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# Thiophosphate bioisosteres of inositol hexakisphosphate enhance binding affinity and residence time on bacterial virulence factors?

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Inositol phosphates are essential for mammalian cell signalling with critical roles in cellular processes. The fully phosphorylated inositol phosphate, *myo*-inositol hexakisphosphate (**IP6**), modulates numerous eukaryotic proteins and bacterial virulence factors. It has been suggested that the high charge density of **IP6** causes restructuring of virulence factors in mammalian cells, activating their enzymatic activity. **IP6** is challenging to study due to its phytase instability and propensity to precipitate. Here we suggest that the thiophosphate bioisostere, *myo*-inositol hexakisthiophosphate (**IT6**), will mitigate these issues, as thiophosphate substitution has been found to be phytase resistant and improve solubility. Assessment of the chemical properties of **IT6** has indeed validated these characteristics. In addition, we performed biophysical characterization of **IT6** binding to the virulence factors *Salmonella enterica* serovar Typhimurium AvrA, *Vibrio parahaemolyticus* VopA, and *Clostridioides difficile* TcdB. Our data show that the higher charge density of **IT6** increased its binding affinity and residence time on the proteins, which improved stabilization of the bound-state. **IT6** is a valuable tool for structural biology research and the described biophysical characteristics of thiophosphate substitution are of value in medicinal chemistry.

# Introduction

Inositol phosphates and their lipidated phosphatidyl inositol congeners are important signaling molecules with crucial roles in cellular processes such as calcium release, insulin signaling, and metabolic signaling pathways. Inositol phosphates are either synthesized from a lipidated inositol core or glucose-6-phosphate *via* a network of kinases, phosphatases, and hydrolases that modulate the attachments on the *myo*-inositol core. Inositol phosphates can exist with various degrees of phosphorylation, ranging from 1 to 6 phosphates, with each species having different functions in the cell. The fully phosphorylated *myo*-inositol hexakisphosphate (IP6) modulates numerous eukaryotic proteins and bacterial virulence factors from mammalian and plant pathogens. Examples of mammalian virulence factors include: large clostridial toxins, 4,5 multifunctional

The physicochemical properties of **IP6** permit its varied roles in biological processes. **IP6** is densely charged, <sup>11</sup> a strong chelator of divalent cations, <sup>12</sup> and susceptible to hydrolysis. This simultaneously permits the tight regulation of the varied inositol phosphate species while also acting as a source of phosphate energy regulation. <sup>13–15</sup> Consequently, the compound is hydrophilic, susceptible to cation precipitation, <sup>16</sup> and low in abundance due to its high turnover rate, <sup>17</sup> making **IP6** challenging to study. Given the importance of **IP6** in biology, the development of biomimetics that can tune-out these challenging properties are of value as both structural biology tools and as therapeutics. <sup>18,19</sup>

In an effort to synthesize an **IP6** biomimetic that satisfies the aforementioned properties, thiophosphate and sulfate substitutions have been previously exploited.<sup>20,21</sup> Historically,

autoprocessing RTX toxin,<sup>6,7</sup> HIV-1 gag-hexamer,<sup>8</sup> *Legionella pneumophila* effector kinase,<sup>9</sup> and the *Salmonella enterica* serovar Typhimurium type III effector AvrA.<sup>10</sup> The virulence factors enter host cells either *via* toxin generated pores or a type III secretion system. It is only upon entering their target that the host cytosolic **IP6** modulates the target function through allosteric regulation, by promoting protein stabilization due to the high charge density. Therefore, the **IP6** binding event can form a target specific catalytically active enzyme by stabilizing the virulence factor.

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thiophosphate substitution has been used in nucleotide synthesis and with lower phosphorylated myo-inositols to circumvent enzymatic hydrolysis. 22-26 Thiophosphate drug mimetics have also been found to have an improved lipophilicity due to a decreased hydrogen bond basicity (HBB) favoring octanol in log P octanol water partition.<sup>27</sup> In high concentrations of divalent cations, like those found in the gastrointestinal (GI) tract, thiophosphate substitution improves compound solubility. 19 These results suggest that a fully thiophosphorylated IP6 analog would satisfy the physiochemical properties required to make a promising IP6 biomimetic. In addition, thiophosphate substitution has been found to improve the potency and stability of the target enzyme(s). 19,28,29 Here, we show that myo-inositol hexakisthiophosphate (IT6), as previously synthesized by Chen et al., 30 is a useful biomimetic of **IP6** with enhanced resistance towards phytase enzymes and solubility in the presence of divalent cations. Notably, IT6 can stabilize the Salmonella enterica serovar Typhimurium effector AvrA and Vibrio parahaemolyticus effector VopA more than their natural co-factor, IP6, which was attributed to better binding affinity and slower dissociation rate.

