

Molecular mechanism for regulating APOBEC3G DNA editing function by the non-catalytic domain

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APOBEC3G, part of the AID/APOBEC cytidine deaminase family, is crucial for antiviral immunity. It has two zinc-coordinated cytidine-deaminase domains. The non-catalytic N-terminal domain strongly binds to nucleic acids, whereas the C-terminal domain catalyzes C-to-U editing in single-stranded DNA. The interplay between the two domains is not fully understood. Here, we show that DNA editing function of rhesus macaque APOBEC3G on linear and hairpin loop DNA is enhanced by AA or GA dinucleotide motifs present downstream in the 3'-direction of the target-C editing sites. The effective distance between AA/GA and the target-C sites is contingent on the local DNA secondary structure. We present two co-crystal structures of rhesus macaque APOBEC3G bound to ssDNA containing AA and GA, revealing the contribution of the non-catalytic domain in capturing AA/GA DNA. Our findings elucidate the molecular mechanism of APOBEC3G's cooperative function, which is critical for its anti-viral role and its contribution to mutations in cancer genomes.

Human APOBEC3G (hA3G), a member of AID/APOBEC family of zinc-containing cytidine deaminases, catalyzes the conversion of cytidine (C) to uridine (U) on DNA. This process generates DNA mutations from unrepaired uridines. hA3G is a well-known host restriction factor that plays a crucial role in restricting human immunodeficiency virus type 1 (HIV-1)¹. In the absence of HIV viral infectivity factor (Vif), hA3G can catalyze excessive C to U editing on the HIV-1 negative cDNA strand, leading to hypermutation in HIV-1 genome^{2–10}. hA3G can also impair HIV-1 replication through deaminase-independent mechanisms^{11–17}.

Deaminases can also induce mutations in the host genome in the context of pathological misregulation in tumorigenesis^{18–24}. Analysis of human cancers revealed hA3G's contribution to mutational signatures in multiple cancer types^{25,26}. In a murine bladder cancer model, transgenic expression of hA3G promotes mutagenesis and genomic

instability²⁵. Additionally, hA3G performs C to U editing on certain types of human and viral RNA^{27–30}.

A3G is composed of two zinc-containing cytidine deaminase (CD) domains in tandem: the N-terminal CD1 domain or NTD (referred to as CD1 hereafter) and the C-terminal CD2 domain or CTD (referred to as CD2 hereafter). Multiple CD1-CD2 domain orientations in full-length A3G have been observed in protein crystal structures and cryo-electron microscopy (cryo-EM) structures^{31–36}. Despite their similar tertiary structures, individual CD1 and CD2 domains have evolved to carry out distinct functions^{37,38}. The CD1 domain is non-catalytic but binds strongly to nucleic acids^{39,40}. Recent studies show that RNA purine dinucleotide sequence motifs rArA and rGrA are preferred RNA binders for the primate rhesus macaque A3G³³. Cryo-EM studies have revealed that the rArA- or rGrA-RNA bound by A3G is a critical part recognized by HIV Vif-E3 ligase for A3G ubiquitination and proteasome

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degradation^{34–36}. These studies provide evidence that CD1, with the assistance of CD2, engages in direct RNA binding. On the other hand, the CD2 domain carries out DNA target-C editing, although it has weak affinity to DNA^{4,5,41–45}. CD2 favors 3' target-C to U editing in the motifs CC or CCC (the target-C is underlined) on single-stranded DNA (ssDNA). X-ray protein crystallography studies of the catalytic CD2 domain bound to the DNA substrate or DNA oligonucleotide inhibitor have revealed the molecular details of the editing motif CCC selection and deamination^{44,46}.

Efficient A3G editing requires cooperativity between its two domains. The catalytic CD2 domain on its own displays nearly three orders of magnitude lower editing efficiency than the full-length protein^{47,48}. Furthermore, full-length A3G processively edits target-C in two CCC motifs located on a ssDNA substrate during one binding event and preferentially edits target-C in the CCC motif near the 5' end of ssDNA substrates^{48–51}. These two editing properties are impaired in the absence of the non-catalytic CD1 domain⁴⁸. Data from experiments with optical tweezers show that A3G binds in multiple steps and conformations to search and deaminate single-stranded DNA⁵². Despite these advances, the precise molecular mechanism used by the two domains to coordinate DNA binding and editing has remained elusive.

In this study, we find that purine dinucleotide AA or GA motif downstream of the target-C editing sites in the 3'-direction facilitates rhesus macaque A3G (rA3G) DNA editing function in linear and hairpin loop DNA. The effective distance between AA/GA motifs and the target-C sites depends on the local DNA secondary structure. We present two co-crystal structures of rA3G in complex with ssDNA containing AA or GA motif, providing a mechanistic understanding of AA/GA motif recognition predominantly through the non-catalytic CD1 domain, and its impact on the target-C selection and editing efficiency. These structures also explain how RNA inhibits DNA editing. Our findings reveal molecular insights into the cooperativity between the two domains of A3G in facilitating efficient DNA editing, which is critical for its antiviral function against foreign pathogens and its mutagenic effects on genomic DNA.

Results

Purine dinucleotide motifs facilitate DNA editing of rA3G

Previously, we have shown that rA3G has a strong binding affinity to rArA dinucleotide containing RNA with K_D between 10 to 17 nM, followed by rGrA dinucleotide with K_D of ~47 nM, and other combinations of dinucleotide containing RNA with K_D of ~124 nM or much worse³³. It turns out that rA3G also binds AA-containing DNA (5'-FAM TTTAATTTT) with K_D of ~318 nM, and GA-containing DNA (5'-FAM TTTTGATTTT) with K_D of ~473 nM (Supplementary Fig. 1). Based on this information, we hypothesized that the presence of AA or GA motifs in DNA may enhance substrate capture by A3G and facilitate the presentation of nearby target-Cs to the active site of the catalytic A3G-CD2 domain.

To study whether and how the AA motifs on DNA can facilitate A3G editing function, we compared editing efficiency between control DNA substrates that carry one editing motif CCC (the target-C is underlined) and AA-DNA substrates that carry both CCC and AA motifs. For simplicity, the control DNA contains only mixed pyrimidine bases, or a combination of mixed pyrimidine and guanine bases, but no adenine base. When designing single-stranded linear DNA substrates (Fig. 1a inset), two variables are considered: (1) substrate length and (2) distance of the editing motif CCC from 3'-end^{48–50}. It has been reported that when distance of the editing motif CCC from 3'-end is less than 30 nt, the editing motif CCC falls into a weakly deaminated 'dead' zone at the 3'-end linear DNA with a specific activity of human A3G less than 1 pmol $\mu\text{g}^{-1} \text{min}^{-1}$ ^{48,50}. We wished to study whether AA motifs could facilitate A3G editing efficiency under such situation.

A linear, 28-nt control DNA in the linear DNA substrate 1 (L1) set was designed with mixed pyrimidine bases (5'-

TTTCCCTTTCTTCTTCTTCTTCTTCTTC-FAM 3', Fig. 1a). A single A3G editing motif, CCC, was placed near the 5'-end with a 22-nt distance from 3'-end, reflecting the polarity preference of the A3G deaminase and falling within the 'dead' zone^{49,50}. Multiple TC motifs were also scattered throughout the sequence. These TC motifs are known to be disfavored by A3G^{5,53} and are unlikely to interfere with editing assays. The nucleotides in the DNA substrate are numbered with the target-C at position '0'. Therefore, we designated this control DNA as L1-CCC₀-N₂₂, where the subscript '22' specifies the 3'-end nucleotide position from the target-C (Fig. 1a inset). Importantly, this value also represents the distance of the editing motif CCC from the 3'-end, as well as the length of the hydrolyzed deamination product (simplified as "product" in this study) from the in vitro UDG-dependent deaminase assay (Supplementary Fig. 2). A 6-carboxyfluorescein dye (FAM) attached at the 3' end facilitates assay quantification.

Three linear AA-containing 28-nt ssDNA in the L1 set were designed with a single AA motif placed at three different locations downstream (in the 3' direction) of the editing motif CCC (Fig. 1a, inset). We designated these AA-containing substrates as L1-CCC₀-A₈A₉-N₂₂, L1-CCC₀-A₁₁A₁₂-N₂₂, and L1-CCC₀-A₁₄A₁₅-N₂₂, where the numbers following the adenine bases specify the adenine base positions from the target-C.

We utilized a soluble variant of rA3G protein, which was purified from *Escherichia coli*, for the deaminase assay. As documented in our previous studies, this purified variant is monomeric and largely free from RNA contamination^{31,33}. It carries a replacement of N-terminal domain loop 8 (139-CQKRDGPH-146 to 139-AEAG-142, designated as rA3G^{R8}) to enhance solubility and has been shown to be catalytically active³¹.

A time course assay was conducted with the control DNA and three AA-containing DNA (Fig. 1b, c). We observed a significant difference in the editing level among the four DNA substrates. The control DNA L1-CCC₀-N₂₂ has only ~4% edits. L1-CCC₀-A₈A₉-N₂₂ has even lower editing, with ~0.8% edits. However, L1-CCC₀-A₁₄A₁₅-N₂₂ has ~91% edits, followed by L1-CCC₀-A₁₁A₁₂-N₂₂ with ~30% edits. Corresponding specific enzyme activities were calculated in the linear product range (Fig. 1d), and they varied dramatically from 0.01 pmol $\mu\text{g}^{-1} \text{min}^{-1}$ (L1-CCC₀-A₈A₉-N₂₂) to 11.81 pmol $\mu\text{g}^{-1} \text{min}^{-1}$ (L1-CCC₀-A₁₄A₁₅-N₂₂). The best and the worst rA3G^{R8} specific activity are comparable to those reported for human A3G, about 12 to 15 pmol $\mu\text{g}^{-1} \text{min}^{-1}$ with a 69-nt single stranded DNA, and about 0.07 pmol $\mu\text{g}^{-1} \text{min}^{-1}$ when the editing motif CCC falling within the 30-nt 'dead' zone^{48,50}.

Next, we extended substrates in the L1 set to include each of the four purine dinucleotide motifs RR (R denotes A or G) and additional RR positions on DNA, while keeping the DNA sequence surrounding the editing motif CCC (5'-TTTCCCTTT) the same in all substrates. Collectively, a panel of 24 ssDNA substrates were derived with six RR positions: R₅R₆, R₈R₉, R₁₁R₁₂, R₁₄R₁₅, R₁₇R₁₈, and R₂₀R₂₁ (Fig. 1e). Evaluation in the linear product range shows that the top edited substrates were with AA motif, followed by GA motif. The substrates with AG motif also showed low but above-background editing. All GG substrates are poorly edited (Fig. 1f). In addition, a pattern of editing efficiency per function of RR position was observed among AA/GA substrates. R₁₄A₁₅ and R₁₇A₁₈ are in the best productive positions to promote target-C editing, whereas R₅A₆ and R₈A₉ are in the non-productive positions.

