Structural insights into non-covalent ubiquitin activation of the cIAP1–UbcH5B–ubiquitin complex

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Ubiquitin (Ub)-conjugating enzymes and Ub ligases control protein degradation and regulate many cellular processes in eukaryotes. Cellular inhibitor of apoptosis protein-1 (cIAP1) plays a central role in apoptosis and tumor necrosis factor signaling. It harbors a C-terminal RING domain that homodimerizes to recruit E2–Ub (where ~ denotes a thioester bond) complex to catalyze Ub transfer. Noncovalent Ub binding to the backside of the E2 Ub-conjugating enzyme UbcH5 has previously been shown to enhance RING domain activity, but the molecular basis for this enhancement is unclear. To investigate how dimeric cIAP1 RING activates E2–Ub for Ub transfer and what role noncovalently bound Ub has in Ub transfer, here we determined the crystal structure of the cIAP1 RING dimer bound to both UbcH5B covalently linked to Ub (UbcH5B–Ub) and a noncovalent Ub to 1.7 Â resolution. The structure along with biochemical analyses revealed that the cIAP1 RING domain interacts with UbcH5B–Ub and thereby promotes the formation of a closed UbcH5B–Ub conformation that primes the thioester bond for Ub transfer. We observed that the noncovalent Ub binds to the backside of UbcH5B and abuts UbcH5B’s α1β1-loop, which, in turn, stabilizes the closed UbcH5B–Ub conformation. Our results disclose the mechanism by which cIAP1 RING dimer activates UbcH5B–Ub and indicate that noncovalent Ub binding further stabilizes the cIAP1–UbcH5B–Ub complex in the active conformation to stimulate Ub transfer.

Post-translational modification of proteins by ubiquitin (Ub),2 achieved via the sequential actions of Ub-activating enzyme (E1), Ub-conjugating enzyme (E2), and Ub-ligase (E3), governs vast arrays of eukaryotic cellular processes (1, 2). E1 activates and transfers the C terminus of Ub to the E2’s catalytic cysteine to produce an E2–Ub thioester intermediate (where ~ denotes a thioester bond). E3 binds E2–Ub and substrate to promote Ub transfer from E2 to a nucleophile, which is usually a lysine side chain. There are three major types of E3s: RING, HECT, and RING-in-between-RING (RBR) (3, 4). RING E3s harbor a RING domain that binds and activates E2–Ub to promote the direct transfer of Ub from E2 to the substrate. In contrast, HECT E3s contain a catalytic cysteine and catalyze a two-step Ub transfer reaction in which Ub is initially transferred from E2 to HECT E3’s catalytic cysteine and then to the substrate. RBR E3s share common features from both RING and HECT E3s, where a RING-like domain (RING1) recruits E2–Ub and transfers Ub to the catalytic cysteine on RING2 prior to transfer to substrate.

Cellular inhibitor of apoptosis protein-1 (cIAP1) is a RING-type E3 and belongs to the inhibitor of apoptosis (IAP) family of proteins. The RING-mediated ubiquitin ligase activity of cIAP1 is essential for its function in both cell death and survival pathways. In cell death pathways, cIAP1 inhibits apoptosis by sequestering and ubiquitinating second mitochondria-derived activator of caspase (SMAC) for degradation by the proteasome, thereby freeing XIAP to bind and inhibit caspases (5–7). Moreover, cIAP1 has been shown to target caspases for ubiquitination and degradation by the proteasome (8). In the cell survival pathway, tumor necrosis factor receptor 1 signaling complex recruits RIP kinase 1 (RIPK1) and various adaptor proteins, including TRADD, TRAF2, and TRAF5, that lead to the recruitment of cIAP1 and cIAP2 (9). cIAP1 and cIAP2 ubiquitinate RIPK1 and components within this complex to enable the recruitment of a linear Ub chain assembly complex that ultimately activates NF-κB signaling (10–16).