## Results and discussion

#### Synthesis and characterization of IT6

The thiophosphorylated IP6 analog, IT6, was synthesized in a two-step process as described previously (Fig. 1).30 First, myoinositol was thiophosphorylated by a PIII method, followed by sulfur oxidation, generating myo-inositol hexakis-dibenzylthiophosphate (IT6-Bn). Next, the benzyl protected thiophosphate groups were removed with sodium in liquid ammonia and the compound was purified via size-exclusion chromatography.

Interestingly, upon purifying IT6-Bn we noticed a sizeable decrease in compound polarity compared to the phosphorylated equivalent, myo-inositol hexakis-dibenzylphosphate (IP6-Bn, Fig. S1A, ESI†). To elaborate on this, we determined the calculated  $\log P$  ( $\operatorname{clog} P$ ) of both compounds and confirmed that IT6-Bn was more lipophilic than IP6-Bn (20.77 vs. 10.69, respectively). To explain these differences, we determined the Hückel charge on each element for both compounds (Fig. S1B, ESI†) and the corresponding compound polar surface area  $(IP6-Bn = 286.56 \text{ Å}^2 \text{ vs. } IT6-Bn = 166.14 \text{ Å}^2)$ . These results corroborate data from Columbus et al. that suggests that thiophosphate substitution of aprotically substituted compounds reduces the hydrogen bond basicity  $(pK_{HB})$  value, improving lipophilicity.27 It should be noted that in respect to IP6 and IT6, this property is not observed as the phosphate and thiophosphate functional groups on IP6 and IT6 have different pK values, and the lipophilicities of both compounds are pH dependent. For example, IT6 has a net charge of -12 at pH 7.4, whereas **IP6** has a net charge of -8, making **IT6** less lipophilic than IP6 at a physiological pH. 19

#### Stability of IT6

First, we evaluated whether IT6 was resistant to enzymatic hydrolysis by a commercial native wheat phytase. Phytases are a class of enzymes that catalyze the hydrolysis of IP6 into lower phosphorylated myo-inositols and inorganic phosphate (Fig. 2B).<sup>31</sup> Dietary wheat phytase is of physiological importance as it significantly contributes to IP6 dephosphorylation in mammals.32 To test whether IT6 was resistant to enzymatic hydrolysis, we quantified the stability of IP6 and IT6 in the presence of phytase-4 over 32 h via 31P NMR with the internal standard trimethyl phosphate (TMP). 31P NMR revealed that IT6 remained completely intact over 32 h, whereas IP6 was hydrolysed within the first hour of phytase exposure (Fig. 2C). The apparent thiophosphate phytase resistance is likely a result of the thiophosphate phosphoryl being less positively charged than on the phosphate, due to the thiophosphate sulfur being

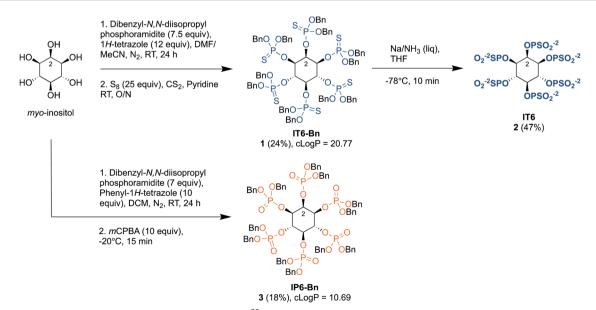


Fig. 1 Scheme of the synthesis of hexakis-thiophosphate (IT6)<sup>30</sup> and hexakis-dibenzylphosphate (IP6-Bn). mCPBA, 3-chloroperbenzoic acid, DCM, dichloromethane; DMF, dimethylformamide; O/N, over night; RT, room temperature; THF, tetrahydrofuran.

