



Published in final edited form as:

*Science*. 2016 June 10; 352(6291): 1334–1337. doi:10.1126/science.aad9633.

## Capture of A Third Mg<sup>2+</sup> is Essential for Catalyzing DNA Synthesis

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### Abstract

It is generally assumed that an enzyme-substrate (ES) complex contains all components necessary for catalysis, and conversion to products occurs by rearrangement of atoms, protons and electrons. However, we find that DNA synthesis does not occur in a fully assembled DNA polymerase-DNA-dNTP complex with two canonical metal ions bound. Using time-resolved X-ray crystallography, we show that the phosphoryltransfer reaction takes place only after the ES complex captures a third divalent cation that is not coordinated by the enzyme. Interestingly, binding of the third cation is incompatible with the basal ES complex and requires thermal activation of the ES for entry. We suggest that the third cation provides the ultimate boost over the energy barrier to catalysis of DNA synthesis.

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Enzymes increase the rate of chemical reaction, which is thought, to occur by reducing the activation energy required to reach the transition state (1–3) (Fig. 1A). Due to their transient and unstable nature, authentic transition states have not been visualized but are assumed to have the same chemical components as the substrate state. DNA polymerases, which catalyze a phosphoryltransfer reaction that incorporates dNTPs into DNA, are known to require two Mg<sup>2+</sup> ions (4–8) (Fig. 1B). Despite extensive kinetic studies using the stopped flow technique and the dNTP analog dNTP $\alpha$ S, it remains controversial whether a conformational transition prior to catalysis (9–14) or the chemistry itself (15–16) is the rate-limiting step in DNA synthesis.

We have recently visualized phosphodiester bond formation catalyzed by human DNA Pol  $\eta$  *in crystallo* (17). Consistent with the two-metal-ion mechanism (6–8), binding of Mg<sup>2+</sup> ions in the A and B sites occurs within 40 s leading to alignment of the 3'-OH of the primer end with the  $\alpha$ -phosphate of dNTP (Fig. 1C) (17). After another 40 s, product starts to appear without discernible conformational change of the enzyme or substrates. However, we observed a third Mg<sup>2+</sup> ion appearing in a third 'C' site after product formation (Fig. 1C) (17). An equivalent third metal ion coordinated by the reaction products and four water molecules has also been observed in the *in crystallo* catalysis by DNA Pol  $\beta$  (18–20). Due to steric clashes with dNTP (Fig. 1C), the third metal ion cannot bind in Pol  $\eta$  enzyme-substrate complexes. Because of low occupancy in the C site and weak diffraction of Mg<sup>2+</sup> ions, it has been unclear when the third Mg<sup>2+</sup> appears and whether it is involved in the phosphoryltransfer reaction.

To determine the reaction coordinates of Pol  $\eta$  and the role of the third metal ion, we replaced  $\text{Mg}^{2+}$  with  $\text{Mn}^{2+}$ , which supports DNA synthesis (21) and is readily detected by X-ray diffraction even at low occupancy. Crystals of native Pol  $\eta$  (1–432 aa) complexed with DNA, dATP and  $\text{Ca}^{2+}$  were grown at pH 6.0 in a non-reactive ground state (17). After exposure to a pH 7.0 reaction buffer containing 1 mM  $\text{Mn}^{2+}$  for 90 to 1800 s, crystals were flash frozen in liquid  $\text{N}_2$  to stop the reaction, and 1.5–1.7 Å X-ray structures were determined at five reaction time points (table S1 and Materials and Methods). All five structures were practically identical except for the gradual replacement of  $\text{Ca}^{2+}$  by  $\text{Mn}^{2+}$  in the B site (fig. S1). By 600 s when ~90% of the A and B sites were occupied by  $\text{Mn}^{2+}$ , the 3'-OH of the DNA primer was aligned with the  $\alpha$ -phosphorus of the dATP, and the structure was identical to that of crystals soaked in 1 mM  $\text{Mg}^{2+}$  for 40 s (fig. S2, A-B). Similar to the reaction in  $\text{Mg}^{2+}$  (17), a water molecule (WatN) hydrogen bonded to the nucleophilic 3'-OH appeared at 90 s, and its occupancy increased with time in correlation with binding of the A-site  $\text{Mn}^{2+}$  (fig. S2, C-D). However, in 1 mM  $\text{Mn}^{2+}$ , the Pol  $\eta$ -DNA complex remained in the substrate state with no product and no C-site  $\text{Mn}^{2+}$  ion for up to 1800s (Fig. 1D).

