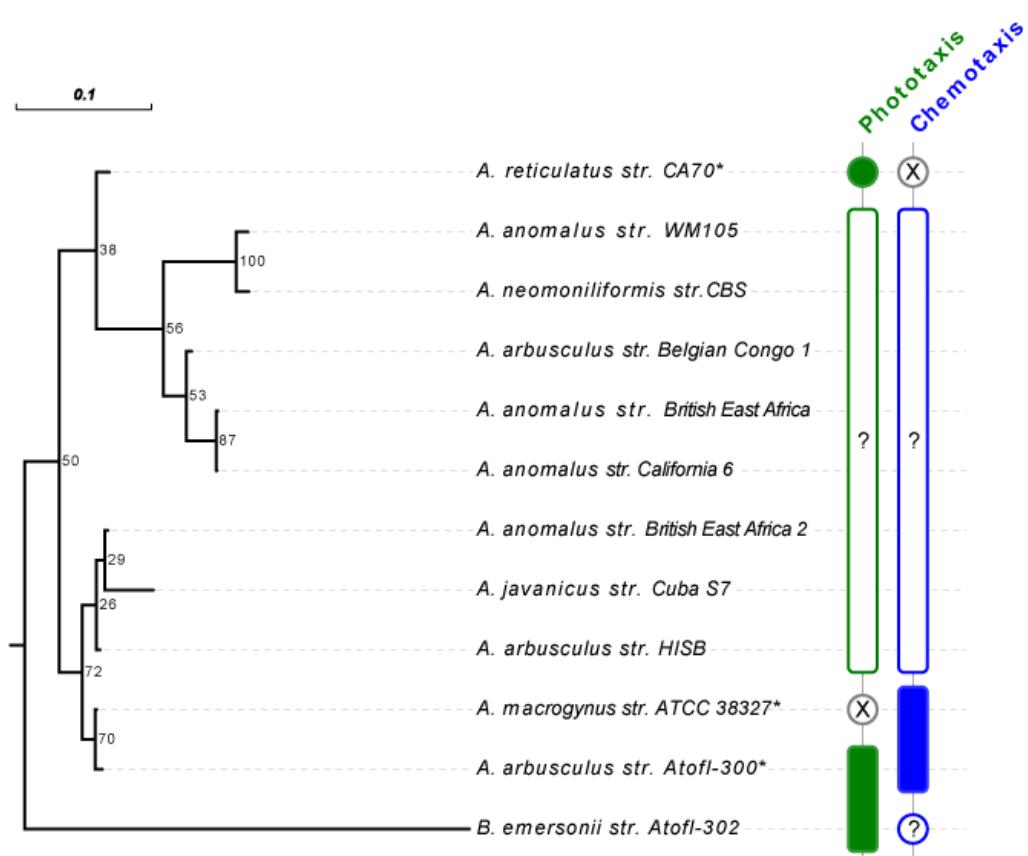


Fig. S3. Maximum Likelihood species tree showing the known distribution of phototactic and chemotactic responses across *Allomyces*, including the outgroup *Blastocladia*. We inferred this tree in RAxML8 with 1000 bootstraps from a combination of 18s, 5.8s, and 28s previously described nucleotide sequences. Species with an “*” are representative of those used in this study. The distribution of phototaxis in *A. arbusculus* str. Atofl-300, *A. reticulatus* str. CA70, and the outgroup *B. emersonii* str. Atofl-302 make an ancestral state of phototaxis in *Allomyces* the most parsimonious explanation given the current data. Trait data is shown in columns to the right. Filled shapes indicate the presence of a trait, while empty shapes with an “X” indicate absence and a “?” indicate that presence/absence has not been tested. Because it is unknown whether *B. emersonii* responds to the chemotactic cues used in this study, we cannot make a prediction about the ancestral state of chemotaxis and if it was gained in the recent ancestor of *A. arbusculus* str. Atofl-300 and *A. macrogynus* str. ATCC 38327 or if chemotaxis was present in the last common ancestor of *Allomyces* and lost in *A. reticulatus* str. CA70.