Dispersed Sites of HIV Vif-Dependent Polyubiquitination in the DNA Deaminase APOBEC3F

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Abstract

APOBEC3F (A3F) and APOBEC3G (A3G) are DNA cytosine deaminases that potently restrict human immunodeficiency virus type 1 replication when the virus is deprived of its accessory protein Vif (virion infectivity factor). Vif counteracts these restriction factors by recruiting A3F and A3G to an E3 ubiquitin (Ub) ligase complex that mediates their polyubiquitination (polyUb) and proteasomal degradation. While previous efforts have identified single amino acid residues in APOBEC3 proteins required for Vif recognition, less is known about the downstream Ub acceptor sites that are targeted. One prior report identified a cluster of polyubiquitinated residues in A3G and proposed an antiparallel model of A3G interaction with the Vif–E3 Ub ligase complex wherein Vif binding at one terminus of A3G orients the opposite terminus for polyUb [Iwatani et al. (2009). Proc. Natl. Acad. Sci. USA, 106, 19539–19544]. To test the generalizability of this model, we carried out a complete mutagenesis of the lysine residues in A3F and used a complementary, unbiased proteomic approach to identify Ub acceptor sites targeted by Vif. Our data indicate that internal lysines are the dominant Ub acceptor sites in both A3F and A3G. In contrast with the proposed antiparallel model, however, we find that the Vif-dependent polyUb of A3F and A3G can occur at multiple acceptor sites dispersed along predicted lysine-enriched surfaces of both the N- and C-terminal deaminase domains. These data suggest an alternative model for binding of APOBEC3 proteins to the Vif–E3 Ub ligase complex and diminish enthusiasm for the amenability of APOBEC3 Ub acceptor sites to therapeutic intervention.

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Introduction

Human APOBEC3F (A3F) and APOBEC3G (A3G) are DNA cytosine deaminases capable of inhibiting human immunodeficiency virus type 1 (HIV-1) reverse transcription and integration, most prominently through their active C-terminal deaminase domains, which introduce massive levels of G-to-A mutations in the nascent provirus that contribute to incomplete reverse transcription and render hypermutated genomes hypofunctional (reviewed in Refs. 1–3). To achieve this restriction activity, A3F and A3G must encapsidate in producer cells during viral budding, but HIV-1 typically circumvents this inhibitory APOBEC3 (A3) activity by utilizing its accessory protein Vif (virion infectivity factor) as a substrate receptor to link A3F and A3G to an E3 ubiquitin (Ub) ligase complex consisting of CBFβ, ELOB and ELOC, CUL5, and RBX2, which results in the polyubiquitination (polyUb) and subsequent proteasomal degradation of these restriction factors (see Refs. 4 and 5 and references therein).

Much effort has been devoted to identifying the determinants of the Vif–A3 interaction critical for this
degradative process, including a variety of changes in Vif that result in the functional inactivation of its anti-A3 activity (e.g., Refs. 6 and 7; reviewed in Refs. 3 and 8). On the A3 side of this direct, host–pathogen interaction, initial efforts suggested that the Vif binding sites in A3F and A3G may be structurally distinct, occurring in the C-terminus of the former and in the N-terminus of the latter at unrelated residues. 9–15 However, independent studies indicated that these single amino acid determinants of Vif recognition typically occur within a common region of a given susceptible A3 deaminase domain centered on the predicted α helix, suggesting that a conserved structural determinant may be targeted by Vif (DPD128–130 in A3G, 9–12,14,15 E324 and E289 in A3F, 16,17 and D/E121 in A3H, 18 as well as multiple residues of a distinct region recently described in A3C, A3D, and A3F 19).

Less is known about the downstream Ub acceptor sites targeted for polyUb during the degradation process. Iwatani et al. have previously reported that four lysines in the C-terminus of A3G are the Ub acceptor sites required for the Vif-mediated degradation of this enzyme. 20 Combined with the aforementioned studies localizing Vif interaction to the N-terminal half of A3G, this led to the proposal of an antiparallel model of A3 binding to the Vif–E3 Ub ligase complex wherein Vif interacts with one deaminase domain, thereby orienting the second domain for polyUb by an activated E2–Ub conjugate at the opposite end of the CUL5 scaffold.

