**Bioinformatic studies of antiviral effects of thiadiazolylcurcumin on covid-19**

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**‌ Statement of Problem:** There is increasing evidence about the antiviral ability of herbal compounds. Treatment and control of viral diseases using plant compounds and derivatives is important because of less side effect. The coronavirus disease is a type of viral pneumonia that broke out in Wuhan, China in December 2019. This disease is a new virus that originated from the family of coronaviruses**.** The covid-19 disease starts with the initial symptoms of fever, cough, shortness of breath and fatigue, it infects the lungs and causes acute respiratory distress syndrome. The structure of the coronavirus includes various proteins, one of which is the Mpro protein. Mpro protein is essential for virus replication and host infection, Mpro has been an important target for coronavirus inhibitors.

**Research Purpose:** The purpose of this project is to investigate the inhibitory potential and binding site of thiadiazolylcurcumin with the main protease of the covid-19.

**Research Method:** In this research, Pubchem and Drugbank databases were used to find Ligands derived from curcumin. To investigate how the compounds bind to the protease active site, energy optimization, docking studies, and final analyzes were performed with Hyperchem, AutoDockTools, and DS Visualizer software, respectively.

**Results and Conclusion:** thiadiazolylcurcumin with a binding energy of -5.60 kcal/mol, was selected as the best compound. In order to confirm the obtained results, it is recommended to use them for clinical trials, along with further investigations. Amino acids involved in the hydrogen bond of histidine 41, glutamic acid 166, cysteine 145, threonine 26 and amino acids involved in the hydrophobic bond of threonine 25, methionine 49, glycine 143, asparagine 142, histidine 164, methionine 165, proline 168, glutamine 189, leucine. 167, arginine 188, glutamine 192, threonine 190.

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