We assayed the metal ion ( $\text{Me}^{2+}$ ) requirements for Pol  $\eta$  catalysis in solution and found that 0.6 mM  $\text{Mg}^{2+}$  or 2.7 mM  $\text{Mn}^{2+}$  is needed to attain the half-maximal reaction rate (Fig. 2A, table S2). We then examined the  $\text{Mn}^{2+}$  affinity of each binding site *in crystallo*. While increasing the  $\text{Mn}^{2+}$  concentration (0.5 to 15 mM) accelerated the rate of metal-ion binding in all three sites (Fig. 2B, table S3), the apparent  $K_d$ 's of the A and B sites were below 0.5 mM. The  $K_d$  for the C site, however, was 3.2 mM, close to the 2.7 mM measured in solution (Fig. 2A).

When *in crystallo* reactions occurred in 10 mM  $\text{Mn}^{2+}$ , catalysis proceeded as in 1 mM  $\text{Mg}^{2+}$  (17), except that the A-site  $\text{Mn}^{2+}$  did not dissociate upon product formation as does  $\text{Mg}^{2+}$  (fig. S3, A-B) and slightly less product accumulated with  $\text{Mn}^{2+}$  than  $\text{Mg}^{2+}$ . However, unlike the reaction in  $\text{Mg}^{2+}$ , the C-site  $\text{Mn}^{2+}$  appeared simultaneously with the reaction product, 30 s after binding of the two canonical metal ions (Fig. 2C). Electron density for the new phosphodiester bond and the C-site  $\text{Mn}^{2+}$ , whose chemical nature was confirmed by its anomalous diffraction and characteristic octahedral coordination geometry (fig. S3C), had one-to-one correlation at every time point and  $\text{Mn}^{2+}$  concentration (Fig. 2D). In  $\text{Mg}^{2+}$  by contrast, with 15% product formed at 80 s the C-site  $\text{Mg}^{2+}$  was at too low occupancy to be observed and was not detected until 140 s when product had accumulated to 40% (fig. S3A) (17). Previous stopped-flow studies indicate that one of the metal ion-binding sites has much lower affinity for  $\text{Mg}^{2+}$  and thus limits DNA synthesis (16). Our *in crystallo* titrations unequivocally show that the low-affinity binding site is neither A nor B, but the C site, which determines the concentration of  $\text{Mg}^{2+}$  or  $\text{Mn}^{2+}$  necessary for the DNA synthesis reaction.

The C-site  $\text{Me}^{2+}$  is coordinated by four water molecules and two oxygen atoms, one each from the product DNA and pyrophosphate, which correspond to the  $\alpha$  pro- $\text{S}_p$  oxygen and the  $\alpha$ ,  $\beta$  bridging oxygen of dNTP (Fig. 1C). Sulfur substitution of the pro- $\text{S}_p$  oxygen ( $\text{S}_p$ -dNTP $\alpha$ S) has been widely used to dissect the reaction kinetics of DNA synthesis (11–14, 22) because the pro- $\text{S}_p$  atom is not directly involved in A- or B-site  $\text{Me}^{2+}$  coordination. The

reduction of the reaction rate by  $S_p$ -dNTP $\alpha$ S has been interpreted to be “conformational” (if < 4 fold reduction) or to affect the chemistry itself (if 4–11 fold) (11–14, 23).

As a ligand of the 3<sup>rd</sup>  $Me^{2+}$ , the sulfur in  $S_p$ -dATP $\alpha$ S was tolerated by Pol  $\eta$  (table S2) but required much higher  $[Mg^{2+}]$  (15 mM) and  $[Mn^{2+}]$  (9 mM) than dATP for catalysis to occur (Fig. 2A, Fig. 3A). Unexpectedly, *in crystallo*  $S_p$ -dATP $\alpha$ S slowed  $Mg^{2+}$  and  $Mn^{2+}$  binding at the A site. After a lengthened delay product started to form, but the C site remained empty (Fig. 3B, fig. S4A-C). We suspect that the third  $Mn^{2+}$  still assisted product formation, but the association was too transient to be observed. In addition, while A-site  $Mg^{2+}$  occupancy was reduced in the presence of dATP $\alpha$ S, an alternative A' site appeared 2.6 Å away (fig. S4, D-E). These data suggest that the reduced reaction rate with  $S_p$ -dATP $\alpha$ S cannot be attributed to “conformational” effects (11–14) but involves impaired A- and C-site  $Mg^{2+}$  binding and altered reaction chemistry.