Following that, we investigated whether increasing distance of the editing motif CCC from 3'-end on longer ssDNA substrates could further facilitate rA3G editing efficiency. We took a low-cost approach and used a panel of unlabeled DNA substrates in combination with a fluorescent SYBR Gold Nucleic Acid Gel Stain detection. Due to relatively weak SYBR Gold signal with pyrimidine only DNA, individual guanine bases (G) were inserted in DNA to boost the staining signal (Fig. 1g). Four groups of unlabeled DNA substrates in the linear DNA substrate 2 (L2) set were designed with the distance of CCC from 3'-end

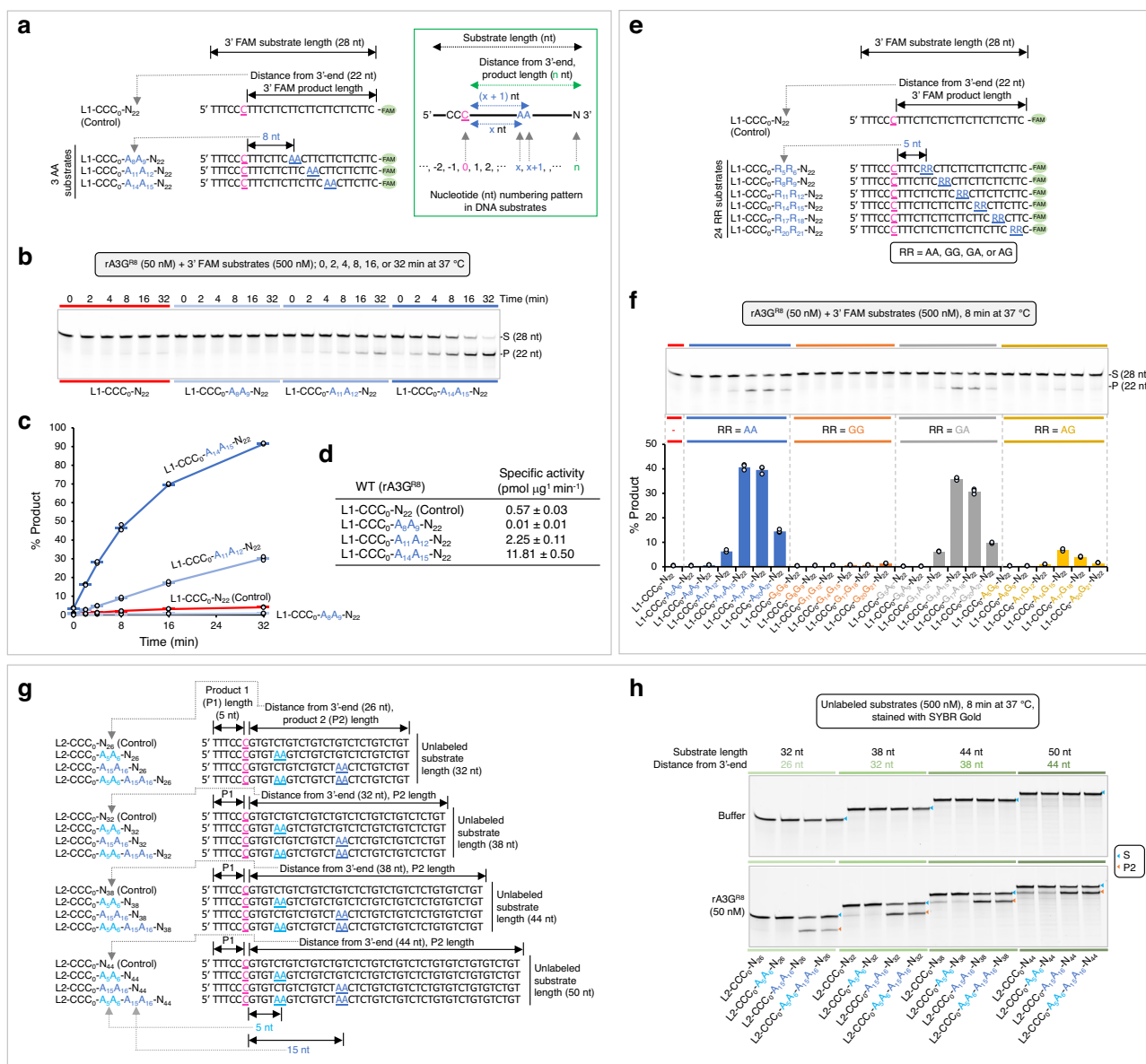


Fig. 1 | Purine dinucleotide motifs facilitate DNA editing by rA3G. The target-C (in pink) is underlined. Reaction conditions are indicated in the relevant data panels. Each plot is presented as mean values ± SD from three independent trials. **a** Design of a control DNA containing mixed pyrimidine bases with one editing motif CCC placed close to the 5'-end. It is designated as L1-CCC₀-N₂₂ with the target-C at position '0'. The subscript '22' specifies the 3'-end nucleotide position relative to the target-C. It also represents the distance (22 nt) between the target-C and the 3'-end, and the length of the editing product. 'L1' represents the linear DNA substrate 1 set. Three 28-nt DNA with a single adenine dinucleotide (AA) motif placed in a distance from the target-C are designated as L1-CCC₀-A_xA_{x+1}-N₂₂, where the subscript 'x' follows the nucleotide numbering pattern depicted in the inset. **b** Gel image and **c** plot of product formation by the four DNA substrates in a time course

assay. **d** Calculated specific enzyme activities using the linear-range data from the first 8 min of each reaction. **e** Design of 25 3' 6-FAM labeled 28-nt DNA substrates. RR denotes AA, GG, GA, or AG. **f** Gel image and plot of product formation of each DNA substrate in the L1 set. **g** Linear DNA substrate 2 (L2) set contains four groups of unlabeled DNA substrates with 32 nt, 38 nt, 44 nt or 50 nt in length. The corresponding distances between the target-C and the 3'-end are 26 nt, 32 nt, 38 nt, and 44 nt. Each group contains four DNA substrates: a control DNA substrate with no AA motifs and three DNA substrates containing individual A₅A₆, A₁₅A₁₆, or a combination of the two AA motifs (A₅A₆ and A₁₅A₁₆). **h** Gel images of the product formation of each DNA substrate in the L2 set. n = 3 independent trials. The quantification data of product formation and specific enzyme activity are presented in Supplementary Fig. 3. Source data are provided as a Source Data file.

increased to 26, 32, 38, or 44 nt. Their substrate lengths were 32, 38, 44, or 50 nt, respectively. Each group contains four substrates including a control DNA without AA motifs and three AA-containing DNA carrying A₅A₆ (in the non-productive position), A₁₅A₁₆ (in the productive position), or both AA motifs (Fig. 1g, h). The results confirmed that substrates with A₅A₆ are poorly edited, whereas substrates with A₁₅A₁₆ are efficiently edited. The enzyme specific activities are improved to -15.14 pmol μg⁻¹ min⁻¹ with L2-CCC₀-A₁₅A₁₆-N₃₂, and then it stays close to this value as the distance of the editing motif CCC from 3'-end increases (such as -14.31 pmol μg⁻¹ min⁻¹ with L2-CCC₀-A₁₅A₁₆-N₄₄,

Supplementary Fig. 3). Additionally, a combination of A₅A₆ and A₁₅A₁₆ generates a reduced editing output. The inhibitory effect of A₅A₆ diminishes as the DNA length increases (Fig. 1h, Supplementary Fig. 3a).

We also observed that, as the distance of the editing motif CCC from 3'-end increases, a substantial number of edits are generated even in the control DNA that contains no AA motifs (such as L2-CCC₀-N₄₄ with the specific enzyme activity of 6.59 pmol μg⁻¹ min⁻¹, Supplementary Fig. 3b). Consequently, AA-facilitated editing is less pronounced, with the specific enzyme activity being about two-fold higher

(14.31 pmol μg^{-1} min $^{-1}$, Supplementary Fig. 3b). These results suggest that with increasing distance of CCC from 3'-end, AA-independent interactions between rA3G and substrate DNA also increase, leading to efficient DNA capture and target-C deamination in the absence of AA dinucleotide motifs.

Control experiments with the purified catalytically inactive protein rA3G^{R8/E259A}, presented in later sections (also see Supplementary Fig. 4a, b), confirmed that the observed editing is solely attributable to rA3G activity and not to other co-purified factors. Additional experiments were conducted to examine whether the substitution in the N-terminal domain loop 8, made to improve solubility, affected AA-facilitated rA3G's editing function. These results are also presented in later sections.

In summary, we find that a single AA or GA motif can facilitate rA3G^{R8} editing efficiency on its target-C. AA/GA-facilitated editing is dictated by their position from the target-C with R₁₄A₁₅ to R₁₇A₁₈ in the best productive positions (specific enzyme activities -11.8 to -15.14 pmol μg^{-1} min $^{-1}$), and with R₅A₆ to R₈A₉ in the non-productive (or inhibitory) positions (specific enzyme activities -0.01 to 0.41 pmol μg^{-1} min $^{-1}$). The magnitude of AA-facilitated editing is also influenced by the distance of the editing motif CCC to the 3'-end. As this distance increases, AA-facilitated editing is attenuated, while AA-independent editing is boosted. Lastly, two adjacent AA motifs can generate a combined effect on a single CCC motif.

Overall structures of rA3G bound with ssDNA containing AA or GA motif

Prior to crystallization trials, we determined the minimal productive AA position of deamination on a target-C. We compared a panel of 17 substrates in the linear DNA substrate 3 (L3) set, each carrying a single AA motif placed from 5 nt to 21 nt downstream of the editing motif CCC (Fig. 2a). The results show that 10 nt (A₁₀A₁₁) is the minimal distance to elicit AA-facilitated editing function (Fig. 2b). Control experiments with catalytically inactive rA3G^{R8/E259A} showed no detectable activity on the DNA substrate containing A₁₄A₁₅ (Supplementary Fig. 4a, c). With this information, crystallization trials were carried out using the catalytically inactive rA3G^{R8/E259A} and ssDNA with AA or GA positioned at R₁₀A₁₁, R₁₁A₁₂, or R₁₄A₁₅. The lengths of the DNA substrate were shortened by removing the last four nucleotides at the 3'-end (Fig. 2c, d). Additionally, GA-containing DNA sequences were further modified to replace guanine bases outside of the GA motif with thymine bases (Fig. 2d). The best diffracting crystals were obtained with A₁₀A₁₁- and G₁₁A₁₂-containing DNA (Fig. 2c, d), and their structures were determined (Supplementary Table 1, Supplementary Fig. 5).

Both structures of the rA3G^{R8/E259A}-DNA complexes are monomers, each with one rA3G^{R8/E259A} molecule bound to one DNA molecule. The resolutions were determined to be 1.93 Å and 1.89 Å, respectively (Fig. 2c, d). Five nucleotides spanning over the AA motif (5'-C₉A₁₀A₁₁T₁₂C₁₃) and four nucleotides over the GA motif (5'-T₁₀G₁₁A₁₂T₁₃) were built into the electron density unambiguously (Fig. 2f, g). However, the editing motif CCC and the remainder of the 5'-end DNA were unresolved in both structures, likely due to their flexibility, as the CCC motif does not strongly bind to the CD2 domain. Superimposition of the two complex structures yielded a root-mean-square deviation (rmsd) of 0.388 Å (2839 to 2839 atoms, Fig. 2e), indicating they are essentially the same structure. A subtle but noticeable difference is seen between A₁₀ of the AA motif (A₁₀A₁₁) and G₁₁ of the GA motif (G₁₁A₁₂) (Fig. 2e, Supplementary Fig. 6), which is expected for the guanine base G₁₁ of the GA motif to fit into the groove that tightly binds the adenine base A₁₀ of the AA motif. The structure of rA3G^{R8/E259A} bound to the AA-containing DNA (resolution 1.93 Å) is used to describe the protein-DNA interactions in the following sections.

To place the editing motif CCC into the context of the full-length A3G structure, we carried out comparative modeling based on our rA3G bound to AA-DNA structure, alongside a previously determined

structure of human A3G-CD2 bound to the editing motif CCC (referred to as 'CCC-DNA', modelled from PDB 6BUX⁴⁴). The comparative model predicted that the AA-DNA fragment (predominately bound by rA3G-CD1) positions its 5'-end (C₉, Fig. 2h) in the general direction of the 3'-end of the editing motif CCC, as modeled with rA3G-CD2 (Fig. 2h). This prediction is consistent with the inherent directionality of CCC and AA motifs in our DNA substrates (Fig. 1e, g). To further validate the polar arrangement, we utilized a panel of 11 unlabeled 47-nt DNA substrates in the linear DNA substrate 4 (L4) set with a single AA motif systematically positioned upstream or downstream of the editing motif CCC (Fig. 2i). Our observations show that AA-facilitated editing occurs only in positions A₁₃A₁₄, A₁₇A₁₈, and A₂₁A₂₂ downstream of the editing motif CCC (Fig. 2j), aligning with the spatial organization predicted in the comparative model. Control experiments with catalytically inactive rA3G^{R8/E259A} showed no detectable activity on the DNA substrate containing A₁₃A₁₄ (Supplementary Fig. 4a, d).

