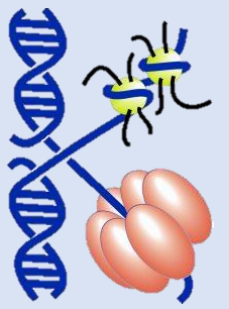




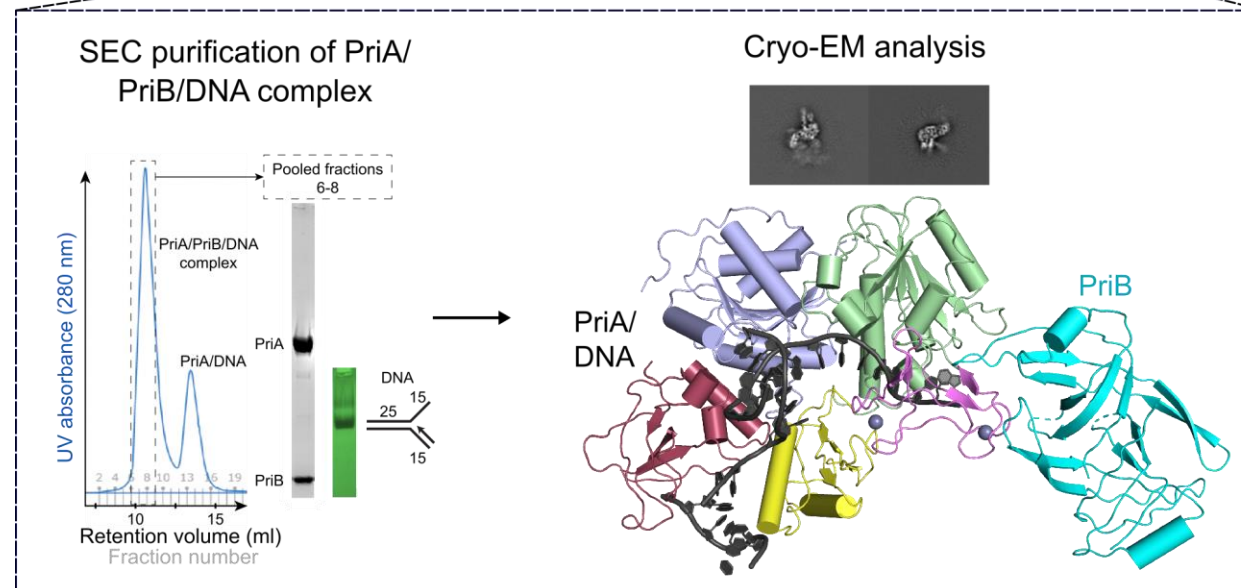
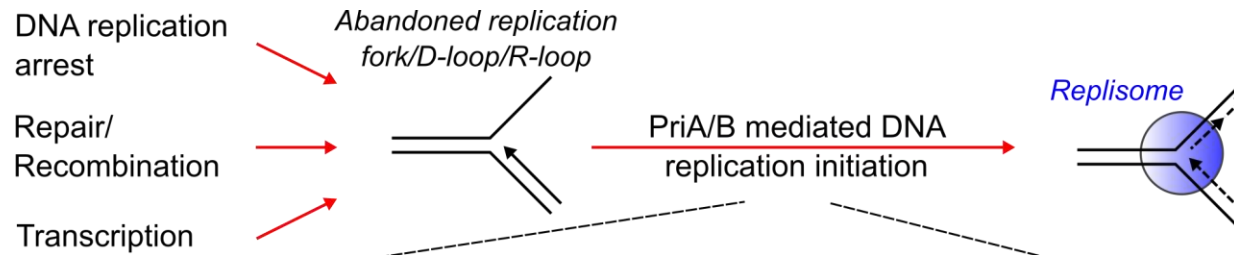
A 3.2 Å structure of the PriA/PriB/replication fork complex reveals mechanistic insight into bacterial DNA replication restart



