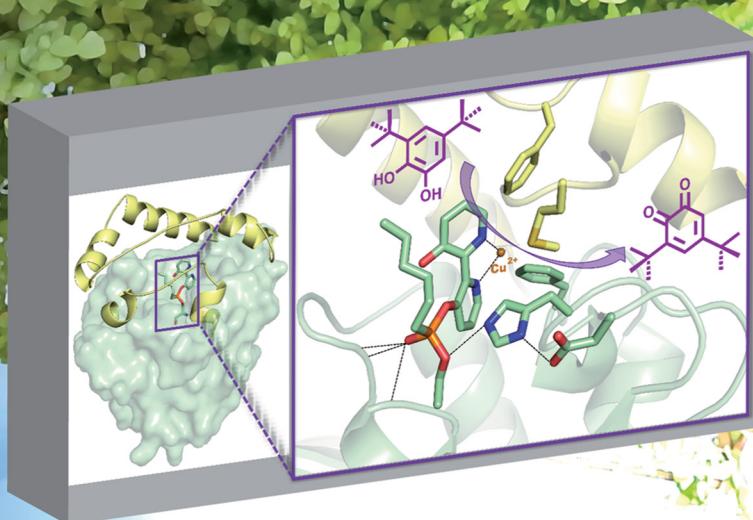


# ChemComm

Chemical Communications

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ISSN 1359-7345

## COMMUNICATION

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Cite this: *Chem. Commun.*, 2023, 59, 9469

Received 20th April 2023,  
Accepted 20th June 2023

DOI: 10.1039/d3cc01946b

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## Transforming an esterase into an enantioselective catecholase through bioconjugation of a versatile metal-chelating inhibitor†

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**Metal complexes introduced into protein scaffolds can generate versatile biomimetic catalysts endowed with a variety of catalytic properties. Here, we synthesized and covalently bound a bipyridinyl derivative to the active centre of an esterase to generate a biomimetic catalyst that shows catecholase activity and enantioselective catalytic oxidation of (+)-catechin.**

Metal complexes can be introduced, through non-covalent or covalent bioconjugation, at specific sites of protein scaffolds to generate versatile biohybrid or biomimetic catalysts. Such systems combine productively structural and functional properties of both biological macromolecules and metal-complex catalysts.<sup>1–6</sup> Using different non-catalytic proteins as scaffolds, biomimetic catalysts supporting a broad range of catalytic activities have been designed. This includes olefin metathesis, ruthenium-catalysed deallylation, iridium-catalysed/siderophore-inspired transfer hydrogenation, dirhodium-catalysed cyclopropanation, C–H activation,<sup>1,5a,b</sup> Diels–Alder reaction and Friedel–Crafts alkylation,<sup>4a,6a,7</sup> redox catalysis,<sup>1,4b,8</sup> enantioselective oxidation of sulfides with H<sub>2</sub>O<sub>2</sub>,<sup>8</sup> metal-dependent hydrolysis,<sup>8</sup> and the hydroformylation of alkenes.<sup>1</sup> This catalytic potential was expanded to selective olefin cyclopropanation, CO<sub>2</sub> hydration, ester hydrolysis, nitrite reduction, enantioselective carbenoid insertion into Si–H bonds, asymmetric cyclopropanation, alkyne polymerization

and metathesis,<sup>1,2b–d,3,8,9</sup> when using nucleic acids and peptides. The capacity for C–H insertion,<sup>1,4a</sup> hydrolysis,<sup>7</sup> oxidation of Mn<sup>2+</sup>,<sup>2a</sup> cofactor reduction,<sup>6a,b</sup> Diels–Alder reaction and Friedel–Crafts alkylation,<sup>6c,7</sup> Hoveyda–Grubbs catalysis, Heck cross-coupling,<sup>7</sup> selective oxidation of aromatic alkenes,<sup>10</sup> ring-opening metathesis polymerization, dihydroxylation and epoxidation,<sup>7</sup> and asymmetric reduction of a cyclic imine,<sup>11</sup> was further incorporated in several enzymatic scaffolds. The environment of a catalytically competent organometallic complex or the orientation of residues into which these catalysts are introduced plays a major role in the catalytic activity of the resulting metalloenzyme.<sup>2c,d,5b,12</sup> This is why amino acid sequences are currently being optimized with respect to the metal coordination geometry and/or the dedicated action of metal ions in protein environments.<sup>13</sup>