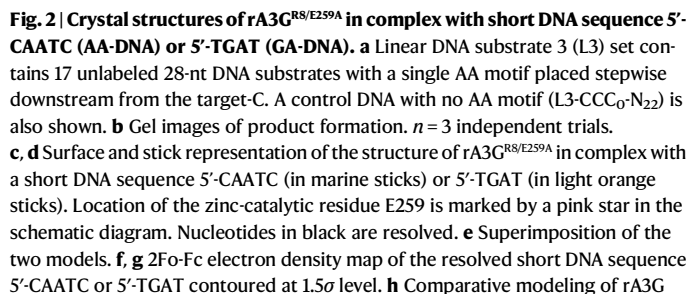
We further estimated the distance between the editing motif CCC and the AA motif by measuring the straight-line distance between A₁ in CCC-DNA and C₉ in AA-DNA (Fig. 2h and its inset), and determined it to be ~36 Å. Using a nucleotide length of 6.3 or 6.76 Å for ssDNA^{54,55}, this distance corresponds to roughly 6 nt between A₁ and C₉. In a real situation, the distance is expected to be longer than 6 nt as it should not follow a straight line connecting A₁ and C₉ due to the protein surface features. Therefore, this estimation aligns well with our experimentally determined minimal distance of 7 nt between A₁ and C₉ for the productive configuration, which is equivalent to A₁₀A₁₁ (Fig. 2b).

Detailed interactions between rA3G and DNA

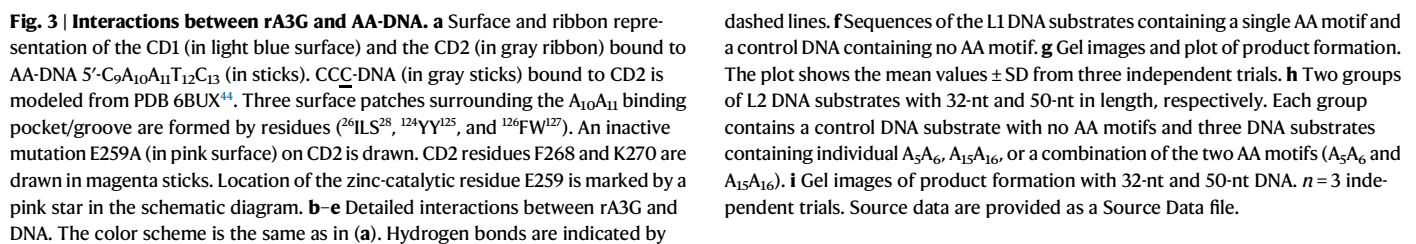
In the co-crystal structure of rA3G^{R8/E259A} bound to AA-containing DNA, the short 5-nt DNA centered around the AA dinucleotide (5'-C₉A₁₀A₁₁T₁₂C₁₃) out of the 21-nt ssDNA are clearly visible (Fig. 2f). The AA dinucleotide bases (A₁₀ and A₁₁) are inserted deep inside the protein, the nucleotides before and after A₁₀A₁₁ (i.e. C₉, T₁₂ and C₁₃) are bound on the protein surface. The rA3G binding interface for the 5-nt DNA is composed of 15 amino acid residues, 13 residues of which are located on the CD1 loops near CD1 Zn-center (loops 1, 3, 5, and 7), with the remaining 2 residues coming from CD2 (Fig. 3a-e). A hydrophobic groove conformed between CD1 and CD2 binds to the 5'-A (A₁₀), and a hydrophobic cave-like pocket on CD1 binds to the 3'-A (A₁₁) of the AA dinucleotide. The groove donates five residues (I26, F126, W127 on CD1, and F268 and K270 on CD2) to interact with A₁₀ through mostly hydrophobic interactions and only one hydrogen bond (Fig. 3b). The cave-like pocket of CD1 interacts with A₁₁ via hydrophobic packing and four strong hydrogen bonds through eleven CD1 residues, including 25-PILS-28 on loop 1, Y59 on loop 3, W94 on loop 5, and 123-LYFW-127 on loop 7 (Fig. 3c, e). Additionally, five CD1 residues, 24-RPILS-28 (loop 1), form a small surface area that interacts with C₉ (Fig. 3d). Two CD1 residues, 59-YP-60 (CD1 loop 3), have weak interactions with T₁₂C₁₃ (Fig. 3e).

To verify the importance of AA binding residues in AA-facilitated editing efficiency, we generated alanine mutations on seven CD1 amino acid residues that engage with the AA dinucleotide of the bound DNA, including I26A/L27A/S28A, Y124A/Y125A, and F126A/W127A. A wild type (rA3G^{R8}) and a catalytically inactive mutant (rA3G^{R8/E259A}) were used as positive and negative controls (Supplementary Fig. 7a). Using a panel of 3' FAM-labeled AA-containing substrates (in the L1 set), the results show that while the catalytically inactive rA3G^{R8/E259A} exhibited no detectable editing, two of the three CD1 mutants, Y124A/Y125A and F126A/W127A, displayed only basal-level editing function (Fig. 3f, g). These results indicate the critical importance of AA binding residues 124-YYFW-127 in CD1 for facilitating efficient editing by CD2. However, AA-facilitated editing is only partially lost in the mutant I26A/L27A/S28A, suggesting that these residues are less critical, and the mutant may still retain partial binding to AA.

Further validation was carried out using two groups of long DNA substrates (in the L2 set) with increased distances between



We also generated alanine mutations on CD2 residues F268 and K270 that participate in binding to the adenine base A₁₀ (Fig. 4a, Supplementary Fig. 7b) and tested it with a panel of 3' FAM labeled RR-containing substrates (Fig. 4b). Comparing to the wild type, the mutant F268A/K270A has an overall reduced editing efficiency when RR is in the productive positions (R₁₁R₁₂, R₁₄R₁₅, R₁₇R₁₈, and R₂₀R₂₁, Fig. 4c, d), indicating that the impairment in AA-binding leads to an impaired



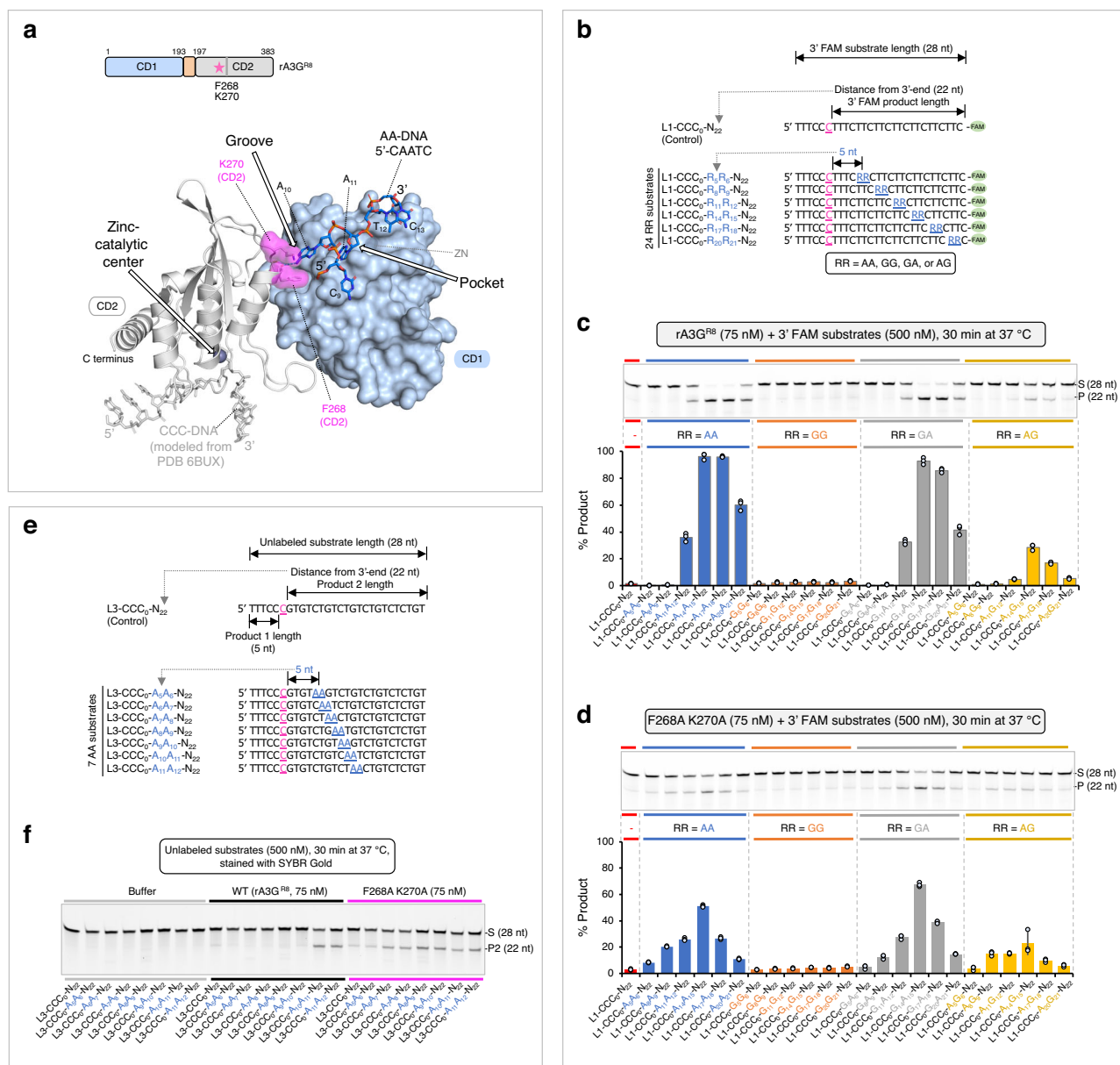


Fig. 4 | AA/GA-facilitated DNA editing performed with rA3G^{RS} carrying F268A and K270A mutations. Each plot is presented as mean values \pm SD from three independent trials. **a** Surface and ribbon representation of the CD1 domain (in light blue surface) and the CD2 domain (in gray ribbon) bound to AA-DNA 5'-CAATC (in marine sticks). CCC-DNA (in light gray sticks) is modeled from PDB 6BUX⁴⁴. Two CD2 residues F268 and K270 are shown (in magenta surface). Location of the zinc-

catalytic residue E259 is marked by a pink star in the schematic diagram. **b** Sequences of the L1 DNA substrates, where RR denotes AA, GG, GA, or AG. **c** Gel image and plot of product formation by the wild-type rA3G^{RS}. **d** Gel image and plot of product formation by the mutant rA3G^{RS} F268A K270A. **e** Sequences of the first 8 DNA substrates in the L3 DNA substrate set. **f** Gel image of the product formation. $n = 3$ independent trials. Source data are provided as a Source Data file.

AA-facilitated editing. Interestingly, it has an overall slightly increased editing efficiency when RR is in the non-productive positions (R₅R₆ and R₈R₉, Fig. 4c, d). Further examination of the minimal AA register using eight DNA substrates in the L3 substrate series (Fig. 4e, f) shows that the minimal AA register for productive DNA editing is shortened to -6 nt (A₆A₇). These observations suggest that the physical barrier between the CCC motif and AA motif has changed, possibly due to weakened interface rigidity between the CD1-CD2 domains. This allows CD2 greater freedom to rotate relative to CD1, enabling it to interact with DNA more flexibly and reach the CCC motif at a shorter distance.

