

Computational Investigation of MAPbI_3 Solvent Intermediate Phases

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Abstract

Methylammonium lead iodide (MAPbI_3) is a solution-processable, three-dimensional hybrid organic-inorganic perovskite (HOIP) that has served as a model structure for early research into perovskite-based photovoltaics. The performance of perovskite-based devices depends on film quality, which is governed by the chemical pathway followed during crystallization. Previous literature has revealed the formation of three possible solvent intermediate phases during the crystallization of MAPbI_3 from dimethylformamide (DMF) solution. The morphological differences between the solvent intermediate phases are maintained in the final perovskite film upon annealing, indicating that some solvent intermediates may be more ideal for forming high-quality perovskite films. While initial work mapping the chemical phase space of this system experimentally is underway, a theoretical treatment of the thermodynamics of this system has not yet been presented. In this report, we discuss the preparation of experimentally refined solvent intermediate crystal structures for chemical phase space mapping using density functional theory. The agreement between experimental and computationally optimized atomic positions and lattice parameters is assessed. Finally, one possible method for the quick identification of solvent intermediate phases in solution without the need for structural refinement is presented.

Introduction

One issue inhibiting the commercialization of hybrid organic-inorganic perovskite (HOIP) photovoltaics is the poor reproducibility of high power conversion efficiencies (PCEs). These PCEs are highly dependent on perovskite film quality, as in other semiconductors^{1,2}. Solution-processed films should be uniformly distributed and pinhole-free for best performance. Large grain sizes are also beneficial to prevent electron impedance and charge carrier

recombination at grain boundaries, although these effects are less pronounced in perovskites compared to other semiconductors^{3,4}. The quality of a perovskite film depends on a large number of methodological parameters that must be controlled during synthesis. These include (anti)solvent choice, the concentration and ratio of precursors, substrate temperature, atmospheric conditions, additive choice and concentration, and annealing temperatures and times. Much attention in the perovskite community has been devoted to the optimization of these parameters using

data-driven approaches, and recently, high-throughput autonomous labs⁵⁻⁸. Despite exciting advances, a fundamental understanding of the chemical processes that lead to high-quality perovskite films is becoming increasingly necessary to sustain the continued improvements in perovskite device performance and longevity.

Multiple studies on perovskite growth have revealed a two-step crystallization pathway, involving the formation of a solvent intermediate phase⁹⁻¹¹. The solvent intermediate phase is then transformed into the final perovskite film upon annealing. Importantly, the morphology of the intermediate phase is often maintained in the final perovskite film^{9,12}. The compositional and morphological differences of these phases indicate that some intermediates may be more ideal for producing high-quality perovskite films than others. It is therefore crucial to identify which phases are desirable and understand the mechanisms associated with their formation.

In 2017, Petrov *et al.* refined the crystal structures of three solvent intermediate phases from MAPbI₃ crystallization in a dimethylformamide (DMF) solution using X-ray diffraction (XRD) data (shown in **Figure 1**)⁹. They recognized that the selective formation of a solvent intermediate phase depended heavily on the PbI₂:MAI ratio in the solution. They also found that the morphologies of the intermediate phases were maintained in the final perovskite upon annealing. Since then, they have also made progress in mapping the chemical phase space of this system experimentally¹³. The availability of crystal structures from XRD opens the door for an atomistic, first-principles computational investigation into the properties of these intermediates. This can provide insight into the thermodynamic nature of these phases, allow for finer control over the crystallization, and enhance the reproducibility of high-quality perovskite films. In this report, we discuss the preparation of the experimental structures from Petrov *et al.* for first-principles thermodynamics calculations using density functional theory (DFT). We also describe a method for the quick identification of these solvent

intermediate states from experimental XRD patterns.

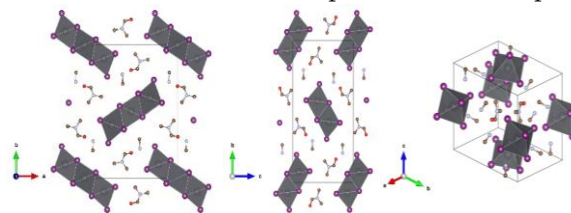


Figure 1. Three crystal structures of MAPbI₃ solvent intermediates from Petrov et al. 2017⁹.