To test this model and potentially enhance our understanding both of A3 binding to the Vif–E3 Ub ligase complex and of how these substrate acceptor sites might be utilized to block the degradation of A3 proteins, we set out to define the sites of polyUb in A3F. Consistent with results previously reported by Iwatani et al., we find that internal lysines are the dominant Ub acceptor sites in both A3F and A3G. Analysis of the specific residues available for functional polyUb, however, reveals that these are dispersed throughout both domains of A3F at lysine residues clustered on one side of predicted structural models of the A3F N-terminal and C-terminal deaminase domains, opposite the Vif interaction site in the latter case. Furthermore, mutation of the lysine residues determined by Iwatani et al. to be the sites of polyUb in A3G confers only partial Vif resistance. Consistent with these genetic data, mass spectrometric analysis demonstrates Vif-dependent Ub modification of at least 6 sites in A3F and 10 sites in A3G localized to both the N- and C-terminal deaminase domains of each. We conclude, therefore, that the lysine residues available for Vif-dependent polyUb in human A3 proteins are diverse and therefore unlikely to be leveraged by novel therapeutics. To explain this flexibility, we further propose an alternative model of A3 binding to the Vif–E3 Ub ligase complex.

**Results**

**The sites of Vif-mediated polyUb in A3F are distributed throughout the protein**

The lysine codons in A3F cluster into three linear groups separated by unique EcoRI and BamHI sites. We first used serial mutagenesis to convert each of these groups from K to R. Next, we joined the three regions together to make a panel of K-to-R mutants including a derivative completely devoid of lysines, A3F-19KR, and tested the restriction activity and Vif susceptibility of the resultant proteins in a single cycle of replication (Fig. 1a).

The restriction activity of all A3F mutants was similar to that of the wild-type protein, and the K-to-R conversion of any single linear region resulted in A3F variants with Vif susceptibility similar to that of the wild-type protein as evidenced both by the recovery of infectivity and by the decrease in steady-state A3F levels in the presence of Vif (Fig. 1b). Similarly, the combination of any two linear regions of K-to-R mutants resulted in somewhat more resistant but still notably Vif-susceptible variants of A3F. Only the variant devoid of all lysines, A3F-19KR, was largely resistant to the effects of Vif. Taken together, these data indicate that at least one lysine residue in each linear region is available for Vif-mediated polyUb.

We also noted that the putative Vif-resistant control protein, A3G-4KR, in which the polyUb residues previously described by Iwatani et al. were changed to arginine, was only partially resistant to HIV-1 Vif (Fig. 1b). To confirm this observation, we cotransfected increasing amounts of Vif with a constant amount of A3G, A3G-4KR, a lysine-free variant of A3G (A3G-20KR), or A3G-D128K and assessed the resultant steady-state levels of A3G. While A3G-4KR is indeed partially resistant to Vif as evidenced by enhanced steady-state levels in the presence of Vif in comparison with the wild-type protein, the decrease in A3G-4KR steady-state levels is greater than that observed for A3G-20KR, particularly considering the greater expression levels of the former in the absence of Vif (Fig. 1c). Furthermore, Vif susceptibility is not due to the epitope tag, as A3G and the lysine-to-arginine mutant derivatives reported here use a single, lysine-free V5 epitope. Thus, while the lysine residues identified by Iwatani et al. are important for the degradation of A3G, A3G appears to also contain alternative sites of polyUb that account for the residual sensitivity of A3G-4KR to Vif.