Editing property of a hyperactive rA3G variant

We investigated whether rA3G carrying a hyperactive catalytic domain could override or escape from the AA-facilitated editing. We

constructed a rA3G^{RS} variant carrying two mutations on its CD2 domain, P247K and Q317K (Fig. 5a, b). Their corresponding mutations from human A3G, P247K and Q318K, have shown to contribute to the hyperactivity of the human A3G CD2 catalytic domain⁴⁴. The rA3G^{RS}/P247K/Q317K variant displays much enhanced editing efficiency on an AA-containing DNA substrate L1-CCC₀-A₁₄A₁₅-N₂₂ (Fig. 5c, d, g). Its enzyme specific activity reached 101.82 pmol μ g⁻¹ min⁻¹, about 8.6-fold higher than that of the wild-type rA3G^{RS}. Dramatic increase in editing efficiency was also observed in other AA-containing DNA and in the control DNA (Fig. 5g). Despite the overall enhanced efficiency, the substrate rank order remained similar to that of the wild type: L1-CCC₀-A₁₄A₁₅-N₂₂ is still the best substrate, followed by L1-CCC₀-A₁₁A₁₂-N₂₂, control DNA, and L1-CCC₀-A₈A₉-N₂₂. Using the complete panel of 25 FAM labeled DNA (Fig. 5e, f), we show that the hyperactive rA3G variant

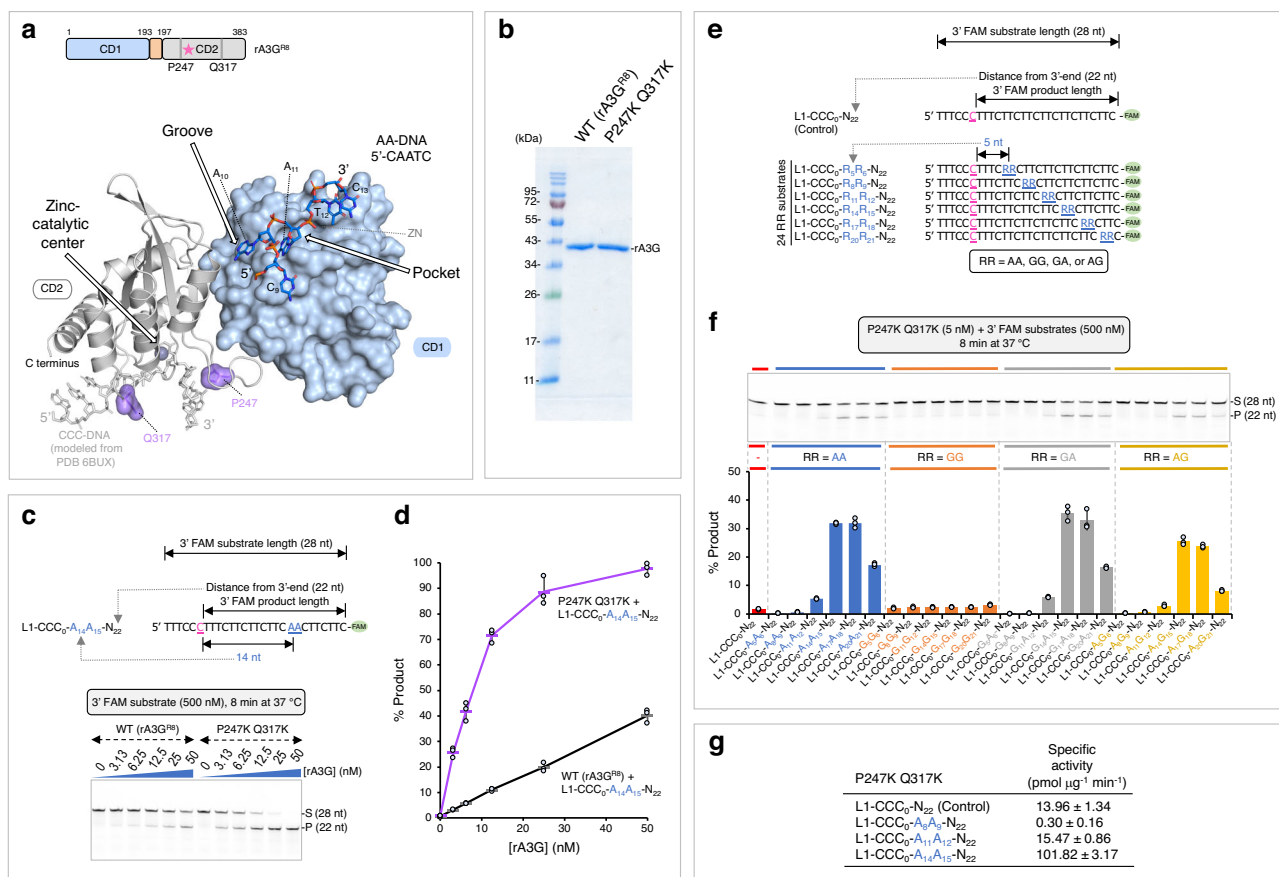


Fig. 5 | AA/GA-facilitated DNA editing performed with rA3G^{RS} carrying P247K and Q317K mutations. Each plot is presented as mean values \pm SD from three independent trials. **a** Surface and ribbon representation of the CD1 domain (in light blue surface) and the CD2 domain (in gray ribbon) bound to AA-DNA 5'-CAATC (in marine sticks). CCC-DNA (in light gray sticks) is modeled from PDB 6BUX⁴⁴. Two previously characterized residues P247 and Q317 (in purple surface) are shown on the CD2 domain (in gray ribbon). Corresponding mutations P247K and Q318K cause a hyperactive phenotype in human A3G CD2 domain⁴⁴. Location of the zinc-

catalytic residue E259 is marked by a pink star in the schematic diagram. **b** SDS-PAGE gel image showing the purified rA3G^{RS}/P247K/Q317K and the wild-type rA3G^{RS}. **c** Gel image and **d** plot of product formation in a dose response assay. The 3' FAM labeled DNA substrate sequence, L1-CCC₀-A₁₄A₁₅-N₂₂, is also shown. **e** Sequences of the L1 DNA substrates, where RR denotes AA, GG, GA, or AG. **f** Gel image and plot of product formation. **g** Calculated specific enzyme activity of four 3' FAM labeled DNA substrates by rA3G^{RS}/P247K/Q317K. Source data are provided as a Source Data file.

displays a pattern comparable to that of the wild type, albeit under a much lower enzyme concentration. GG-containing substrates remained to be poor substrates. Of note, the editing efficiency on AG substrates were disproportionately enhanced.

AA-facilitated DNA editing on editing sites TC and CC

A3G favors the target-C in the context of CCC over CC or TC^{5,53}. We investigated AA-facilitated editing on editing sites TC, CC, and CCC using the hyperactive variant rA3G^{RS}/P247K/Q317K. A panel of three linear AA-DNA substrates containing a single editing site (TC, CC, or CCC) and a single 3' downstream AA motif was designed: L3-TTC₀-A₁₅A₁₆-N₂₂, L3-TCC₀-A₁₅A₁₆-N₂₂, and L3-CCC₀-A₁₅A₁₆-N₂₂ (Supplementary Fig. 8a). Their corresponding control DNA substrates were also included, wherein A₁₅A₁₆ was replaced with a non-AA motif G₁₅T₁₆. A time course assay was conducted, and we observed AA-facilitated editing at all three editing sites (Supplementary Fig. 8b–g). The substrates were ranked from best to worst as CCC-A₁₅A₁₆, CC-A₁₅A₁₆, TC-A₁₅A₁₆/CCC-G₁₅T₁₆, CC-G₁₅T₁₆, and TC-G₁₅T₁₆. A negative control using the catalytically inactive rA3G^{RS}/P247K/E259A/Q317K showed no detectable editing activity. These results demonstrate that under the experimental conditions, editing sites TC or CC with 3' downstream AA motif could be as efficient as, or even more efficient than, editing sites CCC without 3' downstream AA motif.

RNA inhibition of AA-facilitated DNA editing

When comparing the rA3G structures in complex with the AA-DNA (5'-C₉A₁₀A₁₁T₁₂C₁₃) vs rArA-RNA (5'-rU₄rA₅rA₆rU₇U₈)³³, the first four DNA nucleotides (C₉A₁₀A₁₁T₁₂) align well with the four RNA nucleotides (rU₄rA₅rA₆rU₇) and show nearly identical interactions with rA3G, with the fifth DNA nucleotide C₁₃ adopting different interactions with rA3G from the corresponding RNA nucleotide rU₈ (Fig. 6a, Supplementary Fig. 9a). These results indicate that rA3G binds to the AA dinucleotide and the immediate 5' and 3'-side nucleotides similarly for both DNA and RNA. The noticeable differences are that RNA forms hydrogen bonds with the S28 sidechain, the main-chain N, and the G29 main-chain N through the 2'-OH of the sugar moiety of rU₄ and rA₆ (yellow sticks in Supplementary Fig. 9b), which are absent in DNA due to the lack of 2'-OH. For the fifth DNA nucleotide C₁₃, it turns in a different direction from its equivalent RNA nucleotide rU₈ in such a way that C₁₃ packs with T₁₂. Such packing interaction between C₁₃ and T₁₂ should not be allowed in RNA due to the presence of 2'-OH of rU₇ that would clash with rU₈. Another difference includes the 2'-OH of the sugar moiety of the fifth RNA nucleotide rU₈ forming an additional hydrogen bond with the R99 sidechain (Supplementary Fig. 9b).

These observations together with the difference in rA3G affinity between AA-DNA (Supplementary Fig. 1) and AA-RNA³³ suggest that the hydrophobic pocket favors AA-RNA over AA-DNA. It provides a

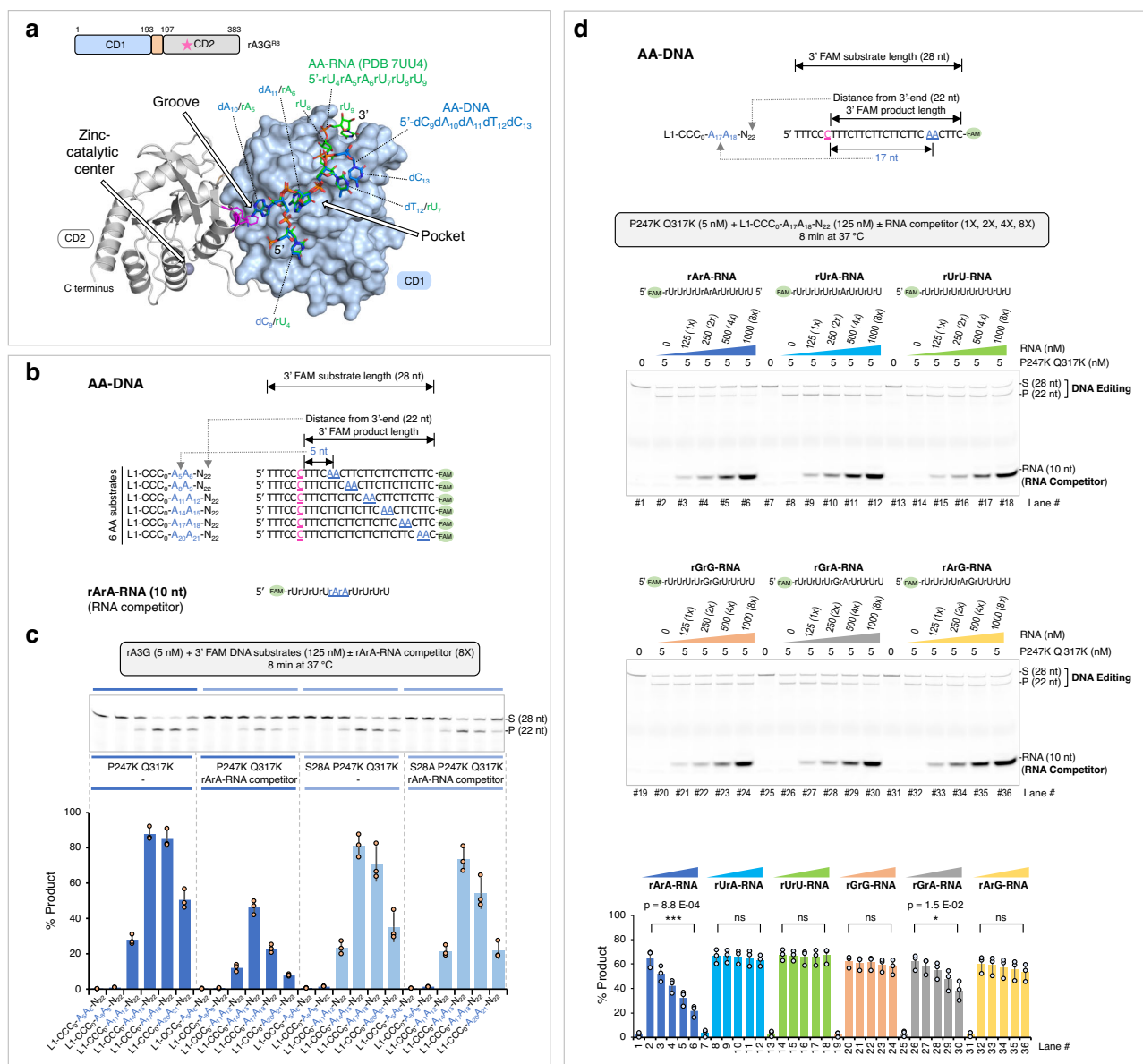


Fig. 6 | Inhibition of AA-facilitated DNA editing by RNA. DNA and RNA were mixed at the indicated molar ratio in the reaction mixture, and the assays were performed using the hyperactive variant rA3G^{R8/P247K/Q317K} and its S28A mutant (rA3G^{R8/S28A/P247K/Q317K}). **a** Overlapping binding surfaces for the AA motif on DNA and the rArA motif on RNA with rmsd 0.193 (2660 atom pairs). See Supplementary Fig. 9 for further details. Location of the zinc-catalytic residue E259 is marked by a pink

star in the schematic diagram. **b** Sequences of six L1-AA DNA substrates and one 10-nt rArA-RNA competitor used in the inhibition assay. **c** Gel image and plot of product formation. **d** Inhibition assay with six 10-nt RNA competitors. Each plot is presented as mean values \pm SD from three independent trials. The *P* values shown for the indicated sets in (**d**) were calculated using a two-tailed Student's *t*-test. Source data are provided as a Source Data file.