It is well-known that hydrogen atoms are systematically misplaced in XRD structures due to their poor X-ray scattering ability¹⁴. This frequently leads to incorrect bond lengths and directions in experimental XRD structures. We have applied the technique introduced by Xie *et al.* to correct the hydrogen positions in these structures¹⁴. This first involves constraining the lattice vector lengths and angles, as well as the positions of all non-hydrogen atoms to their experimentally determined values. The hydrogen atom positions are then computationally relaxed to their most energetically favorable positions using DFT. This method has been shown to produce structures that are in excellent agreement with neutron scattering results¹⁴. Additionally, we conduct a full relaxation of the lattice parameters and atomic positions to determine the nearest energetic minimum for each structure, as determined by DFT. Finally, we conducted a relaxation of the organic and solvent molecules, while holding the cell parameters and inorganic ions fixed. This was done to test the validity of the experimentally refined organic molecule positions and orientations. The all-electron, scalable electronic structure theory package FHI-aims was used with “intermediate” default basis sets for all DFT calculations in this study. All structures were calculated at the Perdew-Burke-Ernzerhof (PBE) level of theory, with the Tkatchenko-Scheffler (TS) van der Waals (vdW) correction to capture long-range electrostatic interactions¹⁵. The Broyden-Fletcher-Goldfarb-Shanno (BFGS) algorithm was used for numerical geometry optimization, with a maximum residual force per atom of 0.005 eV/Å.

Results & Discussion

The average position change for each species during the hydrogen-only and organic-only relaxations, as well as the lattice parameter changes for the full relaxation, are

given in **Table 1** and **Table 2**. The hydrogen displacements during the hydrogen-only relaxation are on the same scale as those reported in other HOIP systems¹⁴. Furthermore, minimal atomic displacements are observed from the experimental structure when the organic molecules (DMF and MA⁺) are relaxed. This indicates that the refined atomic positions of carbon, nitrogen, and oxygen are close to a minimum on the theoretical potential energy surface when other positions and parameters are taken as fixed. The full DFT relaxations also show good agreement with the experimentally refined crystal structures. Two interesting observations appear within this data: the consistently smaller volume of the DFT-relaxed cell and the deviation of the α angle from 90° in fully-relaxed (MA)₂(DMF)₂Pb₃I₈. Both of these observations can be explained by the inherent lack of finite temperature effects in standard DFT calculations. Thermal expansion of the unit cell contributes to the larger volume measured at finite temperature (100K) during the experiment. Likewise, temperature increases are known to lead to the formation of higher symmetry systems. This is readily apparent in 3D perovskite systems such as MAPbI₃, where three distinct phase transitions occur from a lower symmetric phase to higher symmetric phase with increasing temperature¹⁶.

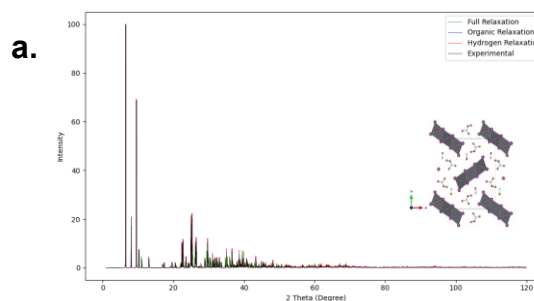
Table 1. Average displacement of each species in the DFT-relaxed structures from the experimentally reported XRD structure in the hydrogen-only and organics-only relaxations. Lead and iodide displacements are not shown as these atoms were constrained in both relaxations.

Intermediate Phase	Species	Hydrogen-only Displacements (Å)	Organics-only Displacements (Å)
(MA) ₂ (DMF) ₂ Pb ₃ I ₈	H	0.13 ± 0.02	0.14 ± 0.06
	C	0.00 ± 0.00	0.05 ± 0.03
	N	0.00 ± 0.00	0.08 ± 0.05
	O	0.00 ± 0.00	0.04 ± 0.00
(MA) ₂ (DMF) ₂ Pb ₂ I ₆	H	0.14 ± 0.02	0.15 ± 0.05
	C	0.00 ± 0.00	0.08 ± 0.03
	N	0.00 ± 0.00	0.07 ± 0.01
	O	0.00 ± 0.00	0.11 ± 0.00
(MA) ₃ (DMF)PbI ₅	H	0.16 ± 0.05	0.17 ± 0.05
	C	0.00 ± 0.00	0.07 ± 0.02
	N	0.00 ± 0.00	0.08 ± 0.02
	O	0.00 ± 0.00	0.11 ± 0.00

Table 2. Unit cell lattice parameters for experimental and fully relaxed DFT structures.

