Review of: "Examination of the roles of a conserved motif in the PriA helicase in structure-specific DNA unwinding and processivity"

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In this elegant study, Duckworth et al. examine the role of a conserved sequence motif in the *E. coli* PriA helicase. PriA initiates structure-specific replication restart at abandoned replication forks. The authors identified a well conserved Trp residue, and two less well conserved Arg and Tyr residues in PriA. The authors mutated each of these residues individually to generate single mutants and also created a triple mutant by replacing these residues with alanines. The authors then characterised the ATPase activities, DNA unwinding and DNA binding activities of these mutants and compared them with the wild type protein. The rationale, logical flow of experiments and simplified explanation of the conclusions make this manuscript a delightful read.

There are a few questions I would like to ask:

1. There are two more non conserved residues between Arg187 and Tyr190. It would be interesting to know if these affect the activity of the conserved residues in any way. Do they tend to belong to a specific group?
2. In figure 1B the red arrow points to the *E. coli* Trp186. Residue 190 is predominantly Leu. What would be the effect of introducing Tyr190Leu mutation on the activity of *E. coli* PriA?
3. Has the additive effect of each mutation been tested in double mutants?
4. Do the mutants have any in vivo phenotype? Do they compromise viability/fitness in any way?
5. Is the loss of strand selectivity specific to the triple mutant or was a similar effect also observed in any of the single mutants?