Engineering a More Thermostable Hemagglutinin H Measles Protein: A Computational Protein Engineering Approach

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The purpose of this project was to determine if a more thermostable Hemagglutinin H protein could be discovered. The research question is: What is the effect of Protein Engineering methods through computation tools on the thermostability of a mutated Hemagglutinin H protein? The independent variable was the residue mutation. The dependent variable was the average ddg score across 10 computational tools. The control in this experiment was the original Hemagglutinin H protein. A variety of mutations were tested. The hypothesis was: Mutating specific residues of the Hemagglutinin H protein using different protein engineering methods will result in increased thermostability with a more favourable ddg score. The null hypothesis was: Mutating specific residues of the Hemagglutinin H protein will not yield any differences in stability. After testing all mutations, two key findings were found, including the high consensus rate of the E90L mutation and the possible stability hotspot of residue G157. The E90L mutation reached a consensus rate of 90%, meaning 9/10 tools deemed this mutation stabilizing, with an average ddg score of -0.74 (stabilizing). Also, position G157 was found to be a potential stability hotspot due to multiple mutations at this position being favourable with a consensus rate of 70%. These findings are novel and not found in preexisting literature. The results agree with the Protein Engineering goal of enhancing and modifying properties of proteins

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