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Structural prediction and comparative studies of psychrophilic α -galactosidase from *Glaciozyma antarctica* against mesophilic and thermophilic enzymes**Shuhaila Mat-Sharani**

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α -galactosidase is an essential enzyme that catalyses the hydrolysis of α -1-6 linked terminal galactosyl residues from oligosaccharides, galacto-polysaccharides and glycol-conjugates. *Glaciozyma antarctica* is an obligate psychrophilic yeast with an optimal growth temperature of 12 °C and able to tolerate high temperature up to 20 °C. Since this yeast able to grow in an extremely cold temperature the enzyme must have special characteristics in adaptation to cold. The objectives of this study are to predict the structure and function of *G. antarctica* cold adapted α -galactosidase and to characterize its adaptation strategies towards the extremely cold environment based on homology modeling and molecular dynamics. It is commonly stated that there is a relationship between the flexibility of an enzyme and its catalytic activity at low temperature. Comparison between the structure of *G. antarctica* α -galactosidase enzymes with their homologs from the mesophilic and thermophilic fungus showed that *G. antarctica* α -galactosidase enzyme is more flexible because it has more loop structure with a lower number of hydrogen and disulfide bonds.

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