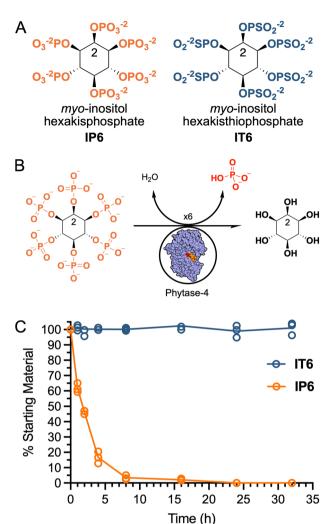


Fig. 2 Stability of **IP6** and **IT6** against phytase-4. (A) Structure of **IP6** and **IT6**. (B) Phytase-4 enzymes remove the phosphate groups from **IP6** via hydrolysis (phytase-4 PDB 6GJ2). (C) Percent of 4 mM of **IP6** or **IT6** detectable via <sup>31</sup>P NMR over 32 h in the presence of phytase-4. n =3 data points are shown.

less electronegative than the oxygen. Since phytase catalysis is initiated by a nucleophilic attack on the phosphorus, the decrease in positive charge reduces the likelihood of said nucleophilic attack. As a result, the thiophosphate esters exhibit greater stability toward neutral and base-catalyzed hydrolysis than the corresponding phosphate esters. These results suggest that **IT6** is more resistant to phytase hydrolysis than **IP6**.

#### Solubility of IT6

It was previously observed that **IT6** was soluble in a simulated GI tract environment whereas **IP6** precipitated in the presence of the concentrations of  $MgCl_2$  and  $CaCl_2$  found in the intestinal lumen. <sup>19</sup> Cummer *et al.* found that the thiophosphate groups on **IT6** have a lower  $pK_a$  than the phosphates on **IP6**, resulting in **IT6** having a higher charge density at pH 7.4. They suggested that the greater charge density of **IT6** gave the compound a higher electroneutrality threshold point, thus enabling solubility at physiologically relevant concentrations

of divalent cations. To explore this theory, we wanted to determine whether IT6 was soluble in all concentrations of CaCl2, or whether a critical point for precipitation existed for IT6 that was previously untested. We determined the concentration of soluble IP6 and IT6 when 4 mM of each ligand was combined with a serial dilution of CaCl<sub>2</sub> at the physiological pH 7.4 in the presence of TMP. Phosphorus NMR with proton coupling (31P-{1H} NMR) was run on the supernatant to determine the concentration of soluble ligand, and these values were plotted against the corresponding CaCl<sub>2</sub> concentration (Fig. 3A and B). We found that IT6 does precipitate out of solution in the presence of CaCl2, although it requires a much higher concentration than IP6 (32 mM vs. 4 mM CaCl<sub>2</sub>). Therefore, IT6 is soluble in physiologically relevant concentrations of CaCl<sub>2</sub>, as its precipitation threshold is outside the physiologically relevant range (1-10 mM).33

While performing the quantification of soluble IT6 via 31P-{1H} NMR an unexpected observation was made. Two species of IT6 were detected, one that corresponded with the <sup>31</sup>P-{<sup>1</sup>H} NMR spectrum of deprotonated IT6,19 and another that only appeared in the presence of CaCl<sub>2</sub>. The second species increased in quantity as CaCl2 was added to the sample, and this change was inversely proportional to that of the deprotonated IT6 species, indicating that the second species was a by-product of calcium chelating to IT6 (IT6 xCa<sup>2+</sup>, Fig. 3C). This observation was not apparent for IP6 bound to Ca<sup>2+</sup>. These results suggest that Ca<sup>2+</sup> first chelates to IT6, forming a complexed species, which then precipitates out of solution, as the concentration of soluble IT6 only decreased after all of the deprotonated IT6 was converted into the complexed form as observed by <sup>31</sup>P-{<sup>1</sup>H} NMR. Of note, IP6 has been found to undergo a ring-flip with five axial substituents in the presence of certain environmental factors, such as metal cation composition.<sup>34</sup> However, <sup>13</sup>C NMR of the IT6 samples indicated that the putative IT6·xCa<sup>2+</sup> species was not a by-product of a "flipped" conformation (Fig. S4, ESI†).

Finally, the presence of precipitate formation was confirmed by dynamic light scattering (DLS, Fig. 3D and E). The mean diameter of **IP6** and **IT6** in solution at pH 7.4 increased as the amount of soluble ligand decreased. The size of the precipitate positively correlated with increased concentrations of CaCl<sub>2</sub>. Collectively, these results support the theory that the increased charge density of **IT6** requires a greater concentration of CaCl<sub>2</sub> to cause charge neutralization of the compound, which initiates precipitation.