plausible structural explanation to prior data on RNA inhibition of A3G DNA editing function^{56–60}. To test this, we conducted rArA-RNA (5'-rUrUrUrUrArUrUrUrU) inhibition study on a panel of AA-DNA substrates (A₅A₆, A₅A₉, A₁₁A₁₂, A₁₄A₁₅, A₁₇A₁₈, and A₂₀A₂₁). We used the hyperactive variant rA3G^{R8/P247K/Q317K} and its S28A mutant rA3G^{R8/S28A/P247K/Q317K} (Supplementary Fig. 7c) to perform in the competition assay (Fig. 6b, c). The results show that (1) rArA-RNA inhibits AA-facilitated DNA editing with the hyperactive variant rA3G^{R8/P247K/Q317K}; (2) The S28A mutation alleviated the rArA-RNA inhibition but not to the full extent. This is likely caused by the loss of hydrogen bonding to 2'-OH of the sugar moiety of rU4 in RNA and the remaining RNA-specific interactions in the S28 mutant. In addition, its DNA editing efficiency is slightly reduced. This is likely caused by the loss of hydrogen bonding to O3' of the sugar moiety of C₉ in DNA (depicted in

Fig. 3d). Human A3G carrying the S28A mutation displays reduced packaging efficiency^{61,62}, supporting the involvement of S28 in RNA binding.

We further tested RNA inhibition of AA-facilitated DNA editing using one of the DNA substrates, L1-CCC₀-A₁₇A₁₈-N₂₂, and a set of six 10-nt RNA competitors (5'-rUrUrUrUrNrUrUrUrU, where rNrN denotes rArA, rUrA, rUrU, rGrG, rGrA, or rArG). The results show that rArA or rGrA-containing RNA competitors cause substantial reduction in the AA-facilitated DNA editing (Fig. 6d), which supports that rArA/rGrA RNA compete with AA-DNA for the same binding site on A3G. Because many cellular RNAs contain unpaired rArA motifs, the cellular rArA-containing RNA bound to A3G-CD1 is expected to inhibit the editing activity of A3G if they are not displaced.

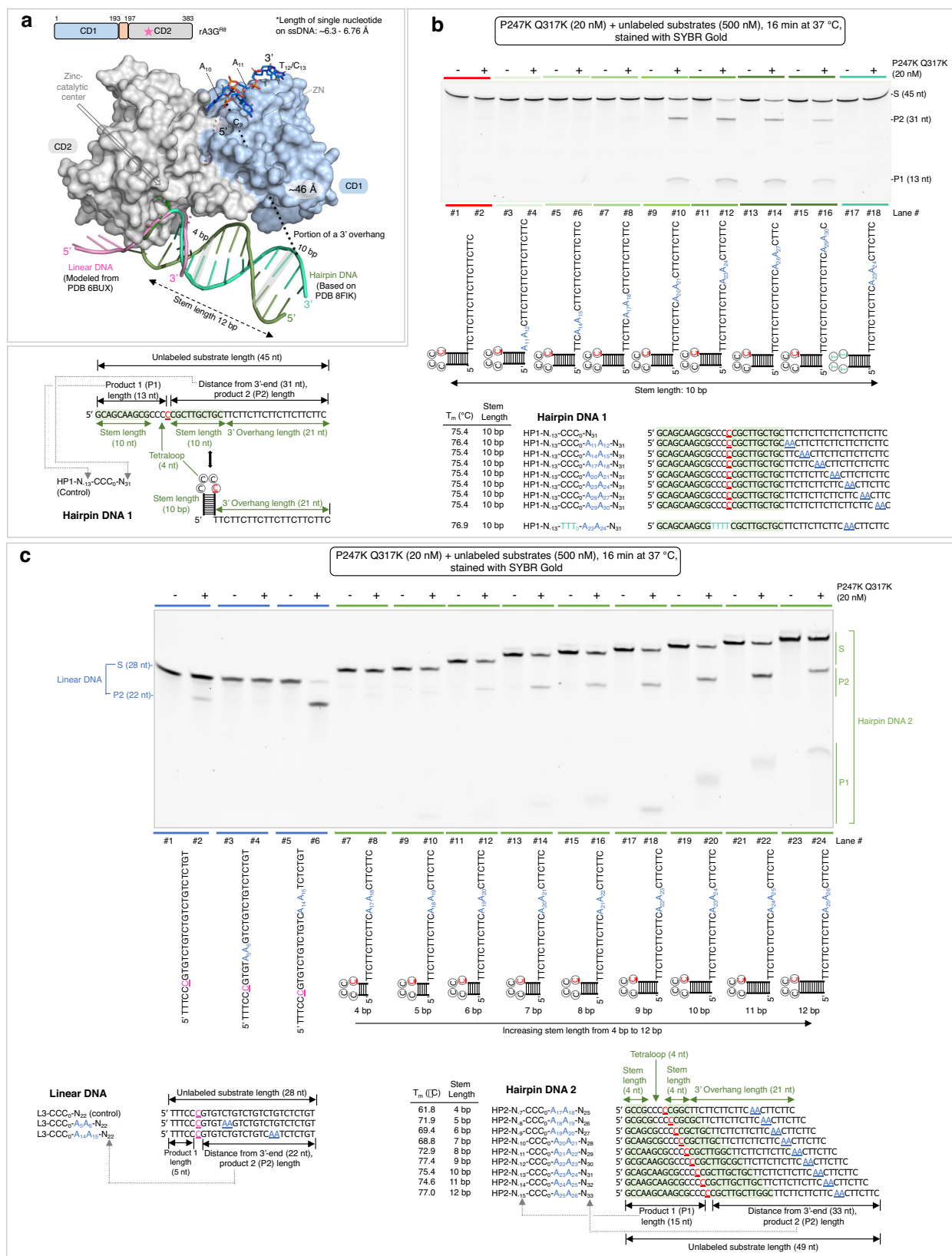


Fig. 7 | AA-facilitated DNA editing in hairpin forming sequences performed with the hyperactive variant rA3G^{R8/P247K/Q317K}. **a** Modeling of the editing motif CCC-DNA (in pink, modeled from PDB 6BUX⁴⁴) and a DNA hairpin structure with a tetraloop and a 12-bp stem (in green, based on PDB 8FIK⁶⁴) mapped on to the AA-bound rA3G structure (this study). A potential connection path (~46 Å) between the hairpin DNA (with a 10-bp stem) and the AA motif is indicated by a black dotted line and labeled as 'portion of a 3' overhang'. Location of the zinc-catalytic residue E259 is marked by a pink star in the schematic diagram. **b** Location of the AA motif on 3'-side affects editing efficiency. Deaminase activity was monitored on hairpin DNA 1

substrates carrying a 10-bp hairpin stem, a tetraloop CCCC, and a 3' overhang. A single AA motif was placed at various locations on the 3'-side. A negative control with 5'-TTTT in the hairpin loop and a single A₂₃A₂₄ motif in the 3'-side was included. *n* = 3 independent trials. **c** Effect of stem length on editing efficiency. Deaminase activity was monitored on hairpin DNA 2 substrates with varying stem lengths from 4 bp to 12 bp. The position of the AA motif was kept the same in all substrates as the position of A₂₃A₂₄ in the 10-bp hairpin DNA substrate. Three linear DNA substrates were included as controls. *n* = 3 independent trials. Source data are provided as a Source Data file.

DNA hairpin substrate with a long stem-length and a 3' overhang (for presenting AA motifs to the non-catalytic CD1 domain) could potentially be edited by rA3G (Fig. 7a). We used the hyperactive variant rA3G^{R8/P247K/Q317K} to test this hypothesis.

We designed a control DNA substrate (hairpin DNA substrate 1 or HP1) carrying an editing motif CCC in the loop region of a hairpin structure with a 10-bp hairpin stem, 5'-GCAGCAAGCG(CCCC)CGCTTGCTGC. The hairpin DNA also carries a 21-nt 3' overhang to boost its interaction with CD1 (Fig. 7b). Seven AA-containing DNA were designed with the AA motifs placed at various locations in the 3' overhang. All annealed hairpin DNA were essentially monomeric (Supplementary Fig. 10a) with the estimated *T_m* between 75.4 to 76.9 °C (Fig. 7b). The results show that the hairpin DNA are not efficiently edited without AA motif or with AA motif located from 11–12 nt to 17–18 nt downstream from the target C (substrates with A₁₁A₁₂, A₁₄A₁₅, or A₁₇A₁₈). Instead, efficient editing was only observed when the AA motif is positioned at a distance longer than 20–21 nt between A₂₀A₂₁ and A₂₉A₃₀. Control experiments using catalytically inactive rA3G^{R8/E259A} showed no detectable activity on the hairpin DNA substrate containing A₂₀A₂₁ (Supplementary Fig. 4a, e).

Comparing with linear DNA substrates, the minimal AA register for the productive DNA editing has changed from A₁₀A₁₁ to be longer than A₁₇A₁₈. This is likely caused by the difference between the rigid form of the hairpin duplex and the flexible linear DNA, as well as their spatial arrangement with the rA3G protein (Fig. 7a). In the comparative model, the straight-line distance between the 3'-end of the hairpin stem and the 5'-end of the AA-DNA is about ~46 Å, which is equivalent to 7 or 8 nt. This model shows that A₁₇A₁₈ does not have sufficient linear space between A₁₇A₁₈ bound at CD1 and the target CCC in the stem-loop bound at CD2 active site. It requires at least A₂₀A₂₁ to cover the distance and support the AA-facilitated editing of the target-C in this hairpin DNA.

We further tested the effect of stem-length on editing efficiency. Nine unlabeled hairpin DNA substrates were designed to carry varies stem-lengths from 4 bp to 12 bp (hairpin DNA 2 or HP2 set, Fig. 7c). Additionally, they all have the same 3' overhang sequence with one AA motif placed at the 13–14 nt position from the 3'-end of the hairpin stem. All annealed hairpin DNA of different hairpin stem lengths were monomeric with the estimated *T_m* between 61.8 to 77.4 °C (Fig. 7c Supplementary Fig. 10b). Three unlabeled linear DNA from the L3 set, L3-CCC₀-N₂₂, L3-CCC₀-A₅A₆-N₂₂, and L3-CCC₀-A₁₄A₁₅-N₂₂ (Figs. 2a and 7c) were also included as the linear DNA controls. Our results show that the linear DNA displayed the expected editing pattern with near complete editing in L3-CCC₀-A₁₄A₁₅-N₂₂ and very little editing in L3-CCC₀-A₅A₆-N₂₂. Nine hairpin DNA2 substrates also displayed a dramatic difference in editing efficiency. Hairpin DNA with short stem lengths is poorly edited (4 bp and 5 bp), whereas hairpin DNA with long stem lengths is efficiently edited (11 bp, 10 bp, and 9 bp). DNA with the longest hairpin stem tested (12 bp) was less efficiently edited.

