Electronic Supporting Information

Title: Towards tailoring hydrophobic interaction with uranyl(VI) oxygen for C-H activation

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Calculations of reduction potential of uranyl complex

Reduction potential was obtained from the calculated Gibbs energy change of the reaction. For instance, for a U(VI)/U(V) couple of aquo complex, the reaction is defined as $[U^{VI}O_2(H_2O)_5]^{2+}$ + 0.5 H_2(aq) + H_2O(aq) —› $[UO_2(H_2O)_5]^+$ + H_3O^+. Details of the calculations are described in our previous publication.[S1] We have extended such calculations to include coordination complexes as well excited state counterparts namely [U(VI)]*/[U(V)] couples. Accuracy of such calculations critically depends on applied solvation models as well as associated radius parameters as thoroughly investigated and discussed by Gutowski and Dixon for uranyl(VI) systems.[S2] We therefore restricted our calculations primarily to DFT methods and applied several different solvation models as shown in Table S1. For all calculations, we employed aug-cc-pVTZ basis sets on all elements except for uranium. For uranium, small-core effective core potential (SC-ECP) developed by Dolg et al. has been used. We first investigated $[U^{VI}O_2(H_2O)_5]^{2+}$ / $[U^{V}O_2(H_2O)_5]^+$ couple using different DFT functionals (B3LYP vs CAM-B3LYP), different solvation radius (UFF vs Pauling), and also with including solute-solvent dispersion/repulsion and solute cavitation energy. Thermal corrections were calculated separately using gas phase geometries to which a pressure parameter of p = 1354 atm has been applied to adjust to concentration in liquid.[S3] These calculations were performed using Gaussian 16 program RevB.01. The UltraFine integration grid was used that correspond to pruned 99 radial shells and 590 angular point per shell for all elements except for uranium for which unpruned grid was employed. Convergence criteria for structure optimization was set as maximum and RMS of force to be less than 0.00045 and 0.00030 Hartrees/Bohr, respectively. The "best" value was obtained using CAM-B3LYP functional with Pauling radius but without including any additional corrections terms. We therefore decided to use this combination of methodology. For open-shell system, spin-orbit interaction was additively included by calculating single-point energy with and without SO effect at the CASSCF level (using Gaussian-optimized geometry) and summing the energy difference to the calculated energetics. This was done using ORCA program version 5.0.3. For instance, for $[U^{V}O_2(H_2O)_5]^+$, CASSCF calculation was performed by distributing one electron in 7 (5f) orbitals setting 7 roots. SO correction was -0.297 eV relative to the spin-free calculations for this system. This value is very close to the one we reported earlier [S1] on the same system which is -0.293 eV.

Table S1 Experimental and calculated reduction potential (in V) for U(VI)/U(V) couples including U(VI) in excited states.

	functional	B3LYP	CAM-B3LYP				exp.
	radius	UFF	UFF	Pauling			
				--	dis	dis, rep, cav	
	$[UO_2(H_2O)_5]^{2+/+}$	-0.269	-0.207	-0.082	-0.114	-0.092	0.088
	$[UO_2(H_2O)_5]^{2+*/+}$	2.066		2.478			2.60

UV-Vis-NIR absorption spectroscopy

The photoreaction between UO_2^{2+} and an amino acid (Gly, Phe, or Val) has been studied by illuminating their mixture under the condition that there are sufficient free ligands to ensure that the side chain of the amino acids can freely access the uranyl oxygen. The initial concentrations of UO_2^{2+} and amino acid were 10.0 mM and 90.4 mM, respectively. The pH of each solution was 1.83 ± 0.01. The sample mixtures were all sealed in 1 cm quartz cuvettes, and illuminated with 365 nm UV light from an LED head (AC8375-365) equipped with a 3 mm spot lens (AC8303C) and an LED controller (8332C). The illumination time ranged from 0 s (no illumination) to 900 s. The UV-Vis-NIR absorption spectra were recorded using a JASCO V-770 spectrophotometer.

Molecular dynamics simulations

MD simulations and data analyses were performed using AMBER 15 program package [S4] with ff99SB force field applied on the protein. For UO_2^{2+} ions,[S5] additional parameters were employed. The starting structure of BSA was taken from a pdb file to which missing residues have been manually added.[S6] Na^+ ions were added to make the system electrostatically neutral. TIP3P waters were then added with minimum water layer thickness of 10 Å. 500 steps of steepest decent and 500 steps of conjugate gradient with 500 kcal mol^{-1} Å^{-1} harmonic restraint on the protein was initially conducted after which 1000 steps of steepest decent and 1500 steps of conjugate gradient were performed without constraints. 40 ps of heating of the system from 0 to 300 K with 10 kcal mol^{-1} Å^{-1} harmonic restraint on the protein, after which another 1 ns preconditioning run was performed at 300 K without restraint on the solutes. Finally, 150 ns MD run was performed in a periodic boundary condition in NPT ensemble. Simulations were terminated and restarted at every 5 ns. The SHAKE algorithm, a 2 fs time integration

step, 12 Å cutoff for non-bonded interactions, and the particle mesh Ewald (PME) method were used. MD trajectory was recorded at each 50 ps.

Fragment molecular orbital calculations

The fragment molecular orbital (FMO) calculations were performed at the scaled third-order Møller–Plesset perturbation (FMO-MP2.5) level available in the ABINIT-MP program,[S7] where a partial renormalization (PR-MP2) [S8] was imposed to reduce overestimations in interaction energies. The fragmentation for peptide was made in a standard segmentation manner (each amino acid as single fragment) and that UO_2^{2+} ion, water molecules, and Na^+ counter ion were treated as single fragments. The basis sets for C, N, O, Na and P atoms was of valence double zeta plus polarization type of the model core potential (MCP) scheme.[S9] Note that the use of MCP basis sets could reduce the basis set superposition error in evaluating interaction energies.[S10] For U atom with large relativistic effect, a special MCP basis set (Miyoshi, unpublished) was used, where the 1s-5p electrons were replaced by the potentials and the valence electrons of 7s, 6d and 5f were described at the double zeta level. The standard 6-31G* basis was adopted for H atoms. All the FMO calculations were performed with ABINIT-MP: Nakano's local version with extended integral ability for the f-shell was used for the peptide plus uranyl system. The basis set superposition error (BSSE) corrections have been also neglected in FMO calculations. Previous studies have shown that BSSE could amount to a quarter of interaction energy for electrostatic interactions even though the comparative strengths of the interactions amongst the residues are generally well-retained even without BSSE corrections.[S11]

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