In this study, we applied the concept of covalent bioconjugation to transform an ester hydrolase enzyme into an oxidoreductase. This was achieved by exploiting the native biocatalytic activity of the enzyme to dock, within the active site of the enzyme, a metal-chelating inhibitor. We recently used the inhibitor **1** to successfully modify the active site of an esterase, which was thereby transformed into a biomimetic chemocatalyst supporting oxidation and Friedel–Crafts alkylation reactions.<sup>14</sup>

The versatility of **1** as catalytic inhibitor is limited by the presence of two phosphoester sites that can be potentially hydrolysed (Scheme 1). The higher reactivity of the bipyridine group compared to the methyl group means that a catalytic biomimetic may not be formed in many cases. We solved this problem by synthesizing phosphodiester **2**. Owing to the symmetry of the molecule, nucleophilic enzymatic hydrolysis can lead to only one hydrolytic product that retains the bipyridine moiety within the active site. To explore the capacity of **2** to transform esterases into biohybrid catalysts, we selected EH<sub>3</sub>, a highly versatile and promiscuous esterase,<sup>15,16</sup> as model enzyme. The inhibitor **2** was produced by reacting 2,2'-bipyridine-3,3'-diol and hexyl phosphonium in *N,N*-dimethylformamide and *N,N*-diisopropylethylamine, characterized using NMR and high-resolution mass spectrometry

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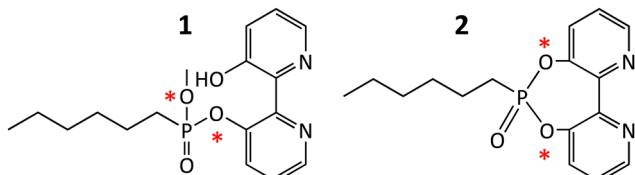
† Electronic supplementary information (ESI) available: Details of synthetic procedures, enzyme inhibition, metal complexation, the activity assay, oxidation reactions, NMR, HRMS, ESI-MS, and HPLC analyses can be found in the Supporting Information. See DOI: <https://doi.org/10.1039/d3cc01946b>

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¶ Equal leading contribution.

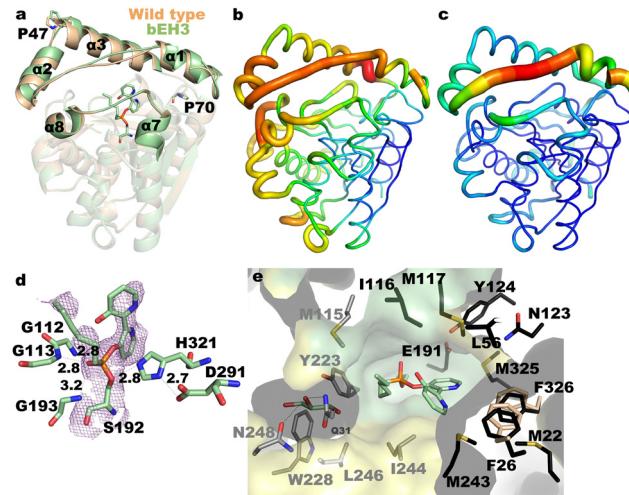




**Scheme 1** Structure of inhibitor **1** (3'-hydroxy-[2,2'-bipyridin]-3-yl methyl hexylphosphonate) and inhibitor **2** (6-hexyl-[1,3,2]dioxaphosphepino[5,4-b:6,7-b']dipyridine 6-oxide). The Figure shows the two sites, marked with a red asterisk, that can potentially be attacked by esterases and through which the molecules that can be covalently linked to the nucleophilic serine.