Additional tests were carried out with hairpin DNA substrates containing a fixed stem length of 4 bp (HP3 set) or 11 bp (HP4 set), with varying AA positions in the 3' overhang (Supplementary Figs. 11 and 12). The results indicate that hairpin DNA with a 4-bp stem length are generally poor substrates, whereas hairpin DNA with an 11-bp stem length yield results similar to those with a 10-bp stem length (Fig. 7b). These findings align with our model predictions (Supplementary Fig. 13), which

suggest that helix rotation of the hairpin stem, in conjunction with the AA motif on the 3' overhang DNA, is likely responsible for the proper orientation (or positioning) of the target C to the CD2's catalytic cavity. It appears that the target C on longer stems, together with the AA motif on the 3' overhang DNA, can effectively reach the catalytic cavity, whereas the target C on shorter stems cannot. Consequently, the principle governing the spatial requirement between the AA motif recognized largely by CD1 and the target cytosine edited by CD2's active site is consistent across both linear DNA and hairpin DNA, despite differences in the number of nucleotides between the AA motif and the target cytosine.

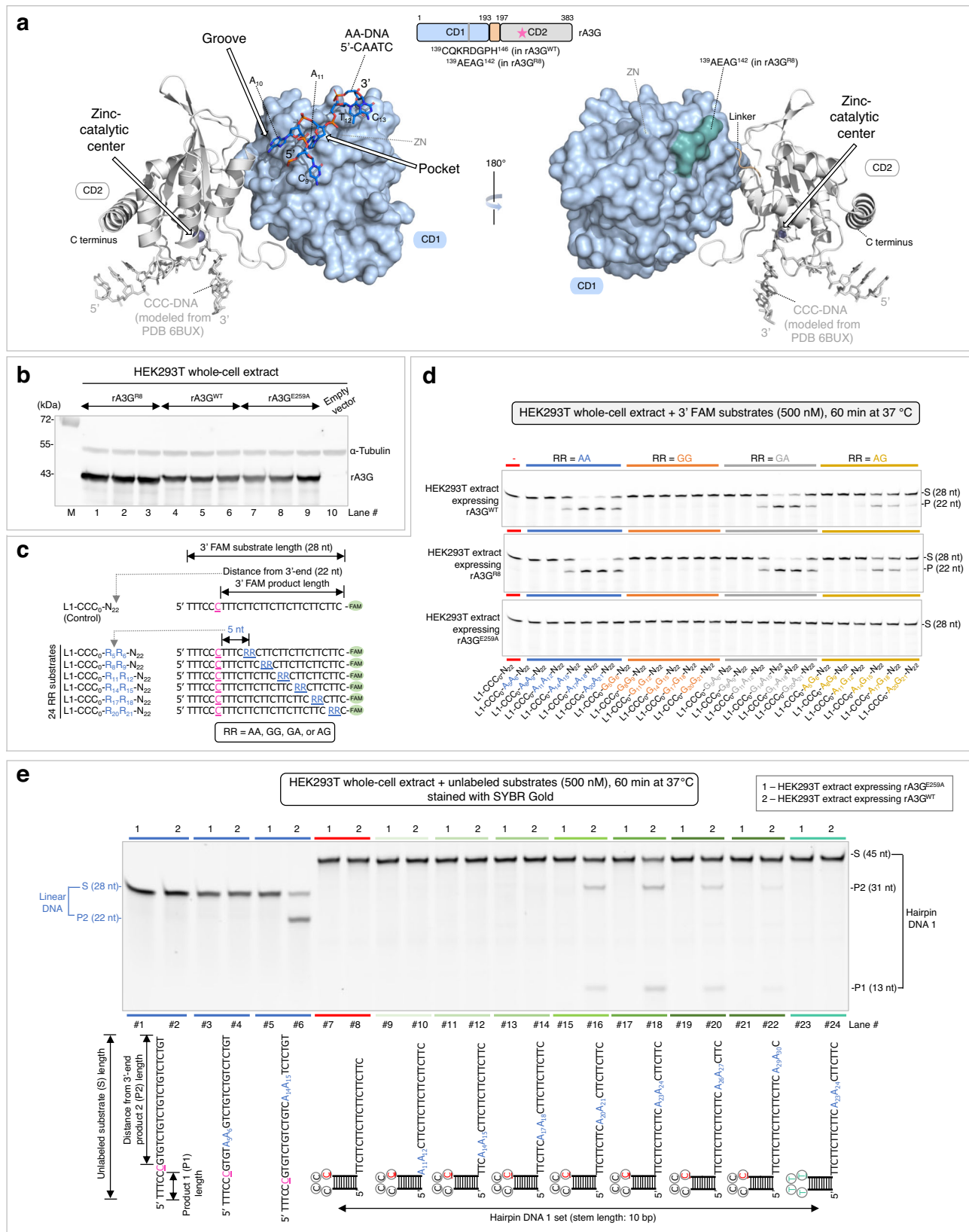
Editing characteristics of the wild-type rhesus macaque A3G and human A3G

Due to the challenging nature of purifying the wild-type rhesus macaque A3G (rA3G^{WT}, with native loop 8), we used whole-cell extracts from HEK293T cells expressing rA3G^{WT} to investigate its AA-facilitated editing function and to evaluate whether the substitution in the CD1 domain loop 8, made to improve solubility, affected this function. Structural analysis reveals that the substituted loop 8 is located remotely from the DNA binding sites, suggesting minimal perturbation on protein-DNA interaction upon substitution of loop 8 (Fig. 8a).

Experiments with the 3' FAM-labeled linear DNA confirmed that rA3G^{WT} and rA3G^{R8} in the HEK293T whole-cell extracts (Fig. 8b–d) displayed similar editing characteristics to each other and to the purified rA3G^{R8} protein (Fig. 1f, Fig. 4c). Experiments with the unlabeled hairpin DNA substrates also showed that rA3G^{WT} in the HEK293T whole-cell extracts (Fig. 8e, Supplementary Fig. 14) displayed similar editing patterns as those from the purified rA3G^{R8} protein (Fig. 7b, c). A negative control using the HEK293T whole-cell extract expressing the catalytically inactive rA3G^{E259A} (with native loop 8) showed no detectable deaminase activity (Fig. 8b, d, e, Supplementary Fig. 14).

Human A3G (hA3G) protein is closely related to rA3G, comprising approximately 77% identical and 85% similar residues (Supplementary Fig. 15a). Comparative modeling of hA3G (PDB 8CX0)⁶⁴ bound to AA-DNA (PDB 8TVC, this study) predicted that the putative binding surface for the AA-DNA motif remains largely the same in hA3G, along with multiple amino acid substitutions at the periphery of the AA-DNA binding area (Fig. 9a). This area also overlaps with the experimentally defined rArA- or rGrA-RNA binding area^{35,36}. HEK293T whole-cell extracts expressing the wild-type hA3G (hA3G^{WT}, Fig. 9b) was used to investigate AA-facilitated editing function due to difficulty of purifying the hA3G^{WT} protein. HEK293T whole-cell extract carrying the empty vector pcDNA was used as a negative control (Fig. 9b).

Experiments with the 3' FAM-labeled linear DNA and unlabeled hairpin DNA substrates revealed that hA3G^{WT} in the HEK293T whole-cell extract can effectively edit the target-C on both linear and hairpin loop DNA. Its editing efficiency exhibited a similar dependence on the AA position on both linear and hairpin DNA substrates (Fig. 9c, d). Additionally, it shows a similar dependence on the stem-length of the hairpin DNA substrates (Fig. 9e). Despite the observed similarity between the two A3G proteins, hA3G^{WT} in the HEK293T whole-cell extract also exhibited its distinct editing features. One notable feature is the elevated AA-independent editing activity towards DNA substrate HP1-N₁₃-CCC₀-N₃₁ (Fig. 9d, lanes 7 and 8). Finally, HEK293T whole-cell extracts carrying an empty vector pcDNA (Fig. 9b–e) or expressing a



catalytically inactive hA3G^{E259A} (Supplementary Fig. 15b–g) showed no detectable deaminase activity.

Discussion

In this study, we demonstrated that the editing of target-C by rA3G in both linear and hairpin loop sequences is significantly influenced by

the presence of AA and GA dinucleotides at a certain distance downstream (but not upstream) of the target-C. We also provided the mechanistic understanding for these biochemical observations through determination of two co-crystal structures of the full-length rA3G in complex with AA- or GA-containing ssDNA sequences. These structures reveal how rA3G predominately uses its non-catalytic CD1

Fig. 8 | Editing function of the wild-type rA3G (rA3G^{WT}, with native loop 8) on linear and hairpin DNA substrates. **a** Surface and ribbon representation of rA3G. The rA3G CD1 domain (in light blue surface) is bound to AA-DNA 5'-CAATC (in marine sticks). The rA3G CD2 domain (in gray ribbon) is bound to CCC-DNA (in light gray sticks, modeled from PDB 6BUX⁴⁴). The four substituted residues in the CD1 domain loop 8, ¹³⁹AEAG¹⁴², are shown as a surface patch (in teal). Location of the zinc-catalytic residue E259 is marked by a pink star in the schematic diagram. **b** Western blot of HEK293T whole-cell extracts expressing rA3G^{R8}, rA3G^{WT} or rA3G^{E259A} (catalytically inactive). HEK293T whole-cell extract with empty vector pcDNA served as a negative control. α -Tubulin served as a loading control. rA3G^{R8} migrated slightly faster than rA3G^{WT} because the substituted loop 8 in rA3G^{R8} is four residues shorter. M indicates protein molecular weight standards. $n = 3$

independent trials. **c** DNA sequences of 3' 6-FAM labeled 28-nt DNA substrates (L1 set). RR denotes AA, GG, GA, or AG. **d** Deaminase activity of HEK293T whole-cell extract expressing rA3G^{WT}, rA3G^{R8}, or rA3G^{E259A} on linear DNA substrates (L1 set). $n = 3$ independent trials. **e** Deaminase activity of HEK293T whole-cell extracts expressing rA3G^{WT} or rA3G^{E259A} on hairpin DNA 1 substrates (HPI set) carrying a 10-bp hairpin stem, a tetraloop CCCC, and a 3' overhang. A single AA motif was placed at various locations on the 3' overhang. A negative control with 5'-TTTT in the hairpin loop and a single A₂₃A₂₄ motif in the 3' overhang was included. Three linear DNA substrates were included as linear DNA controls. Deaminase activity was monitored using 1.6 μ g of HEK293T whole-cell extract on 500 nM DNA substrates in a 20 μ l reaction volume. $n = 3$ independent trials. Source data are provided as a Source Data file.

domain to capture the substrate through recognition of the AA/GA motifs in a specific orientation, thereby presenting the target-C to the distally located active site on the catalytic CD2 domain for deamination. Although most of the work presented here is based on purified rA3G^{R8} (and its derivatives) carrying a substituted loop 8 on the N-terminal domain, we show that rA3G^{WT} in HEK293T whole-cell extracts displays similar editing characteristics as the purified protein rA3G^{R8}. Additionally, hA3G^{WT} in HEK293T whole-cell extracts displays a similar editing property as rA3G^{WT} in terms of AA motif influence on target-C deamination. However, hA3G^{WT} also displays distinct editing features that warrant further investigation.

The AA/GA-facilitated DNA editing is directional and dynamic, supporting previous findings regarding the directionality and processivity features of A3G catalysis on ssDNA. Multiple AA, GA motifs present in the DNA substrates in previous reports would allow A3G to bind at multiple locations on these DNA substrates, thus rationalizes A3G "promiscuous" DNA binding property. The biochemical and structural data described here, together with the prior information from other studies^{44,48,50,52}, support a mechanism (Fig. 10) in which CD1, with the assistance of CD2, scans, recognizes, and captures exposed AA/GA motifs in ssDNA region, which allow CD2 sufficient time to hit on those CCC motifs located 5'-upstream within a 9–20 nt linear distance window (optimal 12–16 nt), for deamination. If CCC motifs are located either at the 5'-side of AA/GA within a 7 nt distance or at the 3'-side of AA/GA, they cannot efficiently reach the catalytic cavity on CD2 for deamination. Additionally, DNA secondary structure can affect the geometric distance between AA/GA and CCC, which in turn, affects the register of the productive distance between AA/GA and the target-C (Fig. 10, Supplementary Fig. 13). Specifically, the editing efficiency of the hairpin loop CCC is influenced by both the stem length and its spatial reach to the CD2 active site from the AA/GA on the 3' overhang, which is primarily captured by CD1.

rA3G also carries out AA/GA independent DNA editing at a reduced efficiency, which requires further study. The editing on ssDNA devoid of AA/GA may be carried out by the action of CD2 without much contribution from CD1, or there could be other DNA binding sites present on CD1 in either sequence specific or non-specific manner. Indeed, the editing level of ssDNA devoid of AA/GA is similar to those by individual CD2 protein alone⁶⁵. However, the editing efficiency of AA/GA-independent editing significantly increases as the DNA length 3'-downstream of the CCC motif increases (Fig. 1h and Fig. 3j), suggesting that the increase of the length of the ssDNA can enhance DNA binding by CD1 to facilitate the substrate capturing and target-C deamination. Additionally, rA3G mutants disrupting the AA/GA specific binding are shown to retain AA-independent DNA editing (Fig. 3g, i).