**Multiple internal lysine residues in the A3F N- and C-termini are suitable substrates for Vif-dependent polyUb**

To map the individual lysines in A3F available for polyUb, we reverted each of the 19 R residues of
A3F-19KR back to K and assessed the sensitivity of these mutants to Vif in comparison with the parent A3F-19KR in a single cycle of replication. Seven individual lysine reversions in A3F-19KR—R40K and R52K in Region 1, R209K in Region 2, and R334K, R337K, R355K, and R358K in Region 3—induced a statistically significant increase in infectivity in the presence of Vif over the parent lysine-free variant (Fig. 2a–c). In addition to these seven residues, it is possible that others in each region might also be functional targets since we noted some variability from experiment to experiment in which R-to-K changes appeared to sensitize A3F-19KR to Vif, the extent of which is indicated by the associated error bars. For example, A3F-19KR R185K appeared Vif-susceptible in the experiment from which the western blots shown in Fig. 2b derived but failed to yield a statistically significant increase in infectivity over A3F-19KR when averaged over three independent experiments. Further examples of this variability are shown in Supplementary Fig. 1, where we have provided the infectivity in the absence or presence of Vif for Region 1 mutants from each of the three experiments averaged in Fig. 2a. This implies that, despite the preferential targeting of certain residues in A3F, the process of Vif-mediated polyUb may be sufficiently promiscuous to find alternative sites with lower efficiency when preferred options are not available. Such a semi-stochastic character is consistent with the distribution of more consistently targeted residues throughout both the N- and C-termini of A3F as well as the generally more efficient degradation of control mutants in which the lysine residues in all but one linear region have been changed to arginine, yielding six or seven potential targets of polyUb in that region rather than the one found in associated individual revertants. The degradative Vif-mediated polyUb of A3F is therefore not a structurally fixed Ub event such as those associated with regulatory functions or that previously described for A3G.20–25 Rather, it may be more accurately described as a flexible sampling of available substrates wherein at least seven residues throughout both the N- and C-termini of A3F can be polyubiquitinated despite binding of Vif at the protein C-terminus13,16,17,19,26 (see Discussion).

Mass spectrometric identification of lysine acceptor sites in A3F and A3G

Previous analyses have relied exclusively on genetic and biochemical techniques for the determination of Ub sites in A3G.20–25 To acquire direct, relatively unbiased biophysical evidence for Ub of the lysine residues identified as functional targets in A3F and to determine whether sites in A3G beyond those previously identified might be modified by Ub, we subjected A3F and A3G to Ub remnant profiling, a technique whereby a monoclonal antibody specific
for the K-GG motif characteristic of trypsinized Ub peptides is used to immunoprecipitate the Ub proteome in a cell lysate prior to mass spectrometric analysis. Peptides harboring Ub on residues 52, 234, 334, 352, 355, and 358 of A3F were highly enriched in the presence of Vif, indicating substantial modifications at the A3F C-terminus despite the binding of Vif to the same end of the protein (Fig. 3a and Supplementary File 1). Moreover, despite a few minor discrepancies in the specific acceptor sites implicated by the mass spectrometric and genetic data sets, the results of these approaches largely overlap and collectively reinforce the notion that the modification of A3 proteins is not restricted to a structurally rigid subset of lysine acceptor sites (see Discussion).

For A3G, peptides corresponding to ubiquitination of five N-terminal and five C-terminal residues were enriched in the presence of Vif (Fig. 3b and Supplementary File 2). These data again implicate residues of both the N- and C-termini as Ub acceptor sites and are further consistent with the inability of K-to-R mutations at the residues previously identified by Iwatani et al. to render A3G fully resistant to Vif (Fig. 1b and c). Importantly, like the variation observed in the genetic analysis of single K-to-R revertants in A3F-19KR, we found that the exact repertoire of modified sites as determined by mass spectrometry differed slightly from experiment to experiment. For example, our previous, unpublished analysis of A3G by this same technique identified modification only at residues 297 and 303 among the four residues reported by Iwatani et al. while also finding no modification at residue 63 (Fig. 3b and see Discussion).