(Fig. S1–S4, ESI†), and used to modify the esterase  $\text{EH}_3$  to yield the corresponding biomimetic ( $\text{bEH}_3$ ). The reaction was carried out in a 50 mM potassium phosphate buffer at pH 6.5 for 10 min and monitored by measuring the inhibition of  $\text{EH}_3$ , following the hydrolysis of glyceryl tripentanoate using the Phenol Red pH indicator assay.<sup>14</sup> Incubating  $\text{EH}_3$  with **2** for 10 min resulted in complete enzyme inhibition, indicating complete bioconjugation of the  $\text{EH}_3$  active site. After the bioconjugation reaction was completed,  $\text{bEH}_3$  was dialyzed against a buffer to remove excess inhibitor. Crystals of  $\text{bEH}_3$  of sufficient quality for single-crystal X-ray crystallography were successfully obtained by co-crystallization, that is, preincubation of  $\text{EH}_3$  with **2**. The crystal structure of this complex was determined (Fig. 1) using the coordinates of unliganded  $\text{EH}_3$  (PDB 6SXP).<sup>16</sup>

A comparison of the structure of  $\text{EH}_3$  with that of the complexed  $\text{bEH}_3$  reveals a shift of the cap domain upon substrate entrance, particularly at helices  $\alpha 1$ ,  $\alpha 2$  and  $\alpha 3$  (Fig. 1a). An equivalent displacement has not been observed for previously reported complexes with methyl-(R/S)-2-phenylpropanoate substrates,<sup>15</sup> or with the  $\text{EH}_3$ -butyl 4-nitrophenylhexylphosphonate complex (B-4NHP),<sup>16</sup> which also mimics the tetrahedral intermediate of the hydrolytic reaction as **2** does. However, we previously reported that the polypeptide chain is highly flexible in the CAP domain, a peculiarity that was supported by an analysis of the B factor values and an ensemble refinement performed using the  $\text{EH}_3$  coordinates.<sup>16</sup> This analysis revealed many potential conformations of the N-terminal segment, mostly comprising  $\alpha 1$  and  $\alpha 2$ , with Pro47 putatively acting as a hinge. The complex reported here shows a shift of a larger CAP region that includes the long helix  $\alpha 3$ , with Pro70 being the putative hinge (Fig. 1a). Thus, the reorganization of the CAP domain observed in this complex appears to be required to accommodate the bulky bipyridyl moiety of **2** and unveils an even higher versatility of the  $\text{EH}_3$  active site cavity. In turn, this reorganization may be feasible because  $\text{EH}_3$  possesses a significantly larger catalytic cavity than its homologues, due in part to the  $\text{EH}_3$  CAP region.<sup>15,16</sup> Nevertheless, the binding of **2** appears to destabilize  $\text{EH}_3$ , as reflected by the high B factor values of **2** (Fig. 1b and c). We previously reported the catalytic residues as the nucleophile Ser192, the acidic residue Asp291 and the basic residue His321.<sup>16</sup> The bipyridine derivative complex mimics the tetrahedral intermediate that is stabilized at the oxyanion site by Gly112, Gly113 and Gly193 (Fig. 1d).  $\text{EH}_3$  has long channels for acyl/alcohol binding that are surrounded mostly by hydrophobic residues and only a few polar

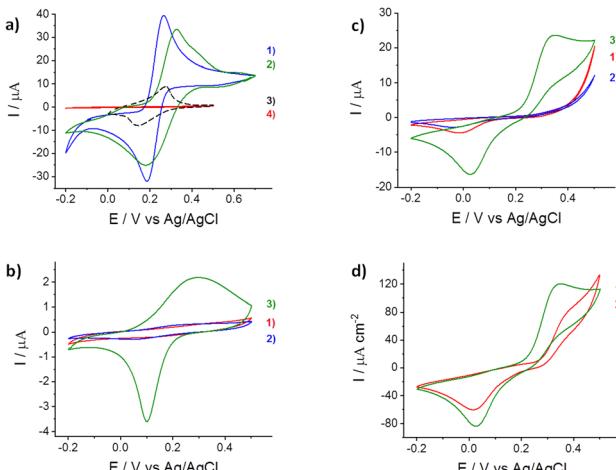


**Fig. 1** (a) Superimposition of unliganded  $\text{EH}_3$  (wheat, PDB Code: 6SXP) onto  $\text{bEH}_3$  (green, PDB Code: 8PC7), highlighting the structural changes at the CAP domain. Residues Pro47 and Pro70, acting as hinges, are shown as sticks. B factors for the complex (b) and the unliganded enzyme (c), with values ranging from low (blue) to high (red). (d) Close-up view of the  $\text{bEH}_3$  complex mimicking the tetrahedral intermediate, and the Polder omit map (2.5  $\sigma$  cut-off) shown in violet. The polar network is shown as dashed lines, with atomic distances in Å. (e) Cross-section of the molecular surface of  $\text{bEH}_3$ , with residues at the alcohol moiety coloured in grey. The cap and catalytic domains are coloured yellow and green, respectively. A glycerol molecule captured at the acyl binding site is shown. The positions of Phe26 and Phe326 in the free enzyme are shown by wheat sticks.