Previous studies have shown that, with the exception of CpG and UpA, other RNA dinucleotides, including UpU and UpC (which translate to ApA and GpA on -cDNA), have normal representation levels in the HIV-1 RNA genome^{66–68}. Therefore, we didn't see evidence to suggest that viruses undergo depletion of the AA/GA motif in the viral -cDNA genome during evolution to evade A3G activity. We speculate that a balanced level of dinucleotides is likely a requirement for maintaining both the

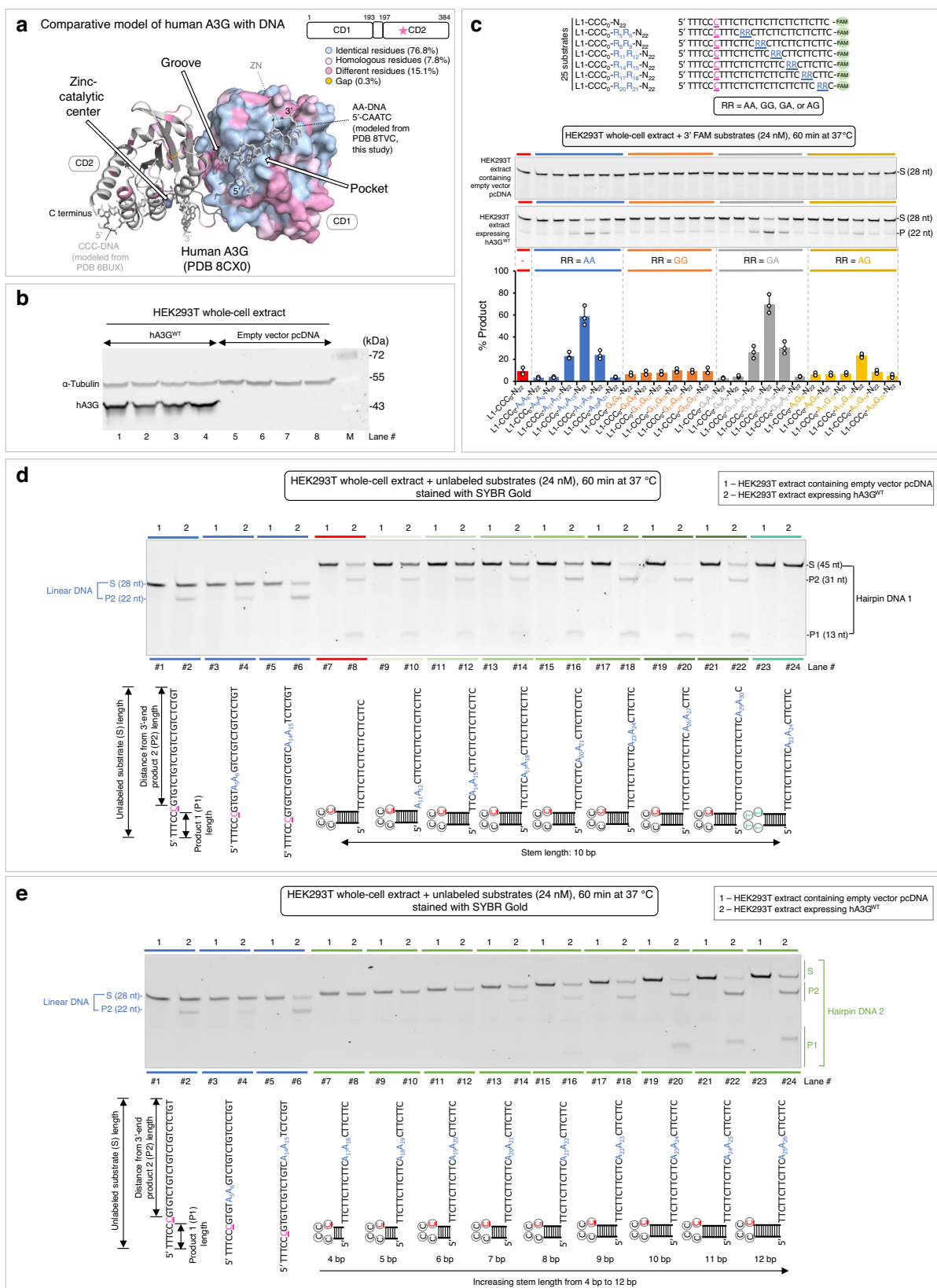
secondary and tertiary RNA structural features as well as efficient transcription and translation⁶⁶. Another concern is that the catalytic enhancement by the AA/GA sequence decreased when longer ssDNA substrates were tested. Our preliminary analysis of the frequency of AA/GA occurrence on the 3' side of most (hot) and least (cold) mutated sites in HIV and SIV cDNA did not reveal any difference between the hot and cold spots. These data suggest that, compared to our controlled experiments with oligos containing a single target site, mutations with the HIV and SIV cDNA during reverse transcription are influenced by several factors, including not only distances from the AA and GA sites but also complex structural features in the RNA-cDNA hybrid, variations in the number of packaged APOBEC3 molecules⁶⁹, presence of other APOBEC3 enzymes such as APOBEC3D, APOBEC3F, and APOBEC3H^{70,71}, interaction between APOBEC3G and RT¹⁷, among other unknown factors. Accurately identifying all these factors and their contributions to the level of C > T mutations warrant further investigation.

We consider the following two factors to be important for AA/GA-facilitated DNA editing: (1) differential binding affinity for purine and pyrimidine motifs on DNA, and (2) a physical barrier between the catalytic cavity and the motif binding pocket. Variations in both binding affinity and flexibility degree between the two domains could influence the enzyme function among A3G homologs. Additionally, multiple factors could potentially shape the contribution of AA/GA-facilitated editing under physiological and pathological situations. Due to the largely shared binding interactions between AA/GA-containing ssDNA and ssRNA, mutants defective in binding to AA/GA ssDNA are also defective in binding to AA/GA ssRNA³³. Cellular and viral ssDNA binding proteins could compete with A3G in binding to ssDNA^{72–75}. Furthermore, temporary formed DNA secondary structures may cause deviation from expected productive configuration for AA-facilitated editing^{7,76,77}. Finally, selection pressure in living cells may promote certain mutations over others and shape the eventual mutational outcome⁷⁸. Further investigation is needed to determine the mechanisms of CD1/CD2 cooperativity and the outcome of target-C editing/mutation carried out by A3G in vivo. Structural studies of double-domain APOBECs in complex with nucleic acids can also provide valuable molecular insights into the cooperative mechanisms that have evolved during conflicts between host restriction factors and retroviruses.

Methods

Protein expression and purification

A soluble variant of rhesus macaque APOBEC3G (rA3G, accession code: AGE34493) with a replacement in the N-terminal domain loop 8 (¹³⁹CQKRDGP¹⁴⁶ to ¹³⁹AEAG¹⁴², designated as rA3G^{R8}) was constructed in the pET-sumo vector (K30001, Thermo Fisher Scientific). This construct generated a SUMO fusion with an N-terminal 6xHis tag and a PreScission protease cleavage site. Protein expression and purification followed previously published protocols³³. In brief, *E. coli* RosettaTM (DE3) pLysS cells (70956, Millipore SIGMA) expressing rA3G were cultured at 37 °C in LB medium with 50 μ g/ml kanamycin. Temperature was lowered to 16 °C when OD₆₀₀ reached ~0.3. Protein expression was induced by 0.1 mM IPTG when OD₆₀₀ reached 0.7 to 0.9. After



overnight growth at 16 °C, cells were harvested by centrifugation. The resulting cell pellet was lysed in buffer A (25 mM HEPES at pH 7.5, 500 mM NaCl, 20 mM MgCl₂, 0.5 mM TCEP, and 60 µg/ml RNase A) using sonication. The protein purification process included Ni-NTA agarose chromatography, RNase A/T1 treatment and PreScission protease cleavage, size-exclusion chromatography, heparin

chromatography, and a second-round of size-exclusion chromatography. The final protein samples were quantified, verified for purity, and stored in buffer B (50 mM HEPES at pH 7.5, 250 mM NaCl, and 0.5 mM TCEP) at -80 °C until use. Sequences of all mutant constructs were verified by Sanger sequencing (Azenta Life Sciences). Mutant proteins were purified using the same protocol.

Fig. 9 | Editing function of the wild-type human A3G (hA3G^{WT}) on linear and hairpin DNA substrates. **a** Comparative modeling of hA3G^{WT} (PDB 8CX0³⁹) bound to DNA. The hA3G CD1 domain (in mosaic-color surface, color key is shown) is bound to 5'-CAATC (in light gray sticks, modeled from PDB 8TVC, this study). The hA3G CD2 domain (in gray ribbon) is bound to CCC-DNA (in light gray sticks, modeled from PDB 6BUX⁴⁴). Location of the zinc-catalytic residue E259 is marked by a pink star in the schematic diagram. **b** Western blot of HEK293T whole-cell extracts expressing hA3G^{WT} or containing an empty vector pcDNA. α -Tubulin served as a loading control. M indicates protein molecular weight standards. $n = 4$ independent trials. **c** DNA sequences of 3' 6-FAM labeled 28-nt DNA substrates (L1 set). RR denotes AA, GG, GA, or AG. Deaminase activity of hA3G^{WT} on linear DNA substrates (L1 set). The plot is presented as mean values \pm SD from three independent trials. **d** Deaminase activity of hA3G^{WT} on hairpin DNA 1 substrates

(HP1 set) carrying a 10-bp hairpin stem, a tetraloop CCCC, and a 3' overhang. A single AA motif was placed at various locations on the 3' overhang. A negative control with 5'-TTTT in the hairpin loop and a single A₂₃A₂₄ motif in the 3' overhang was included. Three linear DNA substrates were included as linear DNA controls. $n = 3$ independent trials. **e** Deaminase activity of hA3G^{WT} on hairpin DNA 2 substrates (HP2 set) with varying stem lengths from 4 bp to 12 bp. The position of the AA motif was kept the same in all substrates as the position of A₂₃A₂₄ in the 10-bp stem loop DNA substrate. Three linear DNA substrates were included as linear DNA controls. Deaminase activity was monitored using 0.18 μ g of HEK293T whole-cell extract on 24 nM DNA substrates in a 20 μ l reaction volume. $n = 3$ independent trials. See Supplementary Fig. 15 for control experiments with a catalytically inactive mutant hA3G^{E259A} on four key unlabeled-DNA substrates. Source data are provided as a Source Data file.