cIAP1 contains three N-terminal baculoviral IAP repeat domains (BIR1–3), followed by a Ub-associated domain (UAB), a caspase-recruiting domain (CARD), and a C-terminal RING domain. Dimerization of its C-terminal RING domain is important for E2–Ub recruitment and ligase activity (17, 18). Studies showed that the N-terminal BIR3–UAB–CARD domain sequesters the RING domain in an inactive conformation to prevent
RING dimerization (19, 20). The addition of SMAC or SMAC mimic induces conformational changes that restore activity by allowing RING dimerization (19, 21). Currently, how RING dimerization activates cIAP1’s ligase activity, and the structure of cIAP1 RING domain bound to E2–Ub, are not known. However, there are several structures of RING E3s bound to E2 covalently linked to Ub (E2–Ub; en dash denotes covalent linkage) (22–32). Collectively, these structures show that the RING domain binds and stabilizes E2–Ub in a closed conformation such that the thioester bond is optimized for UbcH5B transfer (33). For dimeric RING E3s, such as BIRC7, an IAP family protein, the C-terminal tails of each subunit of the RING dimer function to stabilize the closed E2–Ub conformation to enhance ligase activity (23). It seems likely that cIAP1 RING dimer utilizes a similar mechanism for activating E2–Ub.

cIAP1 has been shown to function with the UbcH5 family of E2s to catalyze substrate ubiquitination (34, 35). This family of E2s has a noncovalent Ub binding site on its backside. This backside Ub–UbcH5 interaction is important for processivity of poly-Ub chain formation (25, 36–39). Our recent structural study on the monomeric RING E3 RNF38 showed that backside-bound Ub (Ub$^B$) stimulates RNF38-catalyzed Ub transfer by restricting the flexibility of UbcH5B’s o1 and o1β1-loop to stabilize the closed active RNF38–UbcH5B–Ub complex, thereby enhancing the rate of catalysis (25). It remains unclear whether this mechanism is conserved for dimeric RING E3s.

To better understand how dimeric cIAP1 RING domain (cIAP1R) activates E2–Ub for Ub transfer and how Ub$^B$ could influence this process, we present a crystal structure of cIAP1R bound to UbcH5B–Ub and Ub$^B$. Structural and biochemical analyses showed that cIAP1R forms multiple contacts with UbcH5B–Ub to stabilize it in a closed conformation. Notably, the C-terminal tail of cIAP1R functions in trans to stabilize the closed UbcH5B–Ub conformation, thereby explaining the importance of RING domain dimerization, and consistent with prior examples of dimeric RING E3s. Last, Ub$^B$ restrains UbcH5B’s o1β1-loop conformation to stabilize contacts with donor Ub (i.e. Ub conjugated to UbcH5B; hereafter Ub$^A$). This interaction augments stabilization of the closed UbcH5B–Ub conformation, thereby enhancing Ub transfer. Our results reveal a conserved Ub$^B$-stimulatory mechanism for both monomeric and dimeric RING E3s in mediating UbcH5B–Ub transfer.

Results

Ub$^B$ stimulates cIAP1R-mediated Ub transfer

Previously, we showed that the addition of UbΔGG (lacking the C-terminal diglycine motif) can serve as Ub$^B$ and bind to UbcH5B’s backside to stimulate UbcH5B–Ub discharge catalyzed by the monomeric RING E3 RNF38 and dimeric RING E3 XIAP. To assess whether Ub$^B$ can exert similar effects on cIAP1R-catalyzed Ub transfer, we performed single-turnover lyse discharge assays using WT and S22R UbcH5B. S22R substitution abrogates the Ub$^B$–UbcH5B interaction and was therefore used as a control (25, 36). UbcH5B variants were pre-charged with equimolar concentrations of 32P-Ub and then chased by the addition of cIAP1R alone and in the presence of UbΔGG, which cannot be charged by E1 but can still bind to the backside of UbcH5B WT. The addition of 300 μM UbΔGG stimulated the discharge of UbcH5B–Ub but had no effect on UbcH5B S22R–Ub (Fig. 1A), indicating that Ub$^B$ stimulates cIAP1R-catalyzed Ub transfer.