residues, endowing  $\text{EH}_3$  with broad substrate specificity (Fig. 1e).<sup>15</sup> The binding of **2** to the enzyme locates the bipyridine moiety in the alcohol-binding tunnel, resulting in appreciable reorientation of Phe326 in the catalytic domain and Phe26 at the beginning of the flexible loop  $\alpha 1$ – $\alpha 2$ , which retracts from the catalytic site to prevent steric hindrance (Fig. 1e).

With a well-structurally-characterized conjugate in hand, catechol oxidation, an important transformation for metallo-enzymes,<sup>10–14</sup> was investigated through electrochemical characterization of  $\text{EH}_3$  and  $\text{bEH}_3$ . First, an experiment was performed to compare the electrochemical response of the split components,  $\text{Cu}(\text{NO}_3)_2$  and catechol (1 mM), with that of both of components on the surface of a self-assembled-monolayer (SAM)-modified electrode (Fig. 2a). As some  $\text{Cu}^{2+}$  was stabilized on the carboxylated SAM surface, a broad  $\text{Cu}^{2+}$  signal was observed, which can be attributed to the different kinetics measured for bulk  $\text{Cu}^{2+}$  and bound  $\text{Cu}^{2+}$ . The redox signal of catechol is affected by the presence of  $\text{Cu}^{2+}$ , which makes the redox reaction more irreversible. This behaviour may be attributed to the formation of ligands with the cation that stabilize catechol and shift the oxidation process to more positive values. In a second experiment, the response to immobilized  $\text{EH}_3$  and  $\text{bEH}_3$  was measured, which clearly demonstrated that **2** was located within the  $\text{bEH}_3$  structure (Fig. 2b). As this signal differed from that observed for  $\text{EH}_3$ , it can be concluded that free  $\text{Cu}^{2+}$  was not measured. Addition of catechol produced different behaviour than that observed using the SAM-Au electrode (Fig. 2c):  $\text{EH}_3$  blocked the surface, inhibiting

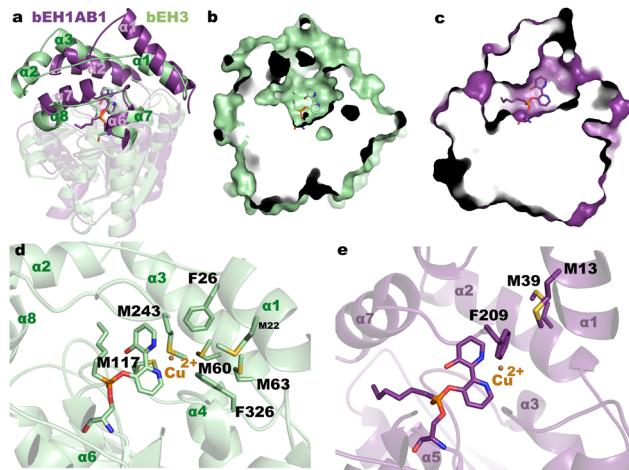




**Fig. 2** (a) The electrochemical response of an 3-mercaptopropionic acid (MPA)-gold electrode in a buffer with catechol (blue solid line, 1) and catechol and  $\text{CuSO}_4$  (green solid line, 2). Cyclic voltammetry (CV) curves for the control electrodes with MPA and  $\text{CuSO}_4$  (dark dashed line, 3) or only MPA (red solid line, 4) are shown. Measurements were performed at a  $20 \text{ mV s}^{-1}$  scan rate with a  $50 \text{ mM}$  phosphate buffer ( $\text{pH} = 6.5$ ) as the electrolyte. (b) The electrochemical response of the MPA-gold electrode before (1) and after absorption of  $\text{EH}_3$  (2) and  $\text{bEH}_3$  (3). (c) The electrochemical response of the electrodes shown in (b) in the presence of  $1 \text{ mM}$  catechol. (d) The electrochemical response of the MPA-gold electrode after absorption of  $\text{bEH}_3$  (1) and  $\text{bEH}_{1\text{AB}1}$  (2) in the presence of  $1 \text{ mM}$  catechol. Data for  $\text{bEH}_{1\text{AB}1}$  are taken from Alonso *et al.*<sup>14</sup>

the catechol redox signal. However, the catechol signal could be measured using  $\text{bEH}_3$ , indicative of catalytic activity for catechol oxidation/reduction.

