**2E07**

# Describing excited states in solution by combining multi-reference perturbation theory with the RISM approach for analyzing bio-imaging probes

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**[Abstract]** Molecules with fluorescence in the "second near-infrared window" (1000-1700 nm) have recently captured attention for improving the performance of bio-imaging, yet are underexplored. Theoretical studies hold a valuable role in accelerating the development of these potential bio-imaging probes by providing information of the excitation; however, high-accuracy determination of state energies is required for meaningful analyses with the energy range being very narrow. Furthermore, these molecules are generally handled in solution, hence consideration of the solvation effect is also essential upon computation. Conventional methods such as PCM-TD-DFT were unable to describe these systems yielding results far from experimental data. Here, we have developed a new method to enable the theoretical analysis of these molecules by combining a solvation theory of a statistical mechanical approach (RISM) and a multi-reference perturbation theory (CASPT2) with the extension of the density matrix renormalization group (DMRG) reference states and have obtained results of higher accuracy.

**[Introduction]** Advances in bio-imaging have been facilitated by the development of new fluorescent molecules. Recently, fluorescence in the so-called "second near-infrared (NIR) window," approximately 1000-1700 nm, have captured attention acquiring higher permeability, yet are underexplored. The difficulty of handling excited states experimentally gives theoretical approaches a vital role in accelerating the development of these molecules by providing information of the excitation. The challenge is that the photochemical properties lie in a narrow energy range requiring highly accurate calculations for meaningful analyses. Additionally, these molecules are generally handled in solution, hence consideration of the solvation effect is also essential. Earlier studies showed that the desired accuracy is not provided by widely used methods such as PCM-TD-DFT. To enable the theoretical study of the molecules of interest, we have developed a new method by employing the complete active space second-order perturbation theory (CASPT2) and the reference interaction site model (RISM) with the extension of the density matrix renormalization group (DMRG) reference states.

**[Methods]** The Helmholtz free energy of the solute in solution computed by the CASPT2 method was defined as,

$$\mathscr{A} \equiv \langle \Psi | \hat{H} | \Psi \rangle + E_2 + \Delta\mu,$$

where the operator $\hat{H}$ is the Hamiltonian defined in the gas phase, $\Psi$ is the CAS reference function determined by a complete active space self-consistent field method (CASSCF) calculation, $E_2$ is the second-order energy from a CASPT2 calculation, and $\Delta\mu$ is the solvation free energy obtained from RISM-SCF-SEDD [1]. $\Psi$ is determined with the following solvated Hamiltonian,

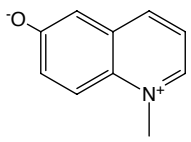
$$\hat{H}^{\mathrm{solv}} \equiv \hat{H} + \sum_{pq} \mathbf{V}^t [\mathbf{\Xi} + (m-1)\mathbf{\Gamma}]^{-1} \mathbf{R}'_{pq} a_p^\dagger a_q.$$

$V_i$ is the electrostatic potential on the $i$-th solute site induced by the solvation structure, $a_p^\dagger$ and $a_q$ are the creation and annihilation operators respectively, and the remaining matrices are as defined in previous work [1].

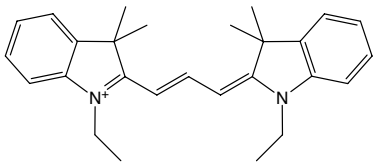
Limitations to the size of the active space in CAS calculations have been eased by employing the DMRG. The DMRG method projects the wavefunction onto the special entanglement structure existing in low-energy physical quantum states. This results in a contracted product of tensors, and the tensorial objects are optimized variationally by repetitive diagonalization of the Hamiltonian in the renormalized basis [2]. For usage of the DMRG with the RISM-CASPT2 method, the reference wavefunction is simply replaced by the active-space DMRG wavefunction $|\Psi_{\mathrm{DMRG}}\rangle$; this is denoted as the RISM-DMRG-CASPT2 method [3].

**[Results and Discussion]** The newly developed method was assessed by calculating the molecules given in Scheme 1. MQZ was selected as a molecule with high solvatochromism in absorption, and CY3 and ICG were selected as molecules with long π-conjugated systems. The calculated absorption energies of MQZ in dimethyl sulfoxide (DMSO), acetonitrile (ACN), methanol (MET), and water (WAT) are summarized in Table 1. Results show that the newly developed method successfully illustrated the solvatochromism in absorption and reproduced the experimental values with errors within 0.2 eV.

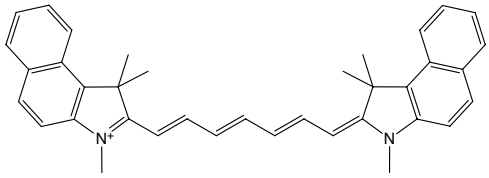
The error in calculated absorption energies relative to experimental values of CY3 and ICG are summarized in Figure 1. With the TD-DFT based methods, errors were approximately 0.65 eV. This exceeds the range of interest, the "second NIR window," which only spans for 0.5 eV. Our method succeeded in reducing the error to within 0.2 eV which seems to be sufficient for the analysis of these systems. Furthermore, the active spaces of CY3 and ICG were (20*e*,19*o*) and (32*e*,31*o*) which cannot be handled with the conventional CASSCF/CASPT2 methods, illustrating the high applicability of RISM-CASPT2 together with the DMRG.




*N*-Methyl-6-oxyquinolone (MQZ)




Modeled indocarbocyanine (CY3)




Modeled indocyanine green (ICG)

**Scheme 1.** Target molecules.

**Table 1.** Absorption energies of MQZ in various solutions [eV].

| | DMSO | ACN | MET | WAT |
|---|---|---|---|---|
| RISM-CASPT2 | 2.38 | 2.38 | 2.73 | 3.21 |
| Exp. | 2.44 | 2.45 | 2.88 | 3.03 |

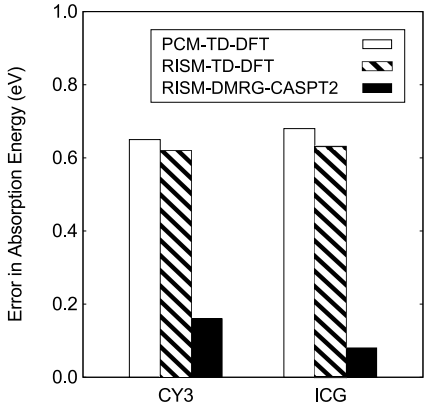



**Figure 1.** Error in calculated absorption energies of CY3 and ICG compared to experimental values.

## [References]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