**Lysine residues in A3F and A3G cluster at distinct predicted surfaces**

To determine whether the susceptibility patterns observed in Figs. 2 and 3 might have a structural

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Fig. 2. Multiple internal lysine residues in A3F are suitable substrates for functional Vif-dependent polyUb. (a–c) Single-cycle infectivity of individual single lysine revertants in an A3F-19KR background in the absence or presence of Vif where data represent the mean and SEM of three independent experiments with associated western blots showing producer cell steady-state levels of Vif-HA and A3-V5 derived from one of these experiments. Statistics represent two-way ANOVA with Dunnett’s post-test comparing the infectivity recovery of each single amino acid revertant (Vif+/Vif−) to that of the A3F-19KR control. ⁎⁎⁎p<0.01; ⁎⁎p<0.05; ⁎p<0.01. Controls that appear in multiple panels of this figure [e.g., A3F in (a), (b), and (c)] are regraphed and rebotted for visual comparison with the mutants of each individual region; all data shown in this figure are the result of one large experiment repeated three times and presented visually as three parts.
The coordination motifs of N- and C-terminal deaminase domains are indicated by boxes. Zinc-ligand residues, however, we sought to create variants that would be predicted to be resistant to N-terminal modification. We therefore indicated that the A3 N-terminal residue is not a major target of Vif function.

**Discussion**

We present here genetic and biophysical evidence for the polyUb of multiple internal lysines distributed throughout both the N- and C-termini of A3F and A3G (Figs. 1–3). The flexibility of the Vif–E3 ligase complex to promote the polyUb of A3 proteins at a wide range of acceptor sites is consistent with an active sampling of A3 lysines by the associated E2–Ub conjugate. Such a sampling model is further consistent with the observation that single R-to-K reversions in A3F-19KR context are generally less efficient in sensitizing A3F-19KR to Vif relative to control mutants in which all the available substrates of a given region are lysines, particularly in Region 1.
This relatively stochastic and indiscriminate process makes intuitive sense since the default mode for Vif should be to rapidly degrade A3 proteins with no apparent need for tight regulation of the kind mediated by more selective Ub events.\textsuperscript{21–25} Consistent with the promiscuous modification of A3F lysines, we observe that mutation of the residues previously reported by Iwatani \textit{et al.} as the sole functional targets of Vif-mediated polyUb in A3G renders the protein only partially Vif-resistant, while many N- and C-terminal lysines in A3G are modified in the presence of Vif (Figs. 1b and c and 3b; compare also the infectivity recovery in the presence of Vif associated with A3G-4KR in Fig. 1b versus that associated with A3G-20KR in Fig. 5b). We therefore think it likely that the antiparallel model for A3 polyUb originally proposed and depicted schematically in\textit{Fig. 6a}, it is more likely that A3 proteins bind Vif in an angled or perpendicular orientation that would expose to activated E2–Ub the entirety of the lysine-rich surfaces predicted to be opposite the Vif binding sites in A3F and A3G (Fig. 6b). It is also possible that multimeric forms of A3 proteins or of the E3 Ub ligase complex might yield results similar to ours, although we have no evidence to directly support such a model. Regardless, while we agree that the four lysines initially identified by Iwatani \textit{et al.} are important substrates for polyUb in A3G, our data suggest that other sites can also be modified, including sites in the N-terminal half of A3G. Moreover, it is clear that both N- and C-terminal residues of A3F can be modified. If these observations are each accurate, then the binding model shown in\textit{Fig. 6a} cannot account for all of the data, while that shown in\textit{Fig. 6b} can.

\begin{figure}[h]
\centering
\includegraphics[width=\linewidth]{fig4.png}
\caption{Lysines in the N- and C-termini of A3F and A3G cluster at distinct predicted surfaces. (a) A model of the A3F N-terminal deaminase domain is shown rotated 180° about the y-axis. (b) A model of the A3F C-terminal deaminase domain is shown rotated 180° about the y-axis. (c) A previously described model of full-length A3G is shown rotated 180° about the \textit{y}-axis.\textsuperscript{31} Orange indicates residues implicated by both genetic and biophysical experiments, while yellow indicates residues implicated by one or the other. A3G residues implicated by Iwatani \textit{et al.} and also identified in Fig. 3b are orange in (c), while additional residues not implicated by Iwatani \textit{et al.} are yellow. Lysine residues not significantly implicated by either data set are gray, while Vif interaction residues are colored red.\textsuperscript{16,17}}
\end{figure}
Alternatively, the ease with which Vif can degrade A3F mutants with one or more linear regions available for polyUb contrasted with the prominent albeit incomplete Vif resistance of A3G-4KR may imply differential binding of Vif to A3F versus A3G. By extension, this may lead to differential availability of acceptable lysine substrates for polyUb. Such a view could be consistent with studies genetically mapping the A3F/G and Vif binding sites in each protein, which suggest that different regions of Vif interact with different regions of A3F versus A3G (reviewed in Ref. 8). Whatever binding model one favors, then, the central question remains one of accessibility.