The electrochemical results provided evidence of catalytic activity of  $\text{bEH}_3$  for catechol oxidation/reduction. We recently used **1** to show that the corresponding biomimetic  $\text{bEH}_{1\text{AB}1}$ , could also catalyse this reaction.<sup>14</sup> The possibility of using the same bipyridine moiety to enable  $\text{Cu}^{2+}$  complexation in two different catalytic environments (as defined by the  $\text{EH}_3$  or  $\text{EH}_{1\text{AB}1}$  active sites) enables evaluation of differences in the catalytic performance. Fig. 2d shows the electrochemical response of the electrodes in the presence of  $\text{bEH}_3$  or  $\text{bEH}_{1\text{AB}1}$  and catechol. The starting potential is less positive and the oxidation wave is much more defined in the presence of  $\text{bEH}_3$  than in the presence of  $\text{bEH}_{1\text{AB}1}$ . This result suggests that  $\text{bEH}_3$  catalyses the oxidation of catechol more effectively than  $\text{bEH}_{1\text{AB}1}$ . This was confirmed by following the oxidation of 3,5-di-*tert*-butylcatechol to 3,5-di-*tert*-butyl-*O*-benzoquinone using high-performance liquid chromatography (Fig. S5 and S6, ESI†), which under the same assay conditions, reached  $72 \pm 2\%$  ( $\text{bEH}_{1\text{AB}1}$ ) and  $97 \pm 1\%$  ( $\text{bEH}_3$ ). The higher performance of  $\text{bEH}_3$  might reflect a favourable role played by the residues near the catalytic site, in agreement with previously reported results on the importance of the second coordination sphere provided by the biomolecular scaffold.<sup>6c</sup> This was confirmed by a structural comparison of the complexes  $\text{bEH}_3$  and  $\text{bEH}_{1\text{AB}1}$  (PDB 6RKY).<sup>14</sup> As shown in Fig. 3a, the bipyridine moiety binds to the alcohol site very similarly as to the corresponding active site cavities, whereas the alkyl chain is allocated to different acyl sites. Indeed, the different topologies of



**Fig. 3** (a) Structural superimposition of the complex  $\text{bEH}_{1\text{AB}1}$  (violet) onto  $\text{bEH}_3$  (green). The different CAP domains shape the active site cavities shown in (b) and (c). (d) and (e) Details of the complexes showing the environment of the bipyridine moiety and the modelled position for a putative  $\text{Cu}^{2+}$ . The  $\text{Cu}^{2+}$  ion has been manually incorporated into the active sites by placing it at a suitable distance from the two nitrogen atoms found in the crystal to depict the different environment found within each enzyme.

the CAP domains of these two complexes result in very different clefts (Fig. 3b and c), which in the case of the  $\text{bEH}_3$  complex appears to be particularly open to the solvent, possibly facilitating access of the substrate to the metal centre and therefore enabling the oxidation/reduction reaction to occur. The close-up view of the  $\text{bEH}_3$  complex in Fig. 3d shows the residues surrounding the catalytic site that could play a role in catalysis. Remarkably, several methionines in the proximity to the bipyridine moiety could well provide a third ligand stabilizing a putative  $\text{Cu}^{2+}$  position. Phe26 and Phe326 could assist in substrate binding through stacking interactions. With the exception of Met117 from the catalytic domain, all these residues are located in the highly flexible CAP, which might enable the different steps of the reaction pathway. Conversely, in the  $\text{bEH}_{1\text{AB}1}$  complex (Fig. 3e), Phe209 is the sole residue close to the putative  $\text{Cu}^{2+}$  position, although two more Met residues are found within the cavity and all three residues are located in the CAP. UV/vis spectra of  $\text{bEH}_{1\text{AB}1}$  and  $\text{bEH}_3$  revealed subtle changes (Fig. S7, ESI†), and further mutagenic, electrochemical and/or Raman analyses, will determine the specific metal ligands in the two enzymes, whose binding environments differ (Fig. 3).

