Fragment molecular orbital calculations for COVID-19 proteins

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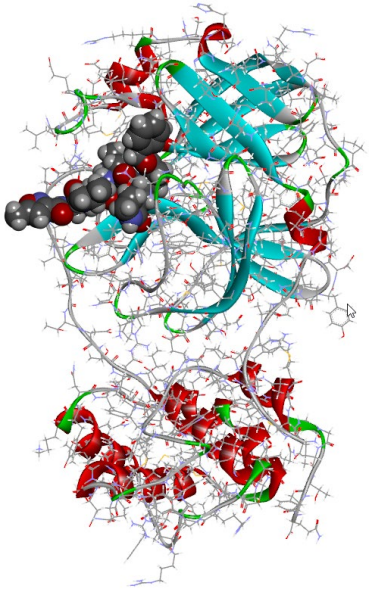
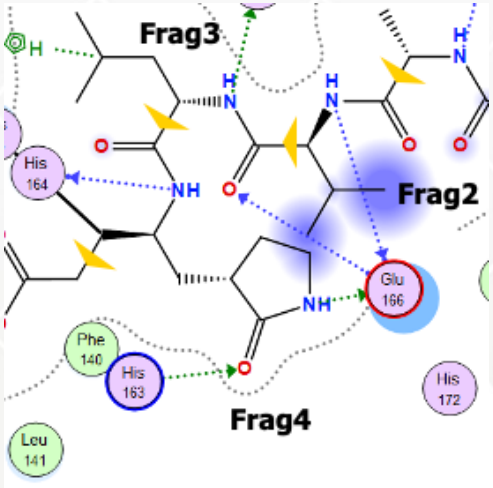
Research group and objectives

Yuji Mochizuki (Rikkyo University) conducts the project in close collaboration with Shigenori Tanaka (Kobe University) and Kaori Fukuzawa (Hoshi Univeristy). By using our ABINIT-MP program, a series of fragment molecular orbital (FMO) calculations are carried out on COVID-19 proteins, and detailed interaction analyses are performed. Resulted data are made public as well.



Evidences

ABINIT-MP has been used in the field of computational drug discovery for the last two decades, and a related consortium activity (FMODD) on the K-computer is organized by Fukuzawa. On the present topic, we have performed FMO-based interaction analyses for a complex formed between a COVID-19 main protease and an inhibitor N3, where FX100 at Nagoya University was employed for computations. The analyzed results were published as a paper at ChemRxiv site, after a month from the release of original PDB structure (6LU7). Crucial residues in interacting with the inhibitor were identified by our analyses.
<https://chemrxiv.org/articles/Fragment_Molecular_Orbital_Based_Interaction_Analyses_on_COVID-19_Main_Protease_-_Inhibitor_N3_Complex_PDB_ID_6LU7_/11988120/1>



Schedule plan

(1) Exploratory FMO calculations and analyses (including structural fluctuations) for complexes between SARS-CoV-2/COVID-19 proteins and inhibitor candidates. (2) Similar studies for related SARS-CoV systems. (3) Data release at FMODD (database) site.

Expected results

(1) Supplemental information for inhibitor candidates based on interaction analyses. (2) Guideline information for development of new inhibitors. (3) Basic data for machine learning toward discovery of effective inhibitors.