To bind the third  $Me^{2+}$ , the R61 side chain, which forms salt bridges with the dNTP (17), moves to vacate the C site (Fig. 1C, 3B). Mutation of R61 to Ala reduces the  $k_{cat}$  by two thirds (table S2) (24–25), but the metal-ion requirement and the general reaction process *in crystallo* were indistinguishable from WT Pol  $\eta$  (fig. S5E-F). However, the delay between binding of two  $Mg^{2+}$  ions and product formation was lengthened from WT's 40 s to R61A's 160 s (Fig. 3C). This delay likely stems from a slight shift of dATP away from the active site and a 0.3 Å increase in separation between the 3'-OH and  $\alpha$ -phosphate (Fig. 3D). The void left by the R61A mutation was occupied by water molecules (25) and not by the abundant  $K^+$  or  $Rb^+$  (identifiable by anomalous diffraction) in the reaction buffer (fig. S5). The subtle misalignment of the substrate, which was repeatedly observed with R61A and R61M mutant Pol  $\eta$  (25) and with dATP $\alpha$ S, led to a prolonged delay before C-site  $Me^{2+}$  binding and product formation (fig. S4, B-C).

Notably a +1 charged side chain at the position equivalent to R61 is found in all A-, B-, and Y-family DNA polymerases and reverse transcriptases despite diverse structures of finger domains surrounding the C-site (fig. S6). Among C- and X-family DNA polymerases, there is no R61 equivalent, but the third metal ion has been observed for the X-family Pol  $\beta$  (18–20). The finger domains, which carry the +1 charged residue, distinguish right from wrong correct from incorrect incoming nucleotides by enclosing only a correct dNTP (26). A closed finger appears to be a prerequisite for C-site metal ion binding and catalysis. The varied environment surrounding the C site may thus be exploited for drug design to increase specificity and reduce toxicity of broadly used nucleoside and nucleotide analogs targeting DNA polymerases in antiviral and anti-cancer therapeutics (27–28).

Because the C site does not exist in the Pol  $\eta$ -substrate complex but is required for product formation, we hypothesized that thermal motion of the well-aligned reactants in the ES may create an opening for the 3<sup>rd</sup> metal ion. If so, elevated temperature would promote C-site metal ion binding and thus catalysis. To test this hypothesis, we designed a two-step *in crystallo* reaction. The Pol  $\eta$  crystals were first soaked in 1 mM  $Mn^{2+}$  to saturate the A and B sites, and then exposed to 5 mM  $Mn^{2+}$  at 4°C to 37°C for 60 s for catalysis to occur (Fig. 4A). The diffusion rate of  $Mn^{2+}$  *in crystallo* was unaffected by temperature as demonstrated by  $Mn^{2+}$  binding at the A-site (Fig. 4B). But in the two-step reaction, no C-site  $Mn^{2+}$  or

product was detected at 4°C (Fig. 4C). At 14°C, low levels of the third  $\text{Mn}^{2+}$  ion and products were observed, and their amounts doubled at 30°C. The temperature dependence of C-site and product formation corroborates that binding of the third metal ion is rate limiting in the DNA synthesis reaction.