Alexander Duckworth^{1*}, Kenneth Satyshur¹, Timothy Grant¹, and James Keck¹

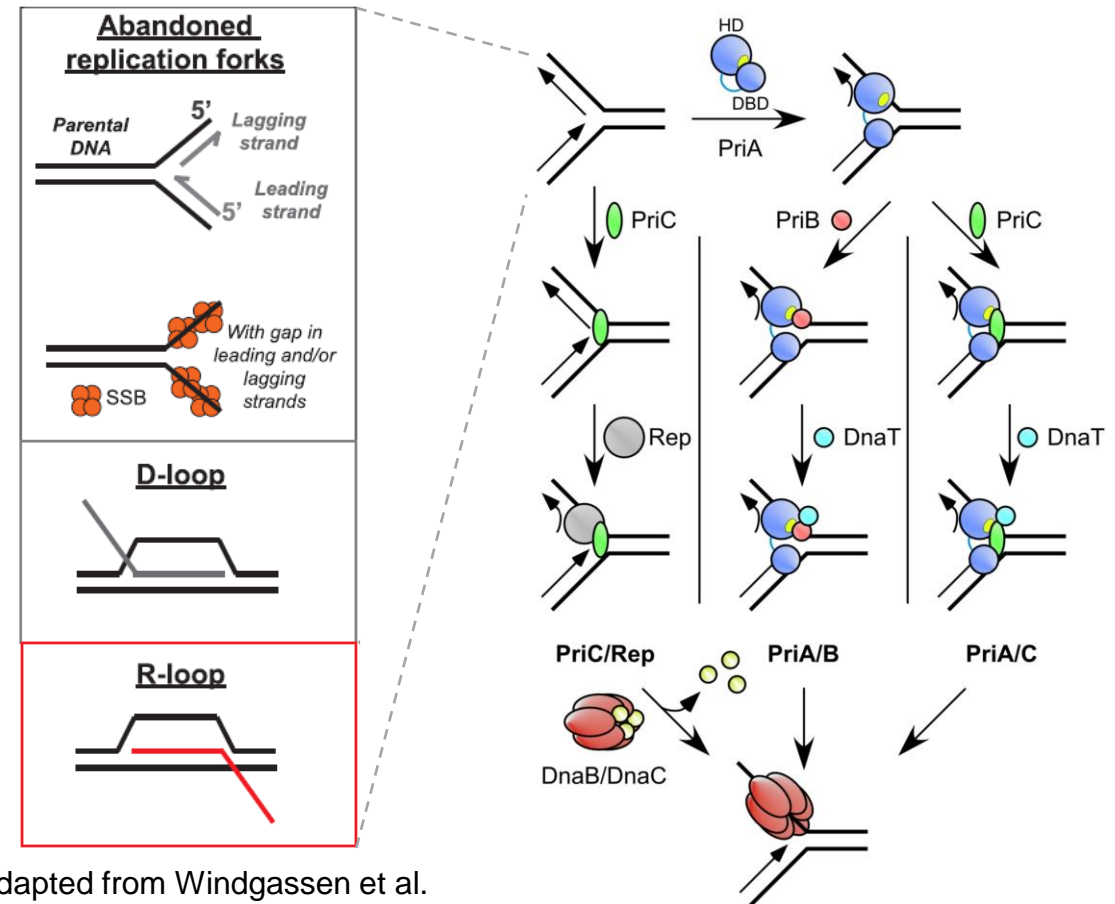
¹University of Wisconsin-Madison

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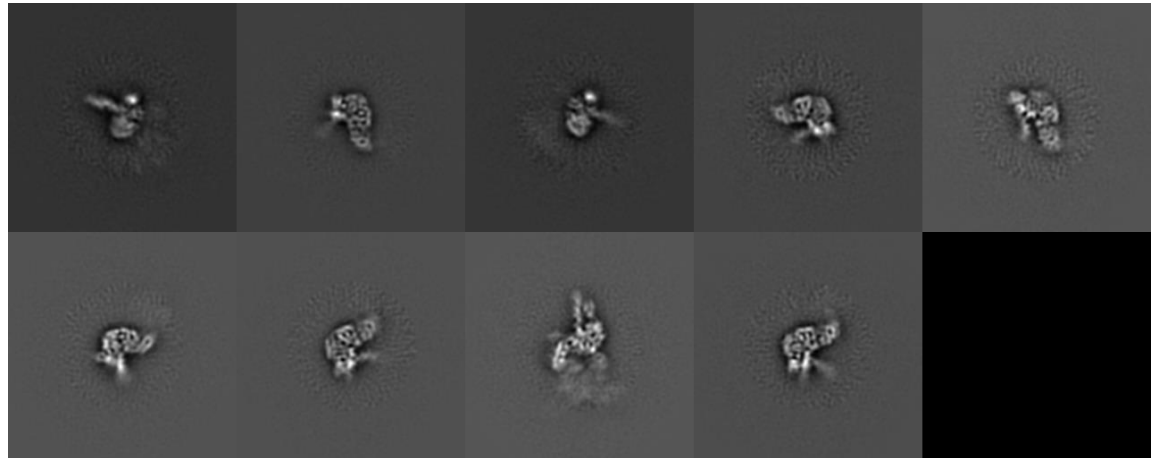
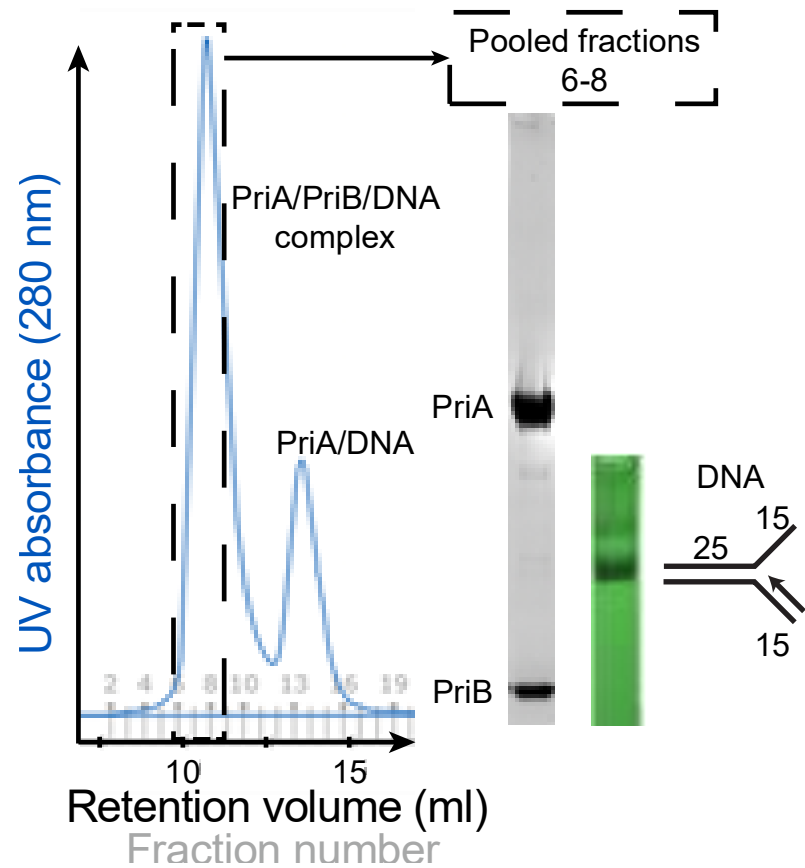
DNA replication restart is an essential process in bacterial cells

- Structure-specific method of DNA replication initiation
 - Replication arrest → abandoned replication forks
 - Repair/recombination → D-loops
 - Transcription → R-loops
- PriA/PriB pathway is thought to be preferred
- Mechanisms of PriB and DnaT remain poorly understood

