PhotOnline'2023
Web-conference organized by and for young researchers – 2nd edition

QM/MM calculations and spectra modelling of the bioluminescent system Nanoluc-Furimamide

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Keywords: Bioluminescence; Force Field; Molecular Dynamics; QMMM; Absorption Spectra

Bioluminescence is a biological phenomenon of light production by living species with many applications[1], notably for the detection of cancer cells[2].The present study deals with a ligand-protein system (furimazine – Nanoluciferase) derived from a shrimp called *Oplophorus gracilirostri* with a very high luminescence intensity[3]. The protein catalyzes an oxidation reaction of furimazine by dioxygen, which leads to a new molecule, furimamide in its excited state. A better understanding of this system will provide insights to tailor new devices with emission of a photon with a red color, and thus a light signal more easily detectable inside the human body.

Simulations of the emission and absorption spectra are relevant tools[4] to comply this goal. We focus here on the absorption spectra of the light emitter system furimamide – Nanoluciferase. In order to take into account the protein environment and the system flexibility, we carry out classical molecular dynamics (MM) with AMBER software. Furimamide is a flexible molecule: standard force fields such as GAFF[5] (General Amber Force Field) are unable to reproduce correctly torsion angles potential energy when compared to in vacuo DFT computations. Thus, we perform a multidimensional fit using 1D and 2D potential energy surface scans with several torsion angles of the molecule in order to parameterize a new force field. Then, we compute electronic transitions at a QM/MM level of theory on a set of 100 snapshots extracted from each MM trajectory. We present analysis of the most important transitions and influence of the cavity. As a perspective, we plan to use the same methodology to simulate emission spectra.

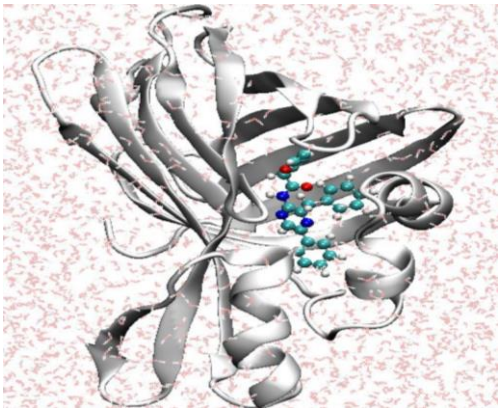

Figure 1. Ligand furimamide (colored molecule) inside the cavity of Nanoluciferase protein (in grey). The system is solvated inside a truncated octahedron water box.

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