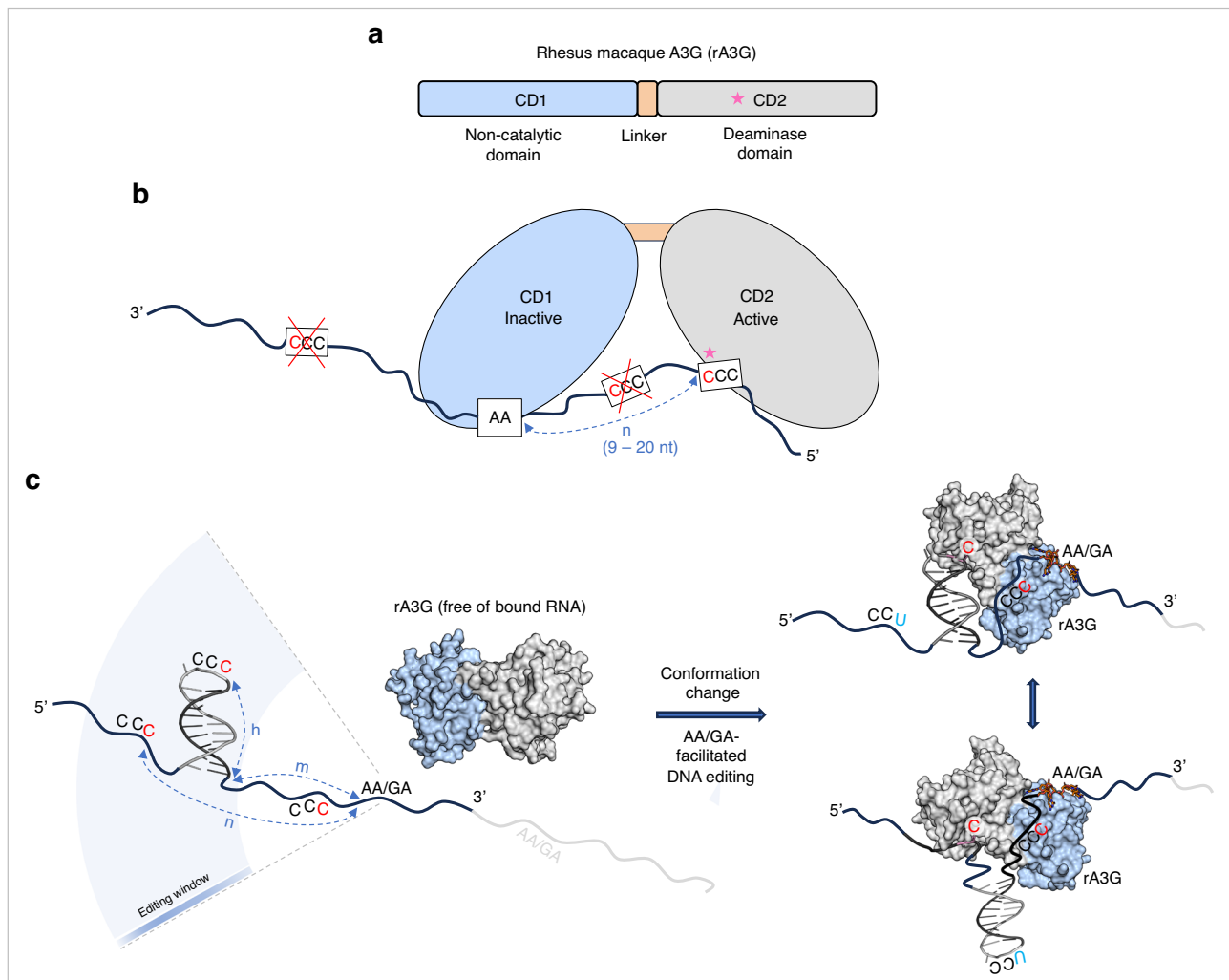


Fig. 10 | AA/GA-facilitated DNA editing by rA3G. rA3G binds the exposed AA/GA motifs on DNA and edits multiple CCCs that are located (1) 5' upstream and (2) within its editing window required for linear or for hairpin DNA. **a** Cartoon depicts the domain organization of rA3G. Location of the zinc-catalytic residue E259 is marked by a pink star in the schematic diagram. **b** Cartoon depicts how rA3G predominantly uses its CD1 domain to capture the AA/GA dinucleotide on linear ssDNA and presents the editing motif CCC, located at the 5'-side (or upstream) of AA/GA, to its CD2 active site within a 9–20 nt window, with an optimal linear distance of 12–16 nt, for deamination. The editing motif CCC located at the

5'-side of AA/GA within 1–7 nt distance or at the 3'-side of the AA/GA cannot reach to the CD2 active site efficiently. **c** Diagram depicts that editing efficiency of CCC on hairpin loop DNA is affected by both stem length (h) and 3' overhang distance (m) to the AA/GA on the 3'-side (downstream). The fate of the editing sites, CCC, whether located on a hairpin loop or on linear ssDNA, will be as follows: the CCC located right next to the 5'-side of AA/GA within 1–7 nt linear distance remains unedited, whereas both the middle CCC on the hairpin loop and the CCC on the 5'-side of the hairpin loop are within the editing distance from the AA/GA for efficient deamination.

Electrophoretic mobility shift assay (EMSA)

DNA labeled with 5' 6-FAM (Integrated DNA Technologies) at 10 nM was titrated by rA3G in 20 μ l reaction volume containing 50 mM HEPES pH 7.5, 250 mM NaCl, 1 mM DTT, 0.1 mg/ml recombinant albumin

(B9200S, New England Biolabs), 0.1 mg/ml RNase A (19101, QIAGEN), and 10% glycerol. Reaction mixtures were incubated on ice for 10 min and analyzed by 8% native PAGE in 4 $^{\circ}$ C. A solution with acrylamide:bis-acrylamide ratio of 72.5:1 was used in preparing 8% native gels.

Typhoon™ Biomolecular Imager (Cytiva) was used to visualize gel images. ImageQuant TL (v8.1, Cytiva) was used for image quantification. Dissociation constant K_D was calculated using GraphPad Prism version 8.0.0 for Windows. Three independent trials were carried out for each DNA molecule.

In vitro UDG-dependent deaminase activity assay

DNA and RNA oligonucleotides were synthesized by Integrated DNA Technologies. Hairpin DNA substrates are annealed overnight in the DNA annealing buffer (10 mM Tris at pH 8, 50 mM NaCl), and their size exclusion chromatography (SEC, Cytiva) elution profiles were checked to ensure no self-dimer formation.

DNA deamination activity assays were performed as described³¹ with minor modifications. Reactions (20 µl) containing the purified protein (rA3G^{RS} or indicated mutants, with specified concentrations) and individual DNA substrates (with indicated sequences and concentrations) were incubated at 37 °C for an indicated duration in DNA deamination buffer [25 mM HEPES at pH 7, 250 mM NaCl, 1 mM DTT, 0.1% Triton X-100, 0.1 mg/ml recombinant albumin (B9200S, New England Biolabs), and 0.1 mg/ml RNase A (19101, QIAGEN)]. Reactions were stopped by heating to 90 °C for 5 min. Uracil was removed by 0.025 U/µl uracil DNA glycosylase (M0280, New England Biolabs) at 37 °C for 15 minutes, followed by abasic site hydrolysis at 90 °C for 10 minutes in 0.13 M NaOH. Reactions were mixed with equal volume of 2× gel loading buffer (95% formamide, 25 mM EDTA) and heated to 95 °C for 5 minutes. DNA fragments was separated on 20% denaturing acrylamide gel (5% crosslinker, 7 M urea, 1× TBE buffer) using Criterion™ cell apparatus (1656001, Bio-Rad) at 300 V for 40 to 60 min. For unlabeled DNA, gels were stained with 1× SYBR™ Gold Nucleic Acid Gel Stain (S11494, Thermo Fisher) for 10 min. Gel images were visualized by Typhoon™ Biomolecular Imager (Cytiva) and quantified by ImageQuant TL image analysis software (v8.1, Cytiva). The percent product formation was calculated by dividing the intensity of the lower product band by the sum of the intensities of the product and substrate bands. RNA competition experiments were conducted with both RNA and DNA present in the reaction mixture, following the same protocol with the addition of an RNase inhibitor (M0314, New England Biolabs).

Crystal growth, data collection, structure determination, and analysis

rA3G^{RS} carrying the inactive mutation E259A (rA3G^{RS/E259A}) was purified using the same protocol as described above. The rA3G^{RS/E259A}-DNA complexes were prepared by mixing protein (4 mg/ml) with DNA at 1 to 1 molar ratio. After incubating on ice for 1 h, precipitation was removed by centrifugation (21,000 × *g*, 2 min, 4 °C). Initial screening was conducted using the sitting-drop vapor diffusion method with the ARI Crystal Gryphon Robot (ARI) and crystallization screening kits (QIAGEN) at 18 °C. Crystallization hits were further optimized using the hanging-drop vapor diffusion method at 18 °C. High-quality crystals of the rA3G^{RS/E259A}-AA DNA complex were obtained with a reservoir solution consisting of 0.1 M Bis-Tris Propane at pH 7.3, 0.2 M Na/KPO₄, and 18% PEG 3350. Similarly, high-quality crystals of the rA3G^{RS/E259A}-GA DNA complex were obtained with a reservoir solution consisting of 0.1 M Bis-Tris Propane at pH 7.5, 0.2 M Na/KPO₄, and 16% PEG 3350. These crystals were transferred to synthetic mother liquor supplemented with suitable amounts of glycerol for cryoprotection and then flash-cooled in liquid nitrogen. X-ray diffraction data were collected at the Advanced Photon Source (GM/CA@APS, Argonne National Laboratory) beamline 23ID-D and at the Advanced Light Source (ALS, Lawrence Berkeley Laboratory) beamline 5.0.3.

Data were processed by automated data processing pipelines at the beamlines. Initial phase information was obtained by molecular replacement method with PHENIX (v1.20.1) using the rA3G crystal structures (PDB 7UU4 or 8EDJ)³³ without bound RNA. DNA was built

manually in COOT. The structural models were refined using PHENIX (v1.20.1) and modified with COOT (v0.9.8.7). Data collection statistics and refinement parameters are summarized in Supplementary Table 1. Hydrogen bonding predictions were done by QtPISA (v2.1.0). Structure images were prepared with PyMOL (v2.5.3).

HEK293T whole-cell extract preparation and Western blot

HEK293T cells were seeded in 12-well plates 24 h before transfection. FLAG-tagged A3G constructs or empty vector pcDNA were transfected using Lipofectamine 3000 Transfection Reagent (L3000008, Thermo Fisher) following the manufacturer's recommendations and incubated for 48 h before harvesting. HEK293T whole-cell extracts were prepared in 100 µl M-PER™ Mammalian Protein Extraction Reagent (78501, Thermo Fisher Scientific) supplemented with 1× Halt™ Protease Inhibitor Cocktail (78429, Thermo Fisher Scientific) and 150 mM NaCl. Total protein concentration in the extracts was estimated using Pierce™ BCA Protein Assay Kit (23225, Thermo Fisher Scientific) following the manufacturer's recommendations, with a typical yield of around 3 mg/ml. Extracts were stored in small aliquots at −80 °C.

For western blot, proteins in HEK293T whole-cell extracts were separated by SDS-PAGE and transferred onto Immobilon® -FL PVDF membrane (IPFL00010, EMD Millipore). The membranes were blotted with primary antibodies: anti-FLAG M2 mAb (F3165, SIGMA, 1:3000) and anti-α-tubulin mAb (GT114, GeneTex, 1:5000). ECL Plex Goat-α-Mouse IgG-Cy3 (PA43009, Cytiva, 1:3000) was used as the secondary antibody. Cy3 signals were detected using the Typhoon™ Biomolecular Imager (Cytiva).

Statistical analysis

We assessed the assumption of equal variances using an *F*-test. Data analysis was performed using a two-tailed Student's *t*-test in Excel (v16.82), assuming homoscedasticity. A significance level of $\alpha = 0.05$ was applied to determine statistical significance.

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

The data supporting the findings of this study are available within the paper and its Supplementary Information files, and available from the corresponding author upon request. Atomic coordinates and structure factors have been deposited in the PDB database under accession codes **8TVK** (rA3G^{RS/E259A} in complex with DNA 5'-CAATC) and **8TX4** (rA3G^{RS/E259A} in complex with DNA 5'-TGAT). The atomic models used in this study are available in the PDB database under accession codes **6BUX**, **7UU4**, **8CX0**, and **8FIK**. Source data are provided with this paper.

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Author contributions

H.Y. and X.S.C. designed the experiments. H.Y. performed crystallization, data collection, structural determination, and functional biochemical analyses. J.P. performed structural work and refinements. K.K. and F.I. assisted the project. D.E. and A.B. analyzed the HIV-1 and SIV genomes. H.Y. and X.S.C. wrote the paper. All authors commented on the paper.

Competing interests

The authors declare no competing interests.

Additional information

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