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Structure-based Virtual Screening for Hinokitiol (β-thujaplicin) Copper Chelatedocked against Profusion structure of 2019-nCoV Spike Glycoprotein with a Single Receptor-binding Domain.

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Abstract: SBDD- Structure Based Drug Discovery is a vital tool for 'In silico' (pseudo-Latin term for in-silicon that refers to huge use of silicon in processor chips as an expression to mean computer simulation) study in medicine. It is a fast and cost-efficient drug discovery and optimization technique and has been proven to be more efficient than conservational techniques since it aims to recognize the molecular basis of a sickness and utilizes the understanding of 3-dimensional structure of the genetic target to design an efficient drug. In this paper we will focus on the virtual screening of Hinokitiol (P-Thujaplicin Copper Chelate docked docked against the profusion structure of 2019-nCoV Spike Glycoprotein with a Single Receptor-Binding domain to study and examine the action of Hinokitiol Copper Chelate as an anti-viral drug against the Spike Glycoprotein of nCoV-2019. [ABSTRACT FROM AUTHOR]

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