To determine the metal ion selectivity at the C site, we varied  $\text{Me}^{2+}$  in the second step of the two-step reaction (Fig. 4A). Catalysis occurred most efficiently with  $\text{Mg}^{2+}$ , followed by  $\text{Mn}^{2+}$  and  $\text{Cd}^{2+}$  (Fig. 4D, fig. S7).  $\text{Ca}^{2+}$  and  $\text{Zn}^{2+}$  seemingly also led to product formation at ~40% efficiency of  $\text{Mg}^{2+}$ . However, the C-site coordination geometry with all five  $\text{Me}^{2+}$  tested appeared identical to that of  $\text{Mg}^{2+}$  and  $\text{Mn}^{2+}$  (fig. S7) despite different coordination distances of  $\text{Ca}^{2+}$  (2.3–2.5 Å) and  $\text{Mg}^{2+}$  or  $\text{Mn}^{2+}$  (2.1 Å). It is thus likely that  $\text{Ca}^{2+}$  and  $\text{Zn}^{2+}$  replaced A or B site  $\text{Mn}^{2+}$  in some Pol  $\eta$  molecules, and the freed  $\text{Mn}^{2+}$  ions may occupy the C site in other Pol  $\eta$  molecules to support the catalysis. The low affinity and strong preference for  $\text{Mg}^{2+}$  at the C site, which cannot be explained by its coordination ligands, suggest a catalytic role for the third metal ion in DNA synthesis.

Based on the requirement for three metal ions in DNA synthesis, we suggest a revision of the catalytic mechanism (Fig. 5). DNA synthesis begins with binding of dNTP along with the B-site  $\text{Mg}^{2+}$  and formation of a ground-state Pol  $\eta$ -DNA-dNTP- $\text{Mg}^{2+}$  complex (GS). Watson-Crick pairing between the template and dNTP favors A-site  $\text{Mg}^{2+}$  binding. The two  $\text{Mg}^{2+}$  ions and the R61 side chain neutralize and align dNTP with DNA in the reaction-ready state (ES), where the juxtaposed and polarized substrates recruit WatN (fig. S2) (17). However, neither deprotonation nor chemistry takes place without the C-site  $\text{Mg}^{2+}$ . Thermal motion may transiently bring the perfectly aligned reactants closer to each other by fractions of an Ångstrom and create an entry for the third  $\text{Mg}^{2+}$ . Close approach of the reactants may also increase negative charge around the  $\alpha$ -phosphate and favor replacement of the +1 charged R61 by the C-site  $\text{Mg}^{2+}$ . We hypothesize that the energy barrier to the transition state is overcome by binding of the third  $\text{Mg}^{2+}$ . The stringent octahedral coordination geometry of  $\text{Mg}^{2+}$  implies that the C-site  $\text{Mg}^{2+}$  may help to break the  $\alpha$ - $\beta$  phosphodiester bond (Fig. 5) in addition to protonating the pyrophosphate leaving group (17). Product formation is coupled to disappearance of WatN (fig. S3D), which likely deprotonates the 3'-OH, and to release of the A-site  $\text{Mg}^{2+}$ , which prevents the reverse reaction (fig. S3, A-B).

It has long been assumed that enzymes stabilize transition states and reduce the energy barrier to product formation (Fig. 1A), but de novo design of enzymes based on this assumption has not been successful (29–32). Notwithstanding its crucial role in catalysis, the C-site metal ion of polymerases has evaded detection by biochemical and structural studies of DNA polymerases for decades. Identification of the essential third metal ion in the Pol  $\eta$  catalysis leads us to anticipate that acquisition of transient metal-ion cofactors in transition states may be a general feature that enables enzyme catalysis.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

## Acknowledgements

Y.G. carried out all experiments; W.Y. conceived and designed the project, and both authors interpreted data and prepared the manuscript. We thank D. J. Leahy and M. Gellert for critical reading and editing the manuscript. This work is funded by NIH intramural program (DK036146–08, W.Y.).

