Structural and Evolutionary Analysis in silico of the Leigh Syndrome-Associated Protein SURF1

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Leigh Syndrome is a disorder that typically appears during childhood or before birth and it is caused by mutations in the mitochondrial protein SURF1. Although more than 80 mutations have been recorded for SURF1, little is known about how they affect the protein structure and function. Here, I used the computational approach AlphaFold2 (AF2) to investigate the impact of some mutations in the 3D structure of SURF1. I found that Single Amino acid Variations do not have any structural effect on the protein. However, in silico protein-protein interaction analysis show that G,p.Gly124Arg mutation disturbs SURF1 association with COX1. Altogether, this data demonstrates that using a structural approach to study the impact of mutations in SURF1 provides useful information to perform in vitro and in vivo studies.

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