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FMO-based Intermolecular Interaction Energy Analysis between SARS-CoV-2 Spike Protein and Its Drug Candidate Molecules

Chiduru Watanabe[1,2] chiduru.watanabe@riken.jp
Yoshio Okiyama[3] okiyama@nihs.go.jp
Shigenori Tanaka[4] tanaka2@kobe-u.ac.j
Kaori Fukuzawa[5] k-fukuzawa@hoshi.ac.jp
Teruki Honma[1] honma.teruki@riken.jp

[1] RIKEN Center for Biosystems Dynamics Research 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
[2] JST, PRESTO, 4-1-8 Honcho, Kawaguchi, Saitama, 332-0012, Japan
[3] National Institute of Health Sciences, 3-25-26 Tonomachi, Kawasaki-ku, Kawasaki City, Kanagawa, 210-9501, Japan
[4] Graduate School of System Informatics, Kobe University, 1-1 Rokkodai, Nada-ku, Kobe 657-8501, Japan
[5] School of Pharmacy and Pharmaceutical Sciences, Hoshi University, 2-4-41 Ebara, Shinagawa-Ku, Tokyo, 142-8501, Japan

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Due to the COVID-19 pandemic, researchers have attempted to identify complex structures of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spike glycoprotein (S-protein) with angiotensin-converting enzyme 2 (ACE2), a blocking antibody, or a drug candidate molecule. We have performed fragment molecular orbital (FMO) calculations on the complexes of S-protein with ACE2 and antibodies to reveal key residues for molecular recognition mechanism [1]. To quantitatively evaluate hydrogen bonds, XH/π interactions (X = N, O, and C), and salt bridges, we performed FMO-based epitope analysis with inter-fragment interaction energy (IFIE) and its energy decomposition analysis (PIEDA). In addition, molecular recognition between S-protein and another drug candidate molecule will be also reported by IFIE/PIEDA analysis. These FMO calculation data will be registered in FMODB (https://drugdesign.riken.jp/FMODB/).

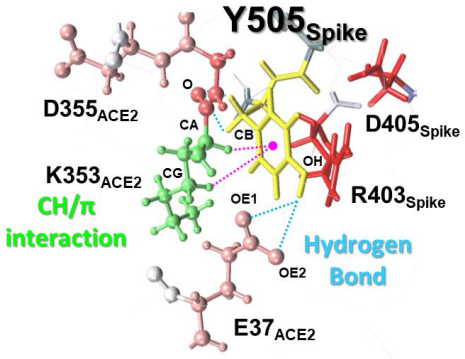

Fig. 1. PIEDA between S-protein and ACE2

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[1] Watanabe C *et al.*, Molecular recognition of SARS-CoV-2 spike glycoprotein: quantum chemical hot spot and epitope analyses, ***Chem. Sci.***, 12, 4722-4739, 2021.