#### Characterizing the binding interaction between IT6 and AvrA

Cummer *et al.* previously found that **IT6** had a higher binding affinity for the *Clostridioides difficile* toxin B (TcdB) cysteine protease domain (CPD) allosteric binding site than its natural co-factor **IP6**. They suggested that this was due to the increased net charge density of **IT6** as the target binding site was electropositive, thus enhancing the electrochemical interaction. Here we aimed to determine whether this property could be ascertained for other **IP6**-dependent virulence factors.

AvrA is an S. typhimurium effector protein, which suppresses c-JUN N-terminal kinase (JNK) signalling in mammals

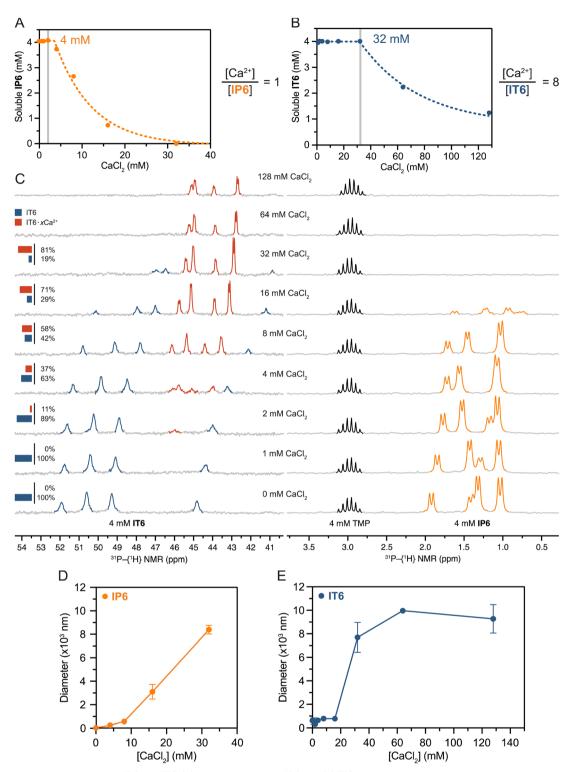


Fig. 3 Solubility differences between IP6 and IT6. (A) Amount of soluble IP6 and (B) IT6 at pH 7.4 in the presence of an increasing concentration of CaCl<sub>2</sub>. The amount of soluble ligand was calculated via  $^{31}P-(^{1}H)$  NMR with TMP as an internal standard. Data are curve fit with a plateau followed by one phase decay in Prism 10. X<sub>0</sub> is noted with the gray line, and the corresponding ratio of CaCl<sub>2</sub> to ligand that induces precipitation is reported. (C) Stacked <sup>31</sup>P-{<sup>1</sup>H} NMR spectra of IT6 (blue/red) and IP6 (orange) with varied concentrations of CaCl<sub>2</sub>. The presence of CaCl<sub>2</sub> elicits the formation of an IT6-Ca complex (IT6 xCa<sup>2+</sup>, red) with a unique  $^{31}P-(^{\overline{1}}H)$  NMR profile. The percentage of IT6 and IT6 xCa<sup>2+</sup> was calculated for each <sup>31</sup>P-{<sup>1</sup>H} NMR spectrum. The average particle diameter (nm) of 4 mM **IP6** (D) and **IT6** (E) at pH 7.4 was calculated at various concentrations of CaCl<sub>2</sub> via DLS.

