

## Computational Model for Predicting Effective siRNA Sequences Using Whole Stacking Energy ( $\Delta G$ ) for Gene Silencing

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**Abstract :** The small interfering RNA (siRNA) alters the regulatory role of mRNA during gene expression by translational inhibition. Recent studies shows that up regulation of mRNA cause serious diseases like Cancer. So designing effective siRNA with good knockdown effects play an important role in gene silencing. Various siRNA design tools had been developed earlier. In this work, we are trying to analyze the existing good scoring second generation siRNA predicting tools and to optimize the efficiency of siRNA prediction by designing a computational model using Artificial Neural Network and whole stacking energy ( $\Delta G$ ), which may help in gene silencing and drug design in cancer therapy. Our model is trained and tested against a large data set of siRNA sequences. Validation of our results is done by finding correlation coefficient of experimental versus observed inhibition efficacy of siRNA. We achieved a correlation coefficient of 0.727 in our previous computational model and we could improve the correlation coefficient up to 0.753 when the threshold of whole tacking energy is greater than or equal to -32.5 kcal/mol.

**Keywords :** artificial neural network, double stranded RNA, RNA interference, short interfering RNA

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