Intermediate Phase	Exp/DFT	Lengths (Å)			Angles (°)			Volume (Å ³)
		a	b	c	α	β	γ	
(MA) ₂ (DMF) ₂ Pb ₃ I ₈	Exp	17.2	22.0	4.6	90.	90.	90.	1717
	DFT	17.4	21.8	4.5	88	90.	90.	1714
(MA) ₂ (DMF) ₂ Pb ₂ I ₆	Exp	4.6	25.5	12.1	90.	97	90.	1398
	DFT	4.5	25.5	12.1	90.	96	90.	1387
(MA) ₃ (DMF)PbI ₅	Exp	10.2	11.4	12.4	111	101	110.	1170.
	DFT	10.2	11.3	12.4	111	101	111	1153

Using the crystallographic visualization software VESTA, we have additionally plotted the simulated powder XRD patterns of each computationally relaxed structure for every intermediate. This allows us to compare how minor displacements within the structure from computational relaxation affect the simulated XRD pattern. Furthermore, by identifying peaks that remain unchanged, we can identify regions that could be useful for quick identification of solvent intermediate phases without the need for structural refinement. These spectra are shown in **Figures 3a-c**. From analysis of these simulated spectra, it is apparent that hydrogen positions play a definite role in peak intensity. Furthermore, lateral peak shifts appear in the fully-relaxed structures. Critically, these spectra can also be divided into two regions. First is a region from $0 < 2\theta < 20^\circ$, which does not appear to change noticeably with minor deviations in lattice parameters or atomic positions. Second is a region $20^\circ < 2\theta$, which could be thought of as a “fingerprint” region, in which any minor deviations can significantly affect the spectrum. It is also worth noting that the spectra for each intermediate phase are noticeably different from each other in the first region. This, combined with the relative invariance of the peaks to minor deviations, suggests that this could be a highly useful region for the quick identification of which intermediate is formed under any given conditions.



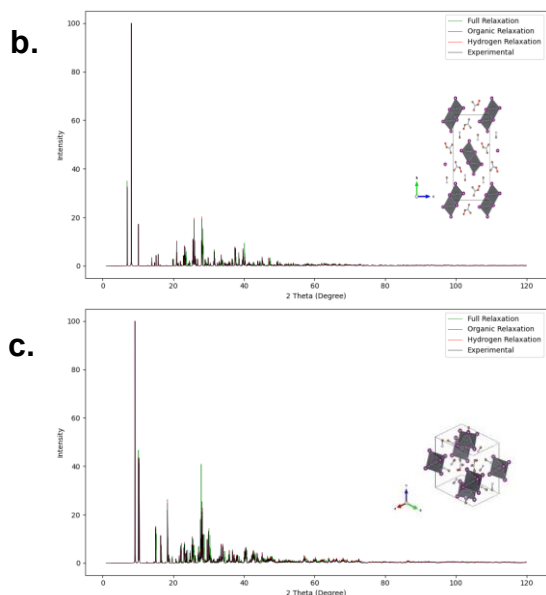


Figure 3a-c. Simulated powder XRD patterns for each relaxed structure of (a) $(MA)_2(DMF)_2Pb_3I_8$, (b) $(MA)_2(DMF)_2Pb_2I_6$, and (c) $(MA)_3(DMF)PbI_5$.

Conclusions

When fully relaxed using DFT, all three solvent intermediate phases show similar lattice parameters to the experimentally refined crystal structures. This indicates that the experimental solvent intermediate structures are near a minimum on the potential energy surface and stable according to theory. The hydrogen atoms show systematic misplacements typical in experimental XRD structures, which were corrected using hydrogen-only DFT relaxation. Relaxing the organic molecules yielded only minimal changes in the structure, indicating that their components have been adequately refined in the XRD structure. These structures can now serve as a basis for further calculations to study the thermodynamic phase space of this system. Finally, we propose that the $0 < 2\theta < 20^\circ$ range of the XRD spectrum can be used for the quick identification of solvent intermediate phases during the two-step crystallization of $MAPbI_3$ from DMF solution.

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