We noted that there was some variability in which specific R-to-K reversions in A3F-19KR sensitized the protein to Vif from experiment to experiment, while linear regional mutants with multiple side chains available for polyUb were consistently Vif-sensitive (Figs. 1 and 2 and Supplementary Fig. 1). Similarly, independent, unbiased mass spectrometric analyses of A3G indicated some variation in the specific residues modified. For example, focusing just on the four residues functionally implicated by Iwatani et al., residues 297, 303, and 334 were identified in one experiment (Fig. 3b), while only residues 297 and 303 were identified in a second and neither experiment produced any evidence for the modification of residue 301. We interpret these data to mean that the Vif-mediated polyUb of A3 proteins is a semi-stochastic affair in which the associated E2–Ub conjugate is able to sample multiple available side chains for polyUb. As a result, changing the residues most efficiently targeted for modification may simply force the modification of less efficiently targeted side chains, consistent with data from other fields indicating that components of the E3 Ub ligase complex may display substantial structural flexibility.

Similarly, there were several discrepancies between the specific residues likely modified according to genetic versus biophysical approaches (Figs. 2 and 3). Three A3F lysines—K40, K209, and K337—were found to be significantly targeted in the genetic

![Fig. 5. Changes at the A3 N-terminus do not alter Vif susceptibility. (a and b) Single-cycle infectivity experiments demonstrate the sensitivity of A3F, A3G, and lysine-free variants thereof to Vif when the second amino acid is altered as shown. Infectivity data represent the mean and SEM of four independent experiments.](image)

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![Fig. 6. An alternative model of A3 binding to the Vif–E3 ligase complex. (a) The antiparallel model previously proposed by Iwatani et al. in which binding of Vif at one deaminase domain orients an A3 protein for polyUb at its second deaminase domain. (b) An alternative, angled/perpendicular model for A3F binding to the Vif–E3 ligase complex in which binding of Vif to a lysine-poor surface orients the lysine-rich surfaces of A3F for polyUb.](image)
data but were not identified by mass spectrometry, while the opposite was true of K234. This may reflect the fact that the wild-type protein used for mass spectrometry simply has more residues available for polyUb and that, consequently, the wild-type protein is preferentially modified at those residues common to the genetic and mass spectrometric data sets. Alternatively, the structures of A3F and A3F-19KR may differ slightly despite their similar restriction activities (Figs. 1 and 2). It is also possible that further experiments may find additional residues modified that are not apparent in the data presented here, as we have observed with A3G. Regardless, the overarching message remains clear: many residues in both the N- and C-terminal domains of both A3F and A3G are suitable substrates for polyUb.

In summary, we report here that the Ub acceptor sites in A3F and A3G are distributed throughout each protein, suggesting that the conjugated E2 enzyme(s) recruited by the Vif–E3 ligase complex are more flexible in their substrate targeting potential than previously proposed and that blocking the modification sites themselves will not be a viable strategy for the therapeutic stabilization of A3 proteins. Of note, the crystal structure of A3C has recently been solved, an effort that further included extensive genetic identification of the Vif interaction surface in A3C. These authors further determined that the residues important for Vif interaction with A3C are conserved in A3F. With a handful of exceptions, mostly notably those residues corresponding to A3F K352, K355, and K358, there is little linear conservation of lysine residues between A3C and A3F (data not shown). On comparing the mapped Vif interaction surface with the available lysine residues, however, it appears that the theme of Vif binding at a lysine-poor surface distinct from available polyUb sites holds true in this single-domain A3 protein. It will be interesting to find whether the apparent clustering of lysines at surfaces distinct from those at which Vif interacts is a general feature of the A3–Vif interaction. It may be that the positively charged Vif protein achieves efficient degradation of A3 proteins, in part, by binding to negatively charged regions of susceptible deaminase domains such as the α4 helix, thereby positioning distinct, lysine-rich surfaces for efficient polyUb in the context of the fully assembled E3 Ub ligase complex.

