The Nature of Protein Aggregation Movement in Saccharomyces cerevisiae
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Abstract
Creutzfeldt-Jakob disease (CJD) is a human disease that stems from misfolded proteins. It is characterized by rapid progressive dementia and is not curable. The disease is caused by prions, which are infectious ages composed entirely of protein material that can fold in multiple different ways. The CJD pion promotes refolding of native proteins into a diseased state; the number of misfolded proteins will grow exponentially and eventually kill the cell. Investigating the nature of misfolded proteins, will help advance the understanding of this disease and similar diseases such as Alzheimer’s. Yeast cells, in particular Saccharomyces cerevisiae, are similar to human cells, except they grow a lot faster – divide every two hours or so versus twelve hours for human cells. These cells have a typical eukaryotic structure, share many genes with the human cell, is safe, and very well understood which make it perfect for studying fundamental biological questions. Drs. Manogaran and Sharma from the Marquette Biology Department, have visualized the prion form of Sup35p, [PSI+], which is the most understood of the yeast prions. When these prions form they come together to form aggregates, and when the mother cell divides these aggregates are moved to the back of the cell and not transferred to the daughter. Dr. Sharma has shown that the aggregates form one of four different shapes, but it is not known how these shapes are formed/how the aggregates come together. The first question that needs to be answered is whether they are moving randomly or not. If they are not moving randomly, then other mechanisms are investigated to determine their movement. Understanding the movement of the prions results gets us one step closer to understanding neurodegenerative diseases such as CJD and Alzheimer’s.