Addendum: Crystal structure of the essential N-terminal domain of telomerase reverse transcriptase

Steven A Jacobs, Elaine R Podell & Thomas R Cech

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The recent paper by Romi *et al.* (*Proc. Natl. Acad. Sci. USA* **104**, 8791–8796, 2007) was in general agreement with our study of the structure and function of the N-terminal domain of *Tetrahymena* telomerase reverse transcriptase. However, the two studies disagreed on the effect of a mutation of Trp187 on catalysis, with our study reporting a severe reduction in activity. Upon sequencing the entire gene encoding our W187A mutant, we found that it had a second distant mutation (R812W) in motif C of the reverse transcriptase domain, and we demonstrated that it was the mutation at position 812 that abolished catalytic activity. In addition, we confirmed that authentic W187A telomerase has catalytic activity similar to that of wild-type telomerase. Both studies concur that Trp187 is physically close to the primer-binding site, and in fact Romi *et al.* have mapped Trp187 as a site of photo-cross-linking to a telomeric DNA primer.

We gratefully acknowledge the work of Arthur J. Zaug (HHMI, University of Colorado-Boulder) in resolving this discrepancy.

Corrigendum: F1-ATPase rotates by an asymmetric, sequential mechanism using all three catalytic subunits

Takayuki Ariga, Eiro Muneyuki & Masasuke Yoshida

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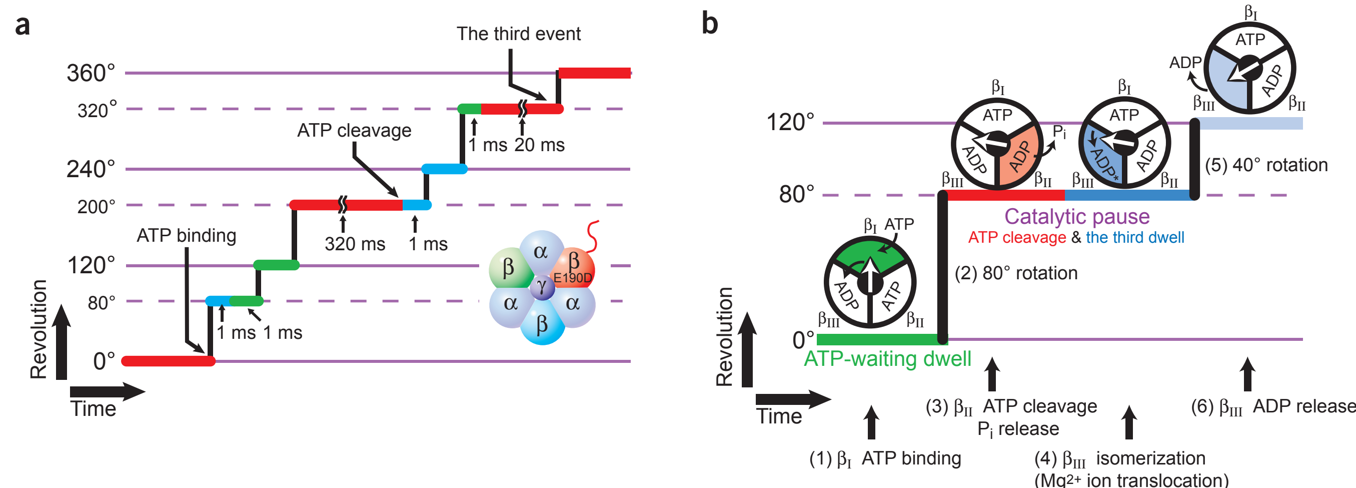
In the version of this article initially published, the proposed model for coupling the rotation and catalysis of the F_1 β subunits to the concerted activity of their active sites shown in Figure 4 was incorrectly drawn. A corrected version is depicted here. The error has been corrected in the HTML and PDF versions of the article.



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