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TBIOMD 410
Abstract of capstone project

Title: Identification of possible phosphorylation sites in Okp1 in Saccharomyces Cerevisiae

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Abstract:
Okp1 stands for the outer kinetochore protein, which is a component of the outer kinetochore complex, COMA (Ctf19p, Okp1, Mcm21p, and Ame1p). The function of COMA is mainly a platform for the attachment of microtubules to centromere. Responsible for chromosomal alignment in metaphase, chromosomal movement in anaphase, and monitor proper kinetochore attachment and regulators. Okp1 is an ortholog to Cenp-Q in humans, a centromeric protein involved in kinetochore assembly. To identify possible homologs from other species, a BLAST search was used (Basic Local Alignment Search Tool). MEGA X was used for multiple sequences alignment (MSA). Conservation sites were identified focusing only on Serines and Threonines. Using protein BLAST, the polypeptide sequence of Okp1 was added and Saccharomyces cerevisiae was excluded. Low percentage identity (30-40%) of the desire sequence was selected, 14 organisms total. Using MEGA X, 14 selected organisms were aligned. A second alignment was done using MEGA X, but this time with 16 organisms, (14 previously selected plus human and Saccharomyces cerevisiae). If one or more phosphorylation sites were mutated, chromosomal missegregation might occur. If one or more phosphorylation sites were mutated, defects in the microtubules attachment to the centromere might occur. From 1st alignment, conservation sites were found at number 5 (exception of 6 organisms), number 18 (exception of 7 organisms) and number 40 (exception of 7 organisms). From 2nd alignment, conservation sites were found at number 5 (exception of 8 proteins), number 14 (exception of 9 proteins) and number 28 (exception of 8 proteins).