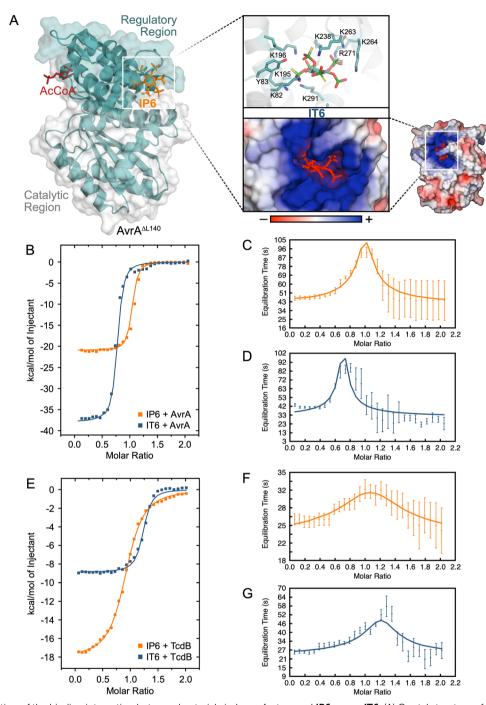


Fig. 4 Characterization of the binding interaction between bacterial virulence factors and IP6 versus IT6. (A) Crystal structure of AvrA<sup>ΔL140</sup> bound to IP6 and AcCoA (PDB 6BE0).<sup>10</sup> IP6 binds to an allosteric binding site in the regulatory region of AvrA that controls the formation of the AcCoA active site. IP6 binds to the very positively charged allosteric binding site. Inset: Docking experiments show that IT6 binds to the same positively charged pocket.<sup>37,38</sup> The binding interaction between AvrA and TcdB CPD with IP6 and IT6 was determined *via* ITC. The resultant thermograms (B) and (E) and the equilibration time curves (C) and (D) are shown for IP6/IT6 with AvrA and IP6/IT6 with TcdB CPD (F) and (G).

through acetylation of mitogen activated receptor kinases 4 and 7 (MKK4/7). Acetylation of MKK4/7 is suspected to reduce the upregulation of the host inflammatory response upon bacterial infection.<sup>35</sup> The acetyltransferase has two closely associated domains: a regulatory region and a catalytic region. The regulatory region mediates binding of the cofactors **IP6** and acetyl CoA (AcCoA), and the catalytic region acetylates the

bound substrate (Fig. 4A).<sup>10</sup> Binding of **IP6** induces structural changes that form the substrate binding sites.<sup>36</sup> The **IP6** allosteric binding site contains many basic amino acids that are positively charged at a neutral pH and are stabilized by the negatively charged co-factor, as observed for TcdB CPD.

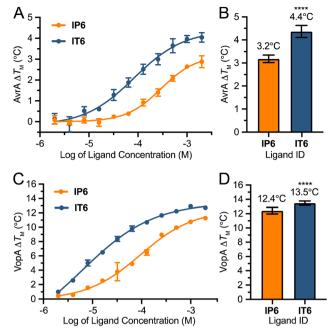
We wanted to determine whether **IT6** had a stronger affinity to AvrA than **IP6**. The equilibrium dissociation constants  $(K_d)$  of

**IP6** and **IT6** were determined *via* isothermal calorimetry (ITC) (Fig. 4B and E). The  $K_{\rm d}$  of **IT6** was 2.5-fold lower than that of **IP6** for AvrA, which was the same fold-change observed for TcdB CPD (Table 1). Of note, the reported  $K_{\rm d}$  of AvrA with **IP6** was significantly lower than previously described (139 nM *versus* 5.18  $\mu$ M). We suspect that this discrepancy arose from the use of different sources of **IP6**. **IP6** needs to be stored in dry conditions, because if water of crystallization is present in the industrial preparation, **IP6** is susceptible to hydrolysis (Fig. S6, ESI†). If **IP6** was in fact a lower phosphorylated species, the resultant decreased net charge would explain the discrepancy with the previously reported  $K_{\rm d}$ .

To look beyond the strength of interaction we can also investigate the durability of the binary ligand-protein complex. The improved electrostatic interaction between IT6 and AvrA/ TcdB CPD is a molecular determinant of the dissociation rate constant  $(k_{\text{off}})$ , and this dissociation process defines the drugtarget residence time  $(\tau_R)^{.39}$  We determined the  $k_{\text{off}}$  of the interactions via the kinetic ITC (kinITC) methodology utilized by the AFFINI meter software.  $^{40,41}$  The equilibration time curves (ETC, Fig. 4C, D, F and G) were curve fit with a one-site model, and the goodness of fit for each measurement had a  $\chi^2$  below 2, indicating a strong fit. The ETC's gave a  $k_{\rm off}$  measurement from the ITC raw data (Table 1). The lower  $k_{\text{off}}$  of IT6 indicated that it had a longer-lived ligand-target complex with both AvrA and TcdB CPD than **IP6** (AvrA  $\tau_R$  = 14.4, 9.7 min; TcdB CPD  $\tau_R$  = 2.4, 0.4 min). Therefore, the increased charge density of IT6 has an effect on the duration of target activation.