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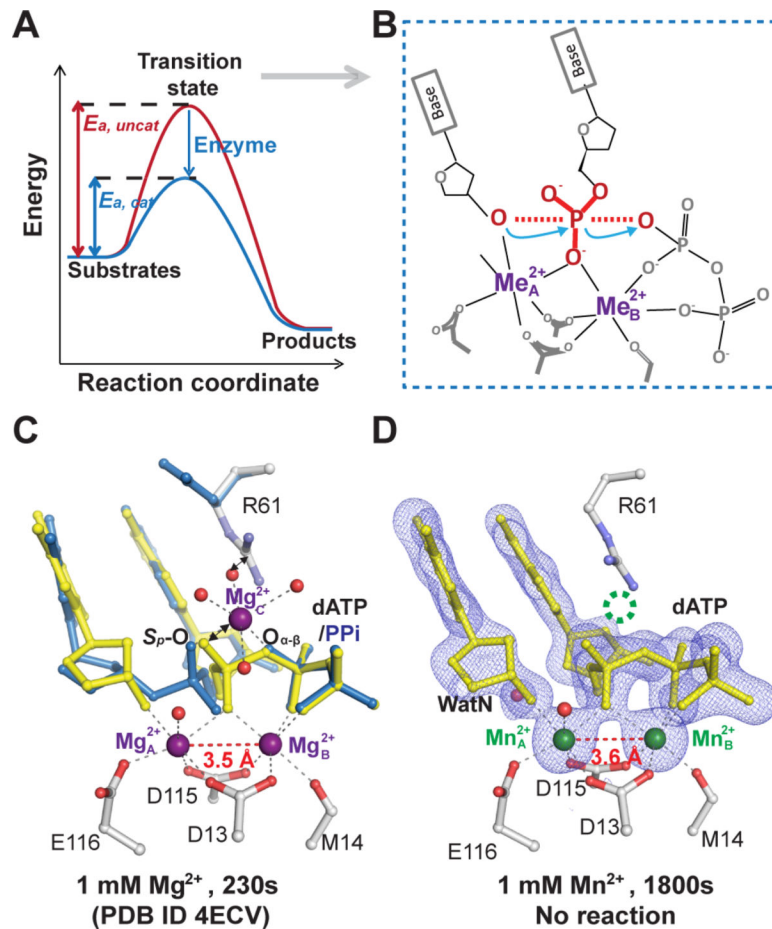
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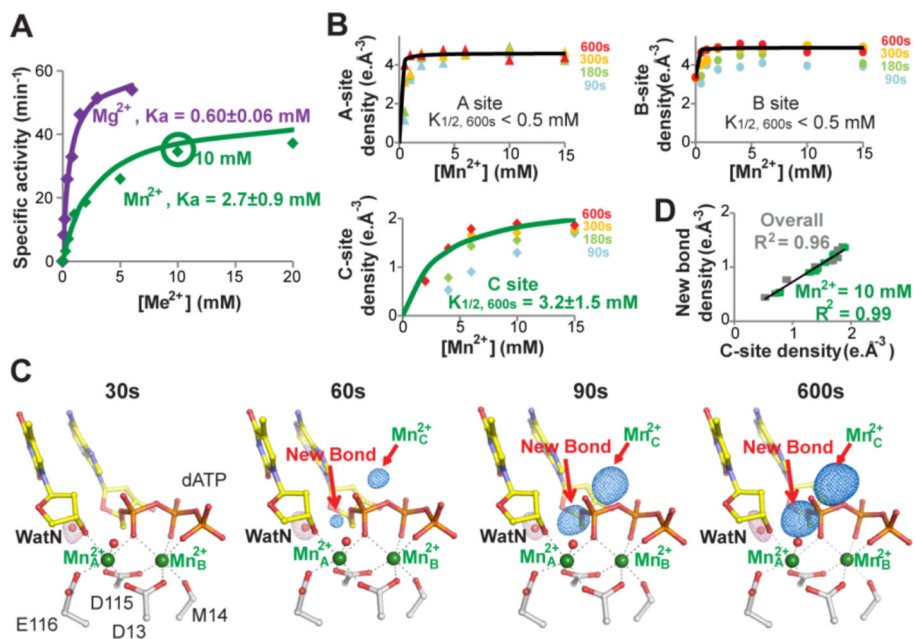
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**Figure 1 |. No DNA synthesis without the third metal ion.**