Synergistic binding enhancement between Ub$^B$, cIAP1R, and UbcH5B–Ub

Our prior study showed that Ub$^B$ stimulates RNF38 and XIAP-catalyzed Ub transfer by enhancing RING E3 affinity for UbcH5B–Ub by ~5–10-fold (25). To determine whether Ub$^B$ functions in a similar manner to stimulate cIAP1R-catalyzed Ub transfer, we performed surface plasmon resonance (SPR) experiments to investigate the effects of Ub$^B$ on cIAP1R’s affin-
Activation of UbcH5B—Ub by cIAP1 and non-covalent ubiquitin

**Table 1**

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<tr>
<th>Immobilized protein</th>
<th>Analyte</th>
<th>Kd (µM)</th>
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<tr>
<td>GST-cIAP1R</td>
<td>UbcH5B</td>
<td>223 ± 4</td>
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<tr>
<td>GST-cIAP1R</td>
<td>UbcH5B—Ub</td>
<td>0.83 ± 0.05</td>
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<tr>
<td>GST-cIAP1R</td>
<td>UbcH5B—Ub + 0.6 mM UbDAG</td>
<td>0.22 ± 0.01</td>
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<tr>
<td>GST-cIAP1R</td>
<td>UbcH5B S22R, F62A, P95D—Ub</td>
<td>0.90 ± 0.01</td>
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<tr>
<td>GST-cIAP1R</td>
<td>UbcH5B S22R, F62A, P95D—Ub + 0.6 mM UbDAG</td>
<td>0.99 ± 0.05</td>
</tr>
<tr>
<td>GST-UbcH5B</td>
<td>UbcH5B—Ub + excess cIAP1R</td>
<td>13 ± 2</td>
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**Table 2**

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<th>Data collection and refinement statistics</th>
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<td><strong>cIAP1R-UbcH5B—Ub—UbB complex</strong></td>
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*Values in parenthesis are for the highest-resolution shell.

ity for UbcH5B—Ub. We generated stable UbcH5B—Ub complex by mutating UbcH5B’s catalytic cysteine (Cys65) to lysine, thereby forming a stable amide linkage that mimics the thioester linkage (22). UbcH5B C85K and UbcH5B S22R C85K covalently linked to Ub (hereafter referred to as UbcH5B—Ub and UbcH5BS22R—Ub, respectively) were generated to assess the effect of backside binding. cIAP1R exhibited weak binding affinity for UbcH5B—Ub (Table 1 and Fig. S1), suggesting that this binding synergy of cIAP1R, we performed single-turnover lysine discharge assays using 20 µM UbDAG, which is just above the Kd of 13 µM, and showed that it was sufficient to stimulate cIAP1R-catalyzed Ub transfer (Fig. 1B). Furthermore, we showed that UbcH5B S22R, F62A, P95D—Ub, a stable isopeptide conjugate that cannot bind RING E3 or UbB but can serve as the UbB source (25), also stimulated cIAP1R-catalyzed Ub transfer at 20 µM (Fig. 1B).

