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# Interaction analysis between cell adhesion factor fimh and its inhibitor by fragment molecular orbital method

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FimH is a critical role for cell-cell adhesion of adherent-invasive *Escherichia coli* (AIEC) and uropathogenic *Escherichia coli* (UPEC) by the interaction with mannose in their host cell. Hence, a number of mannose derivatives are reported for inhibiting the interaction and they become drug candidates for these infections. To find notable information for structure optimization, we calculated inter-fragment interaction energy (IFIE) of their complexes by fragment molecular orbital (FMO) method and analyzed the strength of a correlation by compared with the experimental data. If the correlation is fine in the system, IFIE is a major parameter of the modification to develop more potent inhibitor. In our study, twelve crystal structures of the FimH and mannose derivatives were used for FMO calculation. The complexes for calculation were prepared by MOE (CCG Inc.). One of the crystal waters was included in the complexes. ABINIT-MP6.0+ software, MP2 levels, and 6-31g(d) basis set were used for FMO calculation. Then we considered with the correlation between IFIE and the enthalpy change of ligands. From the result of the calculations, correlation between IFIE of twelve complexes and their enthalpy change ΔH was moderate ($R$=0.51). However, when we removed three outliers, the coefficient $R$ was improved 0.90. It was excellent correlation between IFIE and the enthalpy changes. The results suggested that IFIE is available for the prediction of ΔH in these systems.

## Biography

Norihito Kawashita has completed his PhD in 2005 from Osaka University and then moved to Research Institute for Microbial Diseases, Osaka University. He has been an Assistant Professor of Graduate School of Pharmaceutical Sciences, Osaka University since 2007. His research topics are anti-viral drug design and development, prediction of drug resistance, analysis of protein-protein interaction by quantum chemical calculation and analysis of organic reaction mechanism by computational chemistry.

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