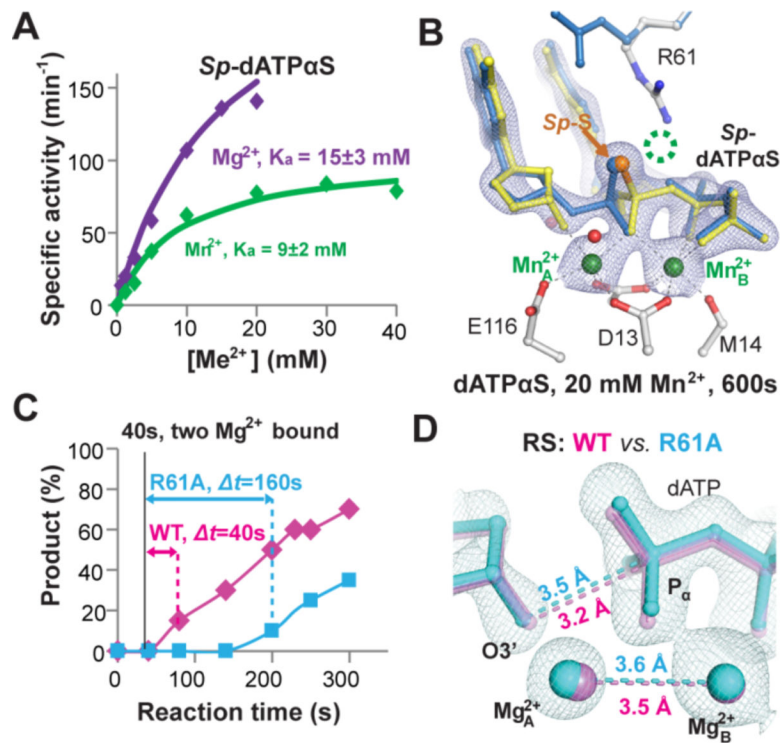
**A**, Reaction coordinate of enzyme catalysis. **B**, The assumed transition state of the two-metal-ion catalysis. **C**, The structure of Pol  $\eta$  catalyzing DNA synthesis *in crystallo* (PDB: 4ECV, 18). The C-site  $Mg^{2+}$  is coordinated by the products (60%, blue) but clashes with the substrate dATP and R61 side chain (40%, yellow). **D**, The structure of Pol  $\eta$  incubated with substrates and 1 mM  $Mn^{2+}$  for 1800s. No C-site metal ion or reaction products were detected. The  $F_o-F_c$  map with the active center omitted contoured at  $3.5\sigma$  level (blue meshes) is superimposed.





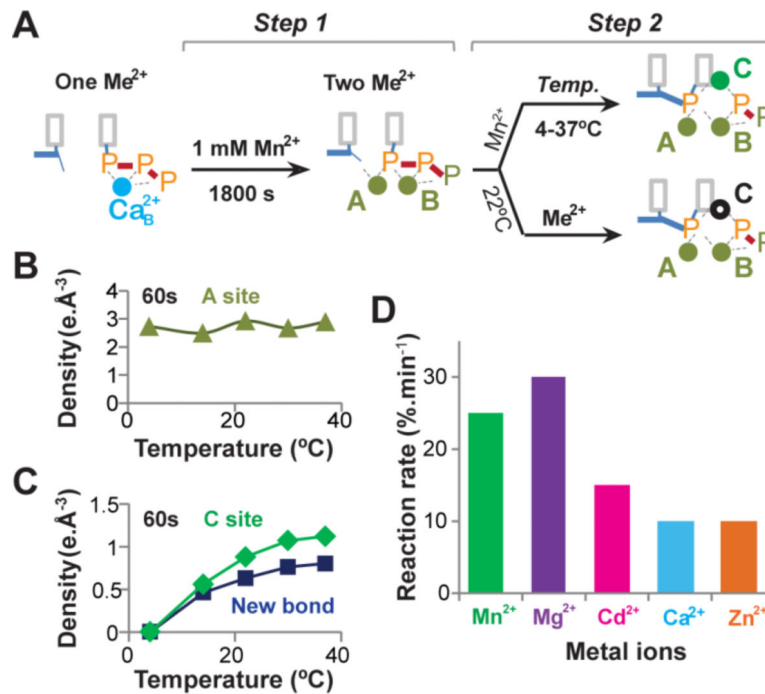
**Figure 2 | Coupled appearance of the third  $\text{Mn}^{2+}$  and reaction products.**

**A**,  $\text{Mg}^{2+}$  (purple) and  $\text{Mn}^{2+}$  (green) dependence of Pol  $\eta$  catalysis in solution. **B**, Titration of the A-, B-, and C-site  $\text{Mn}^{2+}$  binding *in crystallo*. The 600s data were fitted to equilibrium binding modes to yield the  $K_d$ 's. **C**, Structures of Pol  $\eta$  *in crystallo* catalysis with 10 mM  $\text{Mn}^{2+}$ . The  $F_o - F_c$  omit map for the new bond, the C-site  $\text{Mn}^{2+}$  (blue) and the WatN (pink) were contoured at  $3\sigma$  and superimposed onto each structure. **D**, Correlation between the new bond formation and the C-site  $\text{Mn}^{2+}$  binding.