**Overall structure of cIAP1R-UbcH5B—Ub—UbB complex**

To gain insight into how UbB enhances cIAP1R-mediated UbcH5B—Ub transfer, we crystallized and determined the structure of cIAP1R bound to UbcH5B—Ub and UbB. The cIAP1R-UbcH5B—Ub—UbB complex crystals belong to space group C21 with one copy of cIAP1R-UbcH5B—Ub—UbB complex in the asymmetric unit. The structure was refined to a resolution of 1.7 Å (Table 2). Because cIAP1 exists as a biological homodimer via the RING domain (6, 18, 40), we used crystallographic symmetry to generate the structure of dimeric cIAP1R-UbcH5B—Ub—UbB complex (Fig. 2). The structure shows that cIAP1R dimerizes via the RING domain, the C-terminal tail, and a helix that precedes the RING domain similar to other IAP family RING E3s, such as cIAP2, XIAP, and BIRC7 (17, 23, 41). cIAP1R’s RING domain binds both UbcH5B and UbB and stabilizes the UbcH5B—Ub complex in a closed conformation. Additionally, the C-terminal tail of the second subunit in the cIAP1R dimer packs against UbD in trans to stabilize the closed UbcH5B—Ub conformation. These features are similar to those observed in other structures of dimeric RING E3-E2—Ub complexes, such as BIRC7, RNF4, and MDM2-MDMX (22, 23, 30). In our structure, UbB binds to the backside of UbcH5B centering on the Ser222 surface, as reported previously (25, 36).
subtle differences in UbcH5B-RING domain contacts (Fig. 3B). Similar E2 shifts were also observed in the structures of TRAF6 (from human)-Ubc13 and TRAF6 (from Danio rerio)-Ubc13–Ub complexes (31, 42). It is unclear whether this E2 movement results from formation of the closed E2–Ub conformation or is due to crystal packing. Nonetheless, the primary RING-E2 interaction is maintained.

Our structure shows that cIAP1R’s C-terminal tail, RING domain, and UbcH5B stabilize the closed UbD conformation. cIAP1R’s C-terminal tail interactions involve Arg614 and Phe616 from the other cIAP1R protomer in the dimer. Arg614 forms a hydrogen bond with the carbonyl oxygen of UbD’s Asp32, and Phe616 packs against UbD’s Gly35 surface (Fig. 4A). This trans tail packing arrangement is similar to those observed in the structures of BIRC7, RNF4, and MDM2-MDMX bound to UbcH5–Ub (22, 23, 30). These RING E3s all contain a Phe or Tyr corresponding to Phe616 on cIAP1R that disrupted ligase activity when substituted with histidine or alanine. Likewise, substitution on the corresponding Phe in cIAP2 also disrupted activity (17, 23). To determine the importance of this residue, we mutated cIAP1R’s Phe616 to His and performed lysine discharge assays to assess the effect on Ub transfer. cIAP1R F616H was defective in discharging UbcH5B–Ub (Fig. 4B), consistent with an earlier study showing that deletion of cIAP1’s C-terminal residues abrogates activity (20). Thus, the trans tail–UbD interaction explains the importance of RING domain dimerization.

The cIAP1R-UbD interactions primarily involve His588, Ile604, and Cys605 from cIAP1R’s RING domain contacting Leu8 of UbD.
and Ile36 patches of UbD. Crucially, cIAP1R’s Arg606 forms hydrogen bonds with the carbonyl oxygen of Arg72 and the side chain of Gln40 from UbD and the carbonyl oxygen of Gln92 from UbcH5B (Fig. 4A). This Arg606 is commonly known as the “linchpin Arg” (33), and its interaction network is conserved in several structures of RING E3–E2–Ub complexes (22–30). To assess the importance of this interaction in cIAP1R, we generated Ub I36A and cIAP1R R606A and tested their effects in UbcH5B/H11011 Ub discharge assays. Although charging of UbcH5B/H11011 Ub I36A was incomplete, as observed previously (23, 25), in the presence of cIAP1R, UbcH5B/H11011 Ub I36A discharged slower than the WT UbcH5B/H11011 Ub (Fig. 4C). Similarly, cIAP1R R606A was defective in discharging UbcH5B–Ub (Fig. 4B).

The UbD–UbcH5B interaction involves UbD’s Ile44 patch contacting the Ser108 region in UbcH5B’s α2-helix (Fig. 5A). Additional interactions are also observed between Lys18 and Arg42 of UbD and UbcH5B’s Asp42, Lys101, Leu104, and Asp112 (Fig. 5A). To investigate the importance of these interactions, we performed UbcH5B–Ub discharge assays using Ub I44A and UbcH5B S108R. In both cases, cIAP1R-mediated Ub transfer was impaired (Fig. 5B).

