Review of: "Structural Basis for Dimerization and Activation of UvrD-family Helicases"

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Potential competing interests: No potential competing interests to declare.

In the current study, Chadda et al. present the first dimeric structure of a UvrD-family helicase (UvrD1 from *Mycobacterium tuberculosis*), and reveal the novel mechanism of the 2B subdomain in regulating the helicase's activity. This work is quite interesting. Minor revisions are needed to better support the authors' claims.

The authors demonstrate that apo UvrD1 dimers exist in two distinct conformations: "compact" and "extended." Interestingly, after incubation with DNA, the extended conformation of UvrD1 dimers was not observed. Instead, only apo UvrD1 in the compact conformation, along with DNA-bound UvrD1, was detected. It would be valuable if the authors could discuss the significance of the existence of this extended form and its potential implications for the regulation of enzymatic activity.

In Figure 2, it's challenging for readers to connect the full dimeric complex structure in the center with the surrounding zoomed-in views. Clarity would be improved if the authors could add arrows or other markers to pinpoint the locations of each contact (2B:2B, 1A:1A, GIG motif:1B, and Tudor domain) on the central dimeric view.