Materials and Methods

Plasmids

Wild-type A3F and A3G coding sequences are identical with those found in GenBank entries NM_145298 and NM_021822 and previously reported. A3 proteins were expressed from pcDNA3.1-derived vectors with a C-terminal V5 tag in all V5 constructs except the Vif interaction mutants A3F QE323-324EK and A3G D128K, however, the inherent tag lysine was mutated to arginine to prevent artifactual tag Ub such as that previously described. K-to-R mutants were made by sequential site-directed mutagenesis and subcloning; A3G-20KR was graciously provided by Dr. Yong-Hui Zheng and cloned into our lysine-free V5 vector. The HIV-1 Vif-deficient IIIB Vif-XX proviral construct and IIIB Vif-HA expression construct were as previously described. All constructs were verified by restriction digestion and sequencing.

Cell lines

HEK293T cells were maintained in Dulbecco’s modified Eagle medium supplemented with 10% fetal bovine serum (FBS) and penicillin–streptomycin. CEM-GFP reporter cells were obtained from the AIDS Research and Reference Reagent Program and maintained in RPMI medium supplemented with 10% FBS, penicillin–streptomycin, and β-mercaptoethanol.

Single-cycle infectivity protocol

Single-cycle infectivity experiments were carried out as previously described. A total of 250,000 HEK293T cells were plated into 2 mL of supplemented Dulbecco’s modified Eagle medium in 6-well plates. The following day, cells were transfected with 200 ng of either a vector control or an A3-V5 expression construct, 100 ng of a Vif-HA expression construct, and 1.6 μg of replication-competent, Vif-deficient HIV-1IIIB provirus using TransIT transfection reagent (Mirus Bio). Two days after transfection, transfected cells were harvested and lysed as described above, and virus-containing supernatants were filtered through 0.45-μm filters and used to infect CEM-GFP cells in 96-well plates. Three days post-infection, target CEM-GFP cells were fixed with 4% paraformaldehyde and analyzed by flow cytometry for viral infectivity on a FACSCanto flow cytometer (BD Biosciences).

Vif titration experiments

Cells were transfected as in single-cycle infectivity experiments above but with 200 ng of A3-V5 expression construct, 50–200 ng of Vif-HA expression construct balanced to 200 ng total with a Vif expression vector, and 600 ng of pcDNA3.1 (Invitrogen) vector DNA for a total of 1 μg per well. Two days post-transfection, cells were harvested as described above and analyzed by western blot as described below.

Western blot analysis

HEK293T cells transfected as described above were washed in phosphate-buffered saline (PBS) and lysed in 250 μL of a lysis buffer composed of 25 mM Hepes (pH 7.4), 150 mM NaCl, 1 mM MgCl2, 50 μM ZnCl2, 10% glycerol, and 1% Triton X-100 and supplemented with 50 μM MG132 and complete protease inhibitor (Roche). A
5 x sample buffer consisting of 62.5 mM Tris (pH 6.8), 20% glycerol, 2% sodium dodecyl sulfate, 5% β-mercaptoethanol, and 0.05% bromophenol blue was added to each cell lysate to a 2 x concentration, and the mixture was boiled for 5–10 min and subjected to fractionation by 10% SDS-PAGE and transfer to polyvinylidene difluoride membranes. Primary antibodies utilized include mouse anti-V5 (Invitrogen), mouse anti-HA.11 (Covance), and mouse anti-tubulin (Covance). Between probing with different primary antibodies, membranes were stripped with 62.5 mM Tris (pH 6.8), 2% SDS, and 100 mM β-mercaptopethanol at 50 °C and washed in PBS 0.01% Tween.