The C-terminal tail of UbD is extended and lies along UbcH5B’s active site cleft (Fig. 5C). The C-terminal tail of UbD is stabilized by hydrophobic interactions between UbcH5B’s Ile88 and UbD’s Leu73 and numerous hydrogen bonds involving UbcH5B’s Asn77, Asp87, and Asn114 and UbD’s C-terminal tail. To validate the importance of these interactions, we generated Ub L73D and UbcH5B I88A and assessed their effects in UbcH5B–Ub discharge assays. UbcH5B loaded with Ub L73D and UbcH5B I88A charged with WT Ub were defective in discharge catalyzed by cIAP1R (Fig. 5B). Collectively, our data showed that cIAP1R initiates multiple contacts to stabilize UbcH5B–Ub in the closed conformation to promote Ub transfer similar to other RING E3s (22–32).
**Activation of UbcH5B−Ub by cIAP1 and non-covalent ubiquitin**

UbcH5B binds UbcH5B via the Ile44 hydrophobic patch of UbcH5B and UbcH5B’s β1–3 surface surrounding Ser22 (Fig. 6A). This binding mode resembles other available structures of UbH5 family E2s bound to UbH5 (25, 36, 39, 43). In our structure, UbH5 does not contact cIAP1R or UbD (Fig. 2). In addition to UbcH5B’s Ser22 surface, UbH5 also contacts UbcH5B’s α1β1-loop, which in turn packs against UbD (Fig. 6, A and B). Here, UbH5’s Lys6 and His68 form hydrogen bonds with carbonyl oxygens of UbcH5B’s Pro17 and Pro18, respectively, and Leu8 packs against UbcH5B’s Gln20, thereby placing Gln20 within hydrogen-bonding distance of the backbone amide of UbD’s Gly47 (Fig. 6B). To test the importance of Gln20, we used UbcH5B Q20A to perform cIAP1R-mediated UbcH5B–Ub discharge assays. The discharge of UbcH5B Q20A−Ub in the presence and absence of excess of UbK6A remained similar, suggesting that Gln20 plays an important role in UbH5-mediated stimulation of Ub transfer (Fig. 6C).

Previously, we have determined the structures of a monomeric RING E3, RNF38, bound to UbcH5B−Ub alone and in complex with UbH5 (25). These structures showed that in the absence of UbH5, UbcH5B’s α1β1-loop adopts various conformations that are not optimal for interaction with UbH5. The presence of UbH5 locks UbcH5B’s α1β1-loop into a conformation that helps optimize UbD for transfer (Fig. 6, D and E) (25). Superimposition of the structures of cIAP1R–UbH5B–Ub–UbH5 and RNF38–UbH5B–Ub–UbH5 complexes by overlaying the UbcH5B structure reveals that UbH5 in cIAP1R–UbH5B–Ub–UbH5 rotates by ~10° and shifts by ~1.5–4 Å in different regions across UbH5 (Fig. 6F). Whereas the UbH5 Ile44 and UbcH5B Ser22 interacting interface is largely maintained, UbH5’s β1β2-loop packs more closely to UbcH5B’s α1β1-loop in cIAP1R–UbH5B–Ub–UbH5 (Fig. 6F). In this manner, UbH5’s Lys6 moves closer to UbcH5B’s α1β1-loop and forms an additional hydrogen bond with UbcH5B’s Asp16 located at the C terminus of α1; this interaction was not observed in RNF38–UbH5B–Ub–UbH5 (Fig. 6, B and D). To test the importance of the UbH5 Lys6–UbcH5B Asp16 interaction in UbH5-mediated stimulation of Ub transfer, we generated UbcH5B D16A and K6A and performed cIAP1R-mediated UbcH5B–Ub discharge assays. The discharge of UbcH5B D16A−Ub remained similar in the presence or absence of excess of UbK6A (Fig. 6C), suggesting that UbcH5B’s Asp16 plays a role in UbH5-mediated stimulation of Ub transfer. Correspondingly, the addition of excess UbK6A to precharged UbcH5B–Ub was slower than WT Ub in stimulating cIAP1R-mediated UbcH5B–Ub discharge (Fig. 6G). Thus, the additional contact between UbH5 Lys6 and UbcH5B Asp16 contributes to UbH5-mediated stimulation of Ub transfer. Despite this slight difference, the conformation of UbcH5B’s α1β1-loop is nearly identical in both structures, which further supports our proposed UbH5-stimulatory mechanism, whereby UbH5 binding reorganizes UbcH5B’s α1β1-loop to help stabilize UbD in a conformation primed for transfer.