#### Stabilization of virulence factor effector proteins AvrA and VopA

Molecular dynamics simulations have been performed with both TcdB CPD and AvrA to show the structural modifications associated with IP6 binding.36,42 Finn et al. previously found that the conformational changes that accompany allosteric binding of IP6 to the CPD on TcdB and toxin A (TcdA) were stabilized by a network of residue interactions, complementary to the unbound state residue network. The network involves electrostatic interactions between IP6 and arginine and lysine residues in the allosteric binding site. In the IP6-bound conformation, an α-loop formed a 'lid' over the drug binding pocket, which acted to block the escape of the ligand, and a β-flap rotated  $\sim 90^\circ$ , which resulted in the formation of the cysteine protease active site.42 Similarly, Zhang et al. showed that binding of IP6 to the allosteric binding site of AvrA induced structural changes that constrained two α-helices around IP6, which caused two β-strands in the regulatory domain to form the AcCoA and substrate binding sites.36



**Fig. 5** Stabilization of the effector proteins AvrA and VopA. Doseresponse curves for binding of **IP6** and **IT6** with AvrA (A) and VopA (C) and the corresponding temperature stabilization. Stabilization of AvrA and VopA was determined *via* DSF. The melting temperature ( $T_M$ ) was determined for the proteins alone and in the presence of a serial dilution of **IP6** or **IT6**. The difference in melting temperature ( $\Delta T_M$ ) was then plotted and the data were fit with a nonlinear curve fit. Mean  $\pm$  SD, n = 5. Maximal  $\Delta T_M$  (°C) for **IP6** and **IT6** with AvrA (B) and VopA (D), as determined in (A) and (C), respectively. Mean  $\pm$  SD, n = 5; independent t-test \*\*\*\*p < 0.0001.

The simple one-step binding/dissociation model that was used to describe the binding interaction between IT6/IP6 and AvrA/TcdB-CPD may be insufficient to describe the interaction as the ligands induce conformational changes to the proteins. The conformational changes result in greater steric and electronic complementarity between the drug molecule and its binding site on the target and often greater occlusion from the solvent. The conformational changes associated with the transition from unbound to bound strengthen the binding of the ligand to its target and simultaneously decrease the rate of drug dissociation. Consequently, the  $\tau_{\rm R}$  of the drug–protein complex is considerably augmented. Therefore, understanding these changes by other biophysical methods can be of importance.

Here, we determined whether **IT6** was more capable than **IP6** at stabilizing AvrA and VopA, an ortholog of AvrA which is found in other enteric pathogens like *V. parahaemolyticus*. <sup>43</sup> To test this, we performed a differential scanning fluorimetry

**Table 1** Enthalpy ( $\Delta H$ ), equilibrium dissociation constant ( $K_d$ ), and rate of dissociation ( $k_{off}$ ) with the equilibration time curve goodness of fit ( $\chi^2$ ) for **IP6** and **IT6** when bound to the bacterial virulence factors AvrA and TcdB CPD. Mean (SD)

Protein	Ligand	$\Delta H$ (kcal mol <sup>-1</sup> )	$K_{\rm d}$ (nM)	$K_{ m off}\left({ m s}^{-1} ight)$	$\chi^2$
AvrA	IP6	-21.09(0.12)	139.4 (16.4)	$1.711 \times 10^{-3} (1.71 \times 10^{-4})$	0.751
TcdB CPD	IT6 IP6	-35.56 (0.32) $-22.94 (0.05)$	55.39 (15.4) 1918 (34.6)	$1.156 \times 10^{-3} \ (1.91 \times 10^{-4}) \ 4.086 \times 10^{-2} \ (5.52 \times 10^{-3})$	1.300 0.173
1000 010	IT6	-9.386 (0.14)	413.3 (57.8)	$6.912 \times 10^{-3} (7.22 \times 10^{-4})$	1.623

(DSF) experiment to determine the melting temperature ( $T_{\rm M}$ ) of AvrA and VopA alone and in the presence of serial dilutions of **IP6** and **IT6**. We then determined the change in  $T_{\rm M}$  ( $\Delta T_{\rm M}$ ) for each ligand concentration when compared to the  $T_{\rm M}$  of AvrA or VopA alone (Fig. 5A and C, respectively). The sizable leftward shift in the dose response curve corresponding to **IT6** suggests that **IT6** may have an improved binding affinity when compared to **IP6**, and these results are corroborated by the ITC results for AvrA. However, when attempting to assess the binding affinity for VopA *via* ITC, we found that the protein was unstable in the absence of the ligand. VopA rapidly lost functionality or misfolded within hours after purification, leading to inconsistent ITC results.