**Mass spectrometry**

HEK293T cells were labeled using a SILAC approach. Cells were cultured in either "light" SILAC media containing the normal complement of amino acids or "heavy" SILAC media wherein lysine was replaced with 13C6-lysine. FBS was dialyzed in both light and heavy media formulations to remove free unlabeled amino acids. Four 15-cm plates of HEK293T cells cultured in heavy media each were transfected with 2.5 μg of either A3F-V5 or A3G-FLAG. An additional four 15-cm plates of HEK293T cells cultured in heavy media each were also transfected with 2.5 μg of pcDNA4 vector and 2.5 μg of either A3F-V5 or A3G-FLAG. Cells were detached from the plate with 10 mM ethylenediaminetetraacetic acid in PBS, spun down, and snap frozen. The frozen cell pellets were lysed in buffer containing 8 M urea, 0.1 M Tris (pH 8.0), 150 mM NaCl, and a combination of protease inhibitors (Complete tablet, Roche). Protein concentration was measured by Bradford assay (QuickStart 1 x Reagent, Bio-Rad). Fifty milligrams of protein lysate from equal portions of light and heavy culture conditions for A3F-V5 or A3G-FLAG, respectively, were combined and then subjected to reduction with 4 mM TCEP for 30 min at room temperature, alkylation with 10 mM iodoacetamide for 30 min at room temperature in the dark, and overnight digestion with 250 μg of trypsin (Promega) at room temperature. Treated lysates were subsequently desalted using SepPak C18 cartridges (Waters), lyophilized for 2 days, and immunoprecipitated using an antibody specific for the K-GG motif characteristic of trypsinized, Ub-modified peptides (UbiScan, Cell Signaling Technology). Immunoprecipitates were then desalted using C18 STAGE tips (ThermoScientific), evaporated, and analyzed in duplicate with a 2-h gradient on an Orbitrap Elite Mass Spectrometer (Thermo Scientific). The reverse-phase gradient was delivered by an Easy nLC 1000 liquid chromatography system (ThermoScientific) from 5% to 30% acetonitrile in 0.1% formic acid. Columns used were a 100 μm x 2 cm pre-column packed with 5 μm ReproSil Pur C18 particles and a 75 μm x 10 cm analytical column packed with 2 μm ReproSil Pur C18 particles (Thermo Scientific). The Orbitrap Elite continuously collected data in data-dependent acquisition mode, acquiring a full scan in the orbitrap at 120,000 resolution followed by collision-induced fragmentation of the top 20 most intense peaks from full scan in the ion trap. Dynamic exclusion was enabled to exclude repeated fragmentation of peaks for 30 s. Charge state screening was enabled to reject fragmentation of unassigned or singly charged species. Results were analyzed using the MaxQuant software package.

**Homology modeling of the A3F N- and C-terminal deaminase domains**

Modeling of the A3F CTD has been described previously. The A3F NTD model including residues 1–190 was generated using YASARA with the crystal structure of A3G191–384 2K3A (Protein Data Bank ID: 3IR2) as a template. Alignment with the template sequence was iteratively optimized using SwissProt and TrEMBL sequences, the predicted secondary structure, and the three-dimensional structure of the template. Refinement of the model was carried out using knowledge-based and electrostatic interactions in unrestrained molecular dynamics with explicit solvent molecules. Insertions were accounted for by searching the Protein Data Bank for superimposable loop ends with model anchor points and optimized for energy minimization. Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.jmb.2013.01.010

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**Keywords:**

APOBEC3F; APOBEC3G; HIV; Vif; ubiquitin

**Abbreviations used:**

A3F, APOBEC3F; A3G, APOBEC3G; HIV-1, human immunodeficiency virus type 1; Vif, virion infectivity factor; Ub, ubiquitin; polyUB, polyubiquitination; FBS, fetal bovine serum; PBS, phosphate-buffered saline.
References