**Discussion**

The structure of cIAP1R–UbH5B–Ub–UbH5 reported here provides insight into the UbH5-stimulatory mechanism of dimeric RING E3-catalyzed Ub transfer. The cIAP1 RING domain forms a homodimer and utilizes a general mechanism that is shared by other RING E3s to stabilize UbcH5B−Ub in a closed conformation to activate the thioester bond for catalysis (3). UbH5 functions by reorganizing UbcH5B’s α1β1-loop conformation to reinforce UbH5 in the closed conformation, thereby enhancing Ub transfer in a manner consistent with our prior study with the monomeric RING E3 RNF38 (25). Our current work demonstrates that the UbH5-stimulatory mechanism is conserved in both monomeric and dimeric RING E3-catalyzed reactions with the UbcH5 family of E2s.

The closed E2−Ub conformation has been shown to be important for Ub transfer, and the role of the RING domain is to promote the transition to this conformation to enhance the rate of Ub transfer (22, 23, 33, 44, 45). In addition to the established contacts between RING-E2, RING-UbD, and UbD-E2, several RING E3s have evolved different mechanisms to facilitate this process (3). For cIAP1, the RING dimer arrangement enables cIAP1 to utilize the C-terminal tail of the other dimeric cIAP1R protomer to stabilize UbH5. This mechanism is observed in several dimeric RING E3s containing a Phe or Tyr residue in their C-terminal tail, such as BIRC7, RNF4, and MDM2-MDMX (22, 23, 30).

Noncovalent Ub binding to the backside of UbcH5 family E2 has been shown to increase the processivity of Ub transfer (25, 36–39). Mechanistically, we have recently shown that Ub binding improved RING E3’s affinity for the E2−Ub complex and that the RING E3−E2−Ub complex displayed higher affinity for Ub using the monomeric RING E3 RNF38 (25). Here we observed a similar synergistic effect with the dimeric RING E3, cIAP1. We have shown previously that the Kd for the UbH5−UbcH5B interaction was ~280 μM (25). In the presence of the cIAP1R, UbcH5B−Ub complex is primed into the closed conformation, and the Kd for UbH5−UbcH5B binding improved to ~13 μM (Table 1). Our structure showed that the closed UbcH5B−Ub conformation stabilizes UbcH5B’s α1β1-loop, which in turn forms optimal interaction with UbH5 and could explain the drop in Kd. The total cellular Ub concentration is ~20–85 μM, depending on cell type. Within this total concentration, Ub presents as a mixture of monoubiquitinated substrates, free Ub, thioester intermediates of ligation machinery, and poly-Ub chains (46, 47). A previous study (25) and our current study showed that these forms of Ub can serve as sources of UbH5, and hence the total cellular Ub concentration could serve as the guide for the availability of UbH5. The formation of cIAP1–UbcH5B–Ub complex lowers the Kd for the UbH5−UbcH5B interaction to a value in which the UbH5 interaction would be favorable in cells. We anticipate that noncovalent Ub binding would have an impact on cIAP1–UbcH5−catalyzed ubiquitination in cells. In both crystal structures of cIAP1R–UbcH5B–Ub–UbH5 and RNF38–UbcH5B–Ub−UbH5 (25) complexes, UbH5 alters UbcH5B’s α1β1-loop into a nearly identical configuration to buttress UbH5 in the closed conformation. The
subtle differences in Ub^B conformations seen in the two structures could potentially arise from crystal packing. Nonetheless, the clAP1R-UbcH5B–Ub–Ub^B structure presented here provides a more detailed view of how Ub^B could make an additional contact with UbcH5B’s α1 C terminus and α1β1-loop to optimize these elements in stabilizing the closed Ub^D conformation. In conclusion, our work shows that Ub^B serves as an allosteric activator of RING E3-E2–Ub complexes and that the Ub^B-stimulatory mechanism is conserved for both monomeric and dimeric RING E3s.
Experimental procedures