To quantify the stabilizing effect of each ligand, we performed a nonlinear curve fit on the data to determine the maximal  $\Delta T_{\rm M}$  for **IP6** and **IT6** on AvrA and VopA (Fig. 5B and D, respectively). We found that **IT6** had a significantly higher  $\Delta T_{\rm M}$  than **IP6** when bound to both AvrA (3.2 °C  $\nu s$ . 4.4 °C) and VopA (12.4 °C  $\nu s$ . 13.5 °C), which reflected increased protein stabilization. Additionally, the enhanced stabilization of **IT6** over **IP6** was previously observed for TcdB CPD. These results add further support to the theory that the improved charge density of the thiophosphate biomimetic, **IT6**, strengthens the electrostatic interaction with the **IP6**-dependent protein stabilizing the bound state, as observed here and previously with TcdB.

# Conclusions

Here, we propose IT6 as an interesting biomimetic of IP6 due to its suggested phytase stability, improved lipophilicity, solubility, and lower  $K_d$  and increased stabilization of the **IP6**-dependent proteins AvrA and TcdB-CPD. First, we found that IT6 is resistant to phytase-4 degradation due to the thiophosphate phosphoryl group being less positively charged, making a nucleophilic attack unlikely, and circumventing the hydrolysis reaction. Second, we found that aprotic thiophosphates are less polar than phosphates, while protic thiophosphates have a greater charge density; these apparent contradictory properties have manifested themselves in multiple interesting capabilities. The decreased polarity of IT6-Bn in comparison with **IP6-Bn** has resulted in an improved lipophilicity of the functional group. Although this does not put IT6-Bn, or IT6, within the cell permeability range according to Lipinski's rules, other strategies have been developed to optimize the delivery of highly anionic compounds.44 The increased charge density of thiophosphates at pH 7.4 has resulted in IT6 solubility in physiological concentrations of divalent cations due to a higher concentration threshold for charge neutralization. The higher charge density has also improved the  $K_d$ ,  $\tau_R$  and stabilization of IT6 for TcdB CPD, AvrA, and VopA in comparison with IP6. The unique properties of thiophosphate analogs suggest several potential practical applications that warrant further exploration. First, the drug-target  $\tau_R$  model predicts that durable pharmacodynamics can be achieved by developing drug molecules with a long  $\tau_R$  on their target.<sup>39</sup> These results suggest that further research should explore whether thiophosphate substitution of functional groups involved

in electrostatic interactions improves the pharmacodynamic properties of other pharmaceuticals. Second, stabilization of **IP6**-dependent proteins by **IT6** might facilitate the formation of tractable crystal/ligand complexes for X-ray structural analysis.<sup>44</sup>

## **Abbreviations**

AcCoA Acetyl CoA

K Association cons

 $K_{\rm a}$  Association constant clog P Calculated log P

 $\Delta T_{\rm M}$  Change in melting temperature

 $\begin{array}{lll} {\rm JNK} & {\rm c\text{-}JUN\ N\text{-}terminal\ kinase} \\ {\rm CPD} & {\rm Cysteine\ protease\ domain} \\ k_{\rm off} & {\rm Dissociation\ rate\ constant} \\ {\rm DLS} & {\rm Dynamic\ light\ scattering} \\ \end{array}$ 

*K*<sub>d</sub> Equilibrium dissociation constant

GI Gastrointestinal

IP6-Bn myo-Inositol hexakis-dibenzylphosphateIT6-Bn myo-Inositol hexakis-dibenzylthiophosphate

HBB Hydrogen bond basicity ITC Isothermal calorimetry

kinITC Kinetic ITC

MKK4/7 Mitogen activated receptor kinases 4 and 7

 $T_{\rm M}$  Melting temperature

IP6 myo-Inositol hexakisphosphateIT6 myo-Inositol hexakisthiophosphate

 $\tau_R$  Residence time

TcdB Toxin B

TMP Trimethyl phosphate.

# Data availability

The data supporting this article have been included as part of the ESI. $\dot{\tau}$ 

# Conflicts of interest

The authors declare no conflicts of interest.

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