We further determine whether the differences in the topology of the active sites (Fig. 3a–c) and/or the coordination geometry of the  $\text{Cu}(\text{bpy})$  complexes (Fig. 3d and e) play a role in the observed activity and enantioselectivity of  $\text{bEH}_{1\text{AB}1}$  and  $\text{bEH}_3$ . On the latter point, it is well reported that the primary coordination sphere of a metal determines basic reactivity, and the secondary coordination sphere tunes the reactivity through weaker interactions. For that, we measured the conversion of (–)-catechin and (+)-catechin to the corresponding o-quinones by spectrophotometrically monitoring the product formation. Characterization of the reaction product revealed  $\text{bEH}_3$  being enantioselective for (+)-catechin; by contrast,



bEH<sub>1AB1</sub> was found to preferentially oxidize (–)-catechin (Fig. S6 and S8, ESI†). It is generally accepted that the apparent enantioselectivity ( $E_{app}$ ) of soluble enzymes can be calculated as the ratio between the conversion rates of the preferred chiral substrate and the non-preferred substrate obtained by testing the two enantiomers separately. Using the oxidation rates (in  $\text{min}^{-1}$ ) values for each biomimetic and enantiomer (Fig. S8, ESI†),  $E_{app}$  of  $91.9 \pm 0.5$  for bEH<sub>3</sub> ((+), preferred) and  $3.9 \pm 0.7$  for bEH<sub>1AB1</sub> ((–), preferred) were obtained. It is plausible that the higher number of methionine residues in close and flexible regions of the bEH<sub>3</sub> complex compared to that of bEH<sub>1AB1</sub> might provide additional ligands for  $\text{Cu}^{2+}$ , probably stabilizing the metal complex, which has higher accessibility from the solvent (Fig. 3d and e); this may promote the entrance of the substrates influencing the observed catalytic activity and enantioselectivity.

In summary, we synthesized a versatile inhibitor that enables the transformation of esterases into biomimetic catecholases without manipulating the protein sequence by genetic engineering. Indeed, the introduction of Cys,<sup>6a,9</sup> Lys,<sup>4a,6a</sup> His,<sup>4b</sup> non-natural aminoacids,<sup>6c</sup> and other mutations<sup>10</sup> has been reported as being necessary for designing metalloenzymes. It also obviates the use of computational efforts commonly needed to find sites that can accommodate a biomolecule in protein scaffolds.<sup>9–11</sup> We applied this molecule to an esterase and determined the structure of the biomimetics using single-crystal X-ray crystallography. The synthetic relevance and the possibility of using **2** and the resulting biomimetics for enantioselective conversions, either modulated by the orientation of the competent organometallic complex or by the nano-environment of the active site, needs to be further evaluated. Although yet to fully elucidate the nature of the copper site in the biomimetic bEH<sub>3</sub> and how it is modulated for catecholase function, it is plausible that the catalytic cycle of the biomimetic herein designed proceeds as mononuclear copper complexes containing N4 donors,<sup>17</sup> in contrast to natural catecholases that often have binuclear copper centres.<sup>18</sup> In brief, the non-protonated catecholate anion first binds to the  $\text{Cu}^{2+}$  centre of the biomimetic. This intermediate then oxidizes the coordinated catecholate anion forming  $\text{Cu}^+$  species; these species then react with dioxygen to give a copper dioxygen complex which yields catechin quinone and  $\text{H}_2\text{O}_2$ , which would be decomposed to oxygen and two molecules of  $\text{H}_2\text{O}$  and the catalyst is regenerated in its original active form in closing up the catalytic cycle.

We acknowledge the financial support of the European Union's Horizon 2020 (GA 101000327), and the Ministerio de Ciencia e Innovación and Agencia Estatal de Investigación (AEI) (DOI 10.13039/501100011033), and the "NextGenerationEU/PRTR" (PID2020-112758RB-I00, PDC2021-121534-I00, TED2021-130544B-I00, PID2019-105838RB-C31, PID2019-105838RB-C33).

We also thank the staff of the Synchrotron Radiation Source at Alba.

## Conflicts of interest

There are no conflicts to declare.

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