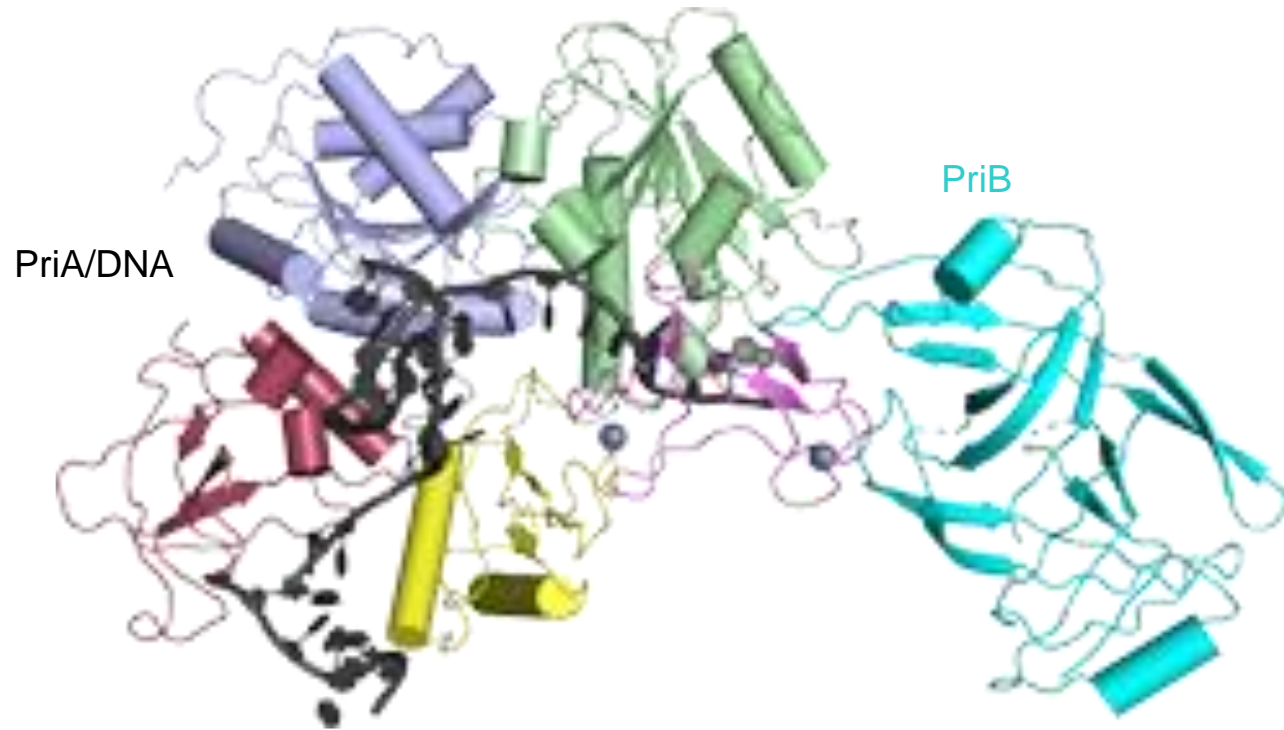


Adapted from Windgassen et al. (2018), *NAR*.

Purification of PriA/PriB/DNA fork and Cryo-EM analysis

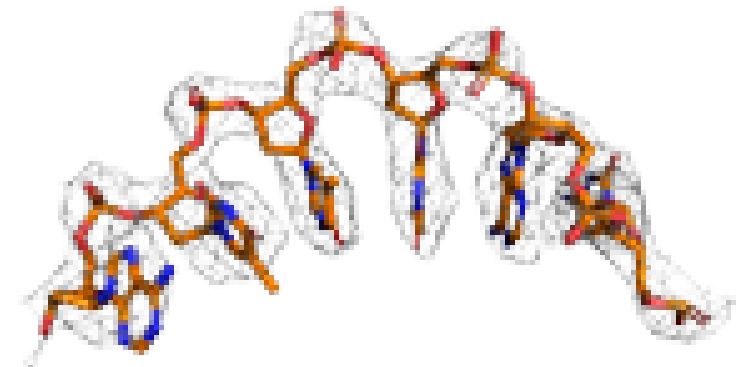


3.2 Å Cryo-EM structure of PriA/PriB/DNA fork resolves ssDNA path

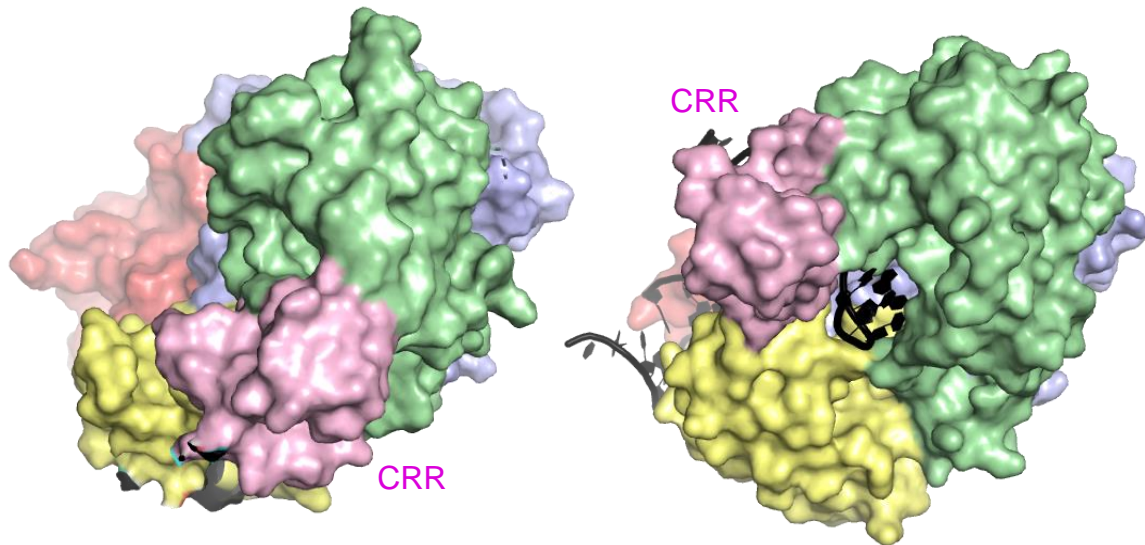


- PriA (colored by domain) and PriB dimer (cyan) resolved bound to DNA (black)
- PriB is bound to PriA's cysteine-rich region (purple)

- Resolved portions of both parental and leading strand dsDNA, 8 nucleotides of lagging strand ssDNA