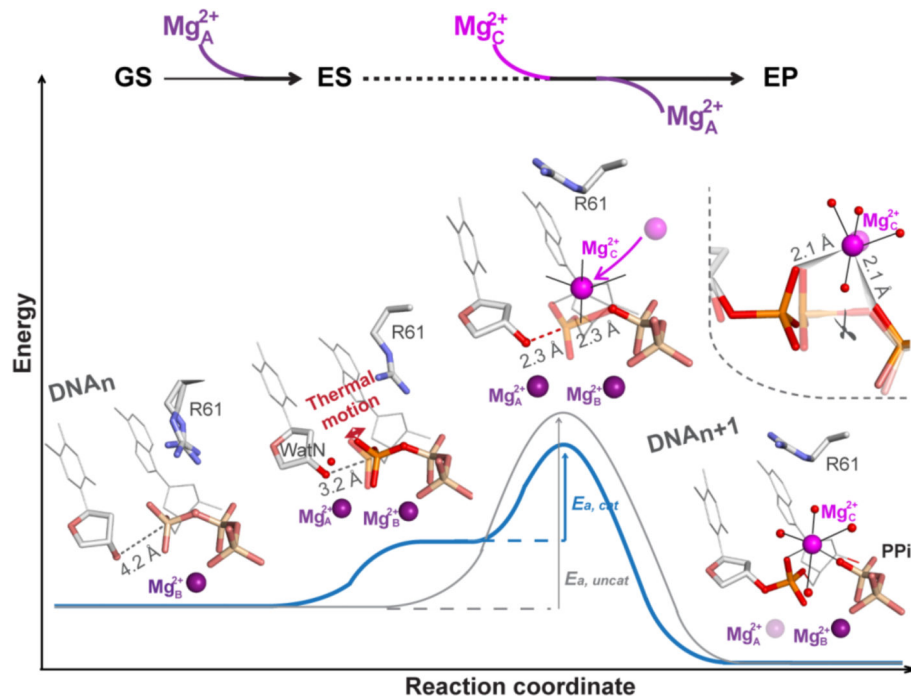
**Figure 3 | Changing the C-site environment alters Pol  $\eta$  catalysis.**

**A**,  $\text{Mg}^{2+}$  (purple) and  $\text{Mn}^{2+}$  (green) dependence of Pol  $\eta$  incorporating  $\text{dATP}\alpha\text{S}$  in solution. **B**, *In crystallo* incorporation of  $\text{dATP}\alpha\text{S}$  by Pol  $\eta$  with 20 mM  $\text{Mn}^{2+}$  at 600s showed product formation (50%) but no C-site  $\text{Mn}^{2+}$ . The  $2F_o - F_c$  map contoured at  $2\sigma$  level (blue meshes) is superimposed. **C**, Time delay in product formation by WT (magenta) and R61A (cyan) Pol  $\eta$  *in crystallo*. **D**, Deviation of  $\text{dATP}$  in the ES of R61A Pol  $\eta$  (cyan with  $2F_o - F_c$  map contoured at  $1.5\sigma$ ) from WT Pol  $\eta$  (magenta).



**Figure 4 | Thermal energy-dependent C-site formation and its metal-ion selectivity.**

**A**, Schematic diagram of the two-step *in crystallo* reactions that probe the C-site formation and ion selectivity. **B**, Binding of the A-site Mn<sup>2+</sup> was unaffected by varying temperature from 4°C to 37°C. **C**, Binding of the C-site Mn<sup>2+</sup> and the product formation increased with the temperature from 4°C to 37°C. **D**, Rates of product formation with five metal ions tested in the second step.



**Figure 5 | Mechanism of Pol η catalysis.**

Pol η binds DNA and an incoming dNTP along with the B-site Mg<sup>2+</sup> to form the ground state (GS). Binding of the A-site Mg<sup>2+</sup> leads to the reaction-ready ES state, in which the 3'-OH is aligned with dNTP and WatN recruited. Thermal motions of the reactants create the C site, leading to the third metal-ion binding and the transition state (TS) formation. The C-site metal ion promotes the phosphoryltransfer from the leaving group to the nucleophilic 3'-OH, thus overcoming the energy barrier to the product state (PS).