Protein expression and purification

All constructs were expressed in Escherichia coli BL21 (DE3) Gold (Stratagene). All proteins used are from humans unless otherwise specified. cIAP1 RING domain (residues 556-C; cIAP1R) was cloned into pGEX4T1 (GE Healthcare), which contains an N-terminal GST tag followed by a tobacco etch virus protease cleavage site. cIAP1R was purified by GSH affinity chromatography, followed by tobacco etch virus cleavage to release the GST tag. The released GST tag was removed by GSH affinity chromatography, and the cleaved cIAP1R was purified by size-exclusion chromatography, Arabidopsis thaliana Uba1, untagged UbcH5B variants, 32P-Ub, Ub, and Ub lacking the C-terminal diglycine motif (UbΔGG) were prepared as described previously (25). Fluorescently labeled Ub was prepared as described previously (30). UbcH5B–Ub, UbcH5B S22R–Ub, and UbcH5B S22R,F62A,P95D–Ub were generated and purified as described previously (25). Protein concentrations were determined by Bradford assay using BSA as a standard. Ub concentration was determined by measuring the absorbance at 280 nm and the molar extinction coefficient calculated from the protein sequence. Proteins were stored in 25 mM Tris-HCl (pH 7.6), 0.15 M NaCl, and 1 mM DTT at −80 °C.

Crystallization

cIAP1R-UbcH5B–Ub–Ub complex was assembled by mixing cIAP1R (8.5 mg/ml), UbcH5B–Ub (20 mg/ml), and Ub (100 mg/ml) at 1:1:1.2 molar ratio. Crystals were obtained by mixing protein complex with an equal volume of reservoir solution containing 0.2 M ammonium fluoride and 15% (w/v) PEG 3350 using sitting drop vapor diffusion at 19 °C. The crystals were harvested and flash-frozen in 0.2 M ammonium fluoride, 18% (w/v) PEG 3350, and 20% (v/v) ethylene glycol.

Data collection and processing

Data were collected at beamline I03 at Diamond Light Source, processed using xia2 pipeline (48), and integrated with automated XDS (49). Initial phases of cIAP1R-UbcH5B–Ub–Ub complex were obtained by molecular replacement with PHASER (50) using UbcH5B and Ub from PDB entry 3ZNI and cIAP2 RING from PDB entry 3EB6. All models were built in COOT (51) and refined using PHENIX (52). cIAP1R-UbcH5B–Ub–Ub complex was refined to a resolution of 1.7 Å. The final model contains one copy of cIAP1R (chain A, residues 556-C), one copy of UbB (chain B residues 1–74), one copy of UbcH5B (chain C residues 2–147), and one copy of Ub (chain D, residues 1–76). All figure models were generated using PyMOL.

Lysine discharge assays

UbcH5B variant (15 μM) was charged with equimolar Ub variant (15 μM), 32P-Ub (15 μM), or fluorescently labeled Ub (15 μM) in a reaction containing 50 mM Tris-HCl, pH 7.6, 50 mM NaCl, Arabidopsis thaliana Uba1 (1 μM), BSA (1 mg/ml), 5 mM MgCl2, and 5 mM ATP for 15 min at 23 °C as described previously (25). The charged reaction was stopped by adding 0.01 units/ml apyrase and 30 mM EDTA for 2 min at 23 °C. The lysine discharge reaction was initiated by adding a mixture containing 50 mM Tris-HCl, pH 7.6, 50 mM NaCl, BSA (1 mg/ml), l-lysine (20 mM), and cIAP1R variant (0.5 μM) in the presence or absence of UbΔGG (300 μM for Figs. 1A, 4 (B and C), 5B, and 6C; 20 μM for Fig. 1B) or UbcH5B S22R,F62A,P95D–Ub (20 μM; Fig. 1B). WT Ub (300 μM) and K6A Ub (300 μM) were used to perform lysine discharge assays in Fig. 6G. Final concentrations are shown in parenthesis except for UbcH5B and Ub variants, which were ~5 μM. Reactions were quenched with 2× SDS-loading buffer at the indicated time points and resolved by SDS-PAGE and visualized by staining with InstantBlue. Reactions performed using 32P-Ub were dried and visualized using autoradiography. Fluorescently labeled UbcH5#–Ub was visualized by a LI-COR Odyssey scanner, followed by staining with InstantBlue.

SPR

All SPR experiments were performed at 25 °C on a Biacore T200 system with a CM-5 chip. For cIAP1R-UbcH5B and cIAP1R-UbcH5B–Ub variant binding experiments, GST-cIAP1R was coupled to CM-5 chips as described previously (25). UbcH5B and UbcH5B–Ub variants were serially diluted in running buffer containing 25 mM Tris-HCl, pH 7.6, 150 mM NaCl, 0.1 mg/ml BSA, 1 mM DTT, and 0.005% (v/v) Tween 20. For experiments with UbΔGG, UbcH5B–Ub variants were serially diluted in running buffer containing 0.6 mM UbΔGG. For the Ub variants, UbcH5B backbone binding experiment, GST–UbcH5B–Ub was captured on a CM-5 chip, and UbcH5B–Ub was mixed with a 2.4-fold molar excess of cIAP1R (100 μM UbcH5B–Ub and 240 μM cIAP1R) and then serially diluted in running buffer containing 10 μM cIAP1R to ensure that all UbcH5B–Ub concentration ranges were saturated with cIAP1R (cIAP1R binds UbcH5B–Ub with a Kd of ~0.83 μM; Table 1). Binding was measured at the indicated concentration ranges as in Fig. S1. Data reported are the differences in SPR signal between GST-cIAP1R and GST alone or GST–UbcH5B and GST alone. The data were analyzed by steady-state affinity analysis using Biacore T200 BIAevaluation software (GE Healthcare) and Scrubber2 (BioLogic Software).

Figure 6. UbB interactions. A, cartoon representation showing the UbcH5B–Ub portion of the structure of the cIAP1R-UbcH5B–Ub–Ub complex. Ile44 of Ub and Ser22 of Ub are indicated. B, close-up view of Ub–Ub–UbcH5B–Ub–Ub binding interface. UbcH5B’s α1β1-loop is indicated by an arrow. Hydrogen bonds are shown as dotted lines. All coloring in A and B is the same as in Fig. 2. C, nonreduced SDS-PAGE of lysine discharge reactions showing the disappearance of Ubβ variant–Ub bands over time in the presence and absence of UbΔGG catalyzed by cIAP1R. *, contaminating band from other reaction components. D, close-up view of Ub–Ub–UbcH5B–Ub–Ub binding interface in the structure of RNF38-UbcH5B–Ub–Ub complex (PDB entry 4V3L). UbcH5B is shown in cyan, Ub in yellow, and UbB in wheat. E, close-up view of Ub–Ub–UbcH5B’s α1β1-loop in the structure of RNF38-UbcH5B–Ub–Ub complex (PDB entry 4V3L). UbB is shown in cyan and Ub in yellow. F, close-up view of Ub–Ub–UbB’s α1β1-loop in the structure of RNF38-UbcH5B–Ub–Ub complex. Superimposition was performed on all Cα atoms of the UbcH5B portion of the structure. Ribbon representations of the UbcH5B–UbB portion from both structures are shown. UbB’s β1β2-loop is indicated by an arrow. UbB and Ub are colored in cyan and gray, respectively. G, nonreduced SDS-PAGE of lysine discharge reactions showing the disappearance of the UbcH5B–Ub–UbB complex. WT Ub and UbB from RNF38-UbcH5B–Ub–UbB structure are colored in cyan and gray, respectively.
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Structural insights into non-covalent ubiquitin activation of the cIAP1-UbcH5B–ubiquitin complex
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