# Supporting online information for: Anisotropy enhanced X-ray scattering from solvated transition metal complexes 

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## 1. Additional Figures



Fig. S1. Full X-ray scattering pattern arising from a 80 mM water solution of PtPOP, after corrections for X-ray polarization, solid angle coverage and masking. The magnitude of the difference scattering signal shown in the main article (Fig. 4b) is found $\sim 1 \%$ of total scattering.


Fig. S2. top) Comparison between the isotropic (left) and anisotropic (right) difference scattering signals arising from a $0.25 \AA$ contraction of the $\mathrm{Pt}-\mathrm{Pt}$ bond (blue line) and from this contraction with an additional $0.04 \AA$ contraction of the four-phosphorous planes (magenta line). This additional deformation involves mostly changes of intra-molecular distances that are parallel to the $\mathrm{Pt}-\mathrm{Pt}$ axis and add a positive contribution to both the isotropic and anisotropic difference scattering signal. bottom) Comparison between the isotropic (left) and anisotropic (right) difference scattering signals arising from a $0.25 \AA$ contraction of the Pt-Pt bond (blue line) and from this contraction with an additional $0.02 \AA$ contraction of each Pt-ligand distance (green line). This additional deformation involves mostly changes of intra-molecular distances that are perpendicular to the Pt - Pt axis and add a positive contribution to the isotropic difference scattering signal and a negative contribution to the anisotropic signal, accordingly to Eq. 10 .

## 2. DFT calculations in vacuum

The set of molecular structures used to simulate the solute difference scattering signal ( $\Delta S^{\text {solute }}$ ) was obtained from a DFT-optimized geometry of ground state PtPOP by varying the Pt-Pt distance from 2.700 to $3.300 \AA$ in steps of $0.001 \AA$ while keeping all the other atoms fixed.

The geometry optimization was performed in the Atomic Simulation Environment (Bahn \& Jacobsen, 2002; Larsen et al., 2017) and employing the Grid-based Projector Augmented Wave (GPAW) DFT code (Mortensen et al., 2005; Enkovaara et al., 2010). The exchange-correlation functional was BLYP (Becke, 1988; Lee et al., 1988), while a linear combination of atomic orbitals (LCAO) with tzp basis for Pt and dzp for the rest of the atoms was used to represent the Kohn-Sham wave functions (Larsen et al., 2009). We employed a grid spacing of $0.18 \AA$. The geometry was optimized until the maximum force on all individual atoms was less than $0.02 \mathrm{eV} / \AA$. A vibrational analysis using the finite difference method implemented in ASE was carried out on the optimized geometry to confirm that it is a true minimum of the potential energy surface. The resulting structure has approximate $C_{4 h}$ symmetry, and features a PtPt distance of $3.005 \AA$. In comparison, the values found from X-ray crystallographic studies lie in the range 2.913-2.979 $\AA$ (Pinto et al., 1980; Che et al., 1983; Ozawa et al., 2003; Yasuda et al., 2004), while previous X-ray diffraction measurements in water solution delivered a Pt-Pt distance of $2.98 \AA$ (Christensen et al., 2008).

## 3. Simulation of $\Delta S^{\text {cage }}$ and $\Delta S^{\text {solvent }}$

$\Delta S^{\text {cage }}$ in Eq. 15 is calculated from solute-solvent RDFs of QM/MM simulations performed in the ground and excited states, as detailed in the next section, and following the procedure described by Dohn et al. (Dohn et al., 2015). $\Delta S^{\text {solvent }}$ in Eq. 15 is
calculated as following:

$$
\begin{equation*}
\Delta S^{\text {solvent }}(Q)=\left.\Delta T \frac{\partial S(Q)}{\partial T}\right|_{\rho} \tag{S1}
\end{equation*}
$$

where $\Delta T$ is the change in temperature and $\left.\frac{\partial S(Q)}{\partial T}\right|_{\rho}$ is the water solvent differential, that was measured in separate experiment and archived (Kjær et al., 2013; Sørensen \& Kjær, 2013). The fit of Eq. 15 to the isotropic scattering signal in Fig.5(right) yields $\beta \sim 1.9 \%$ and $\Delta T \sim 0.28 \mathrm{~K}$.

## 4. $\mathrm{QM} / \mathrm{MM}$ MD simulations

The solute-solvent RDFs for PtPOP in water were obtained from a previous QM/MM Born-Oppenheimer Molecular Dynamics (BOMD) investigation (Dohn et al., 2017). The DFT level of theory and atomic orbital basis set used to the describe the complex were the same as those utilized here for the geometry optimization in vacuum. The ground state RDFs were calculated from 230000 MD frames spanning a total simulation time of around 460 ps . A detailed account of the $\mathrm{QM} / \mathrm{MM}$ interfacing strategy, MM force field and MD protocol that were used in the QM/MM BOMD simulations is provided in (Dohn et al., 2017). To compute the RDFs for PtPOP in the first singlet excited state, 99 excited-state $\mathrm{QM} / \mathrm{MM}$ trajectories were started from uncorrelated frames of the equilibrium ground state trajectories collected in (Dohn et al., 2017). In these simulations the excited state was described with a modified version of $\Delta \mathrm{SCF}$ (Ziegler et al., 1977) in the spin unpolarized formalism (Maurer \& Reuter, 2011; Himmetoglu et al., 2012). The method uses Gaussian smeared constraints of the orbitals occupation numbers (Maurer \& Reuter, 2011) to achieve stable convergence of the density at each step of the dynamics and is implemented in a local version of GPAW. Time step and thermostatting scheme were the same as those used for the ground state equilibrium simulations in (Dohn et al., 2017). Equilibrium excited-state RDFs were calculated from around 80000 MD snapshots, corresponding to 160 ps remaining
after having removed the non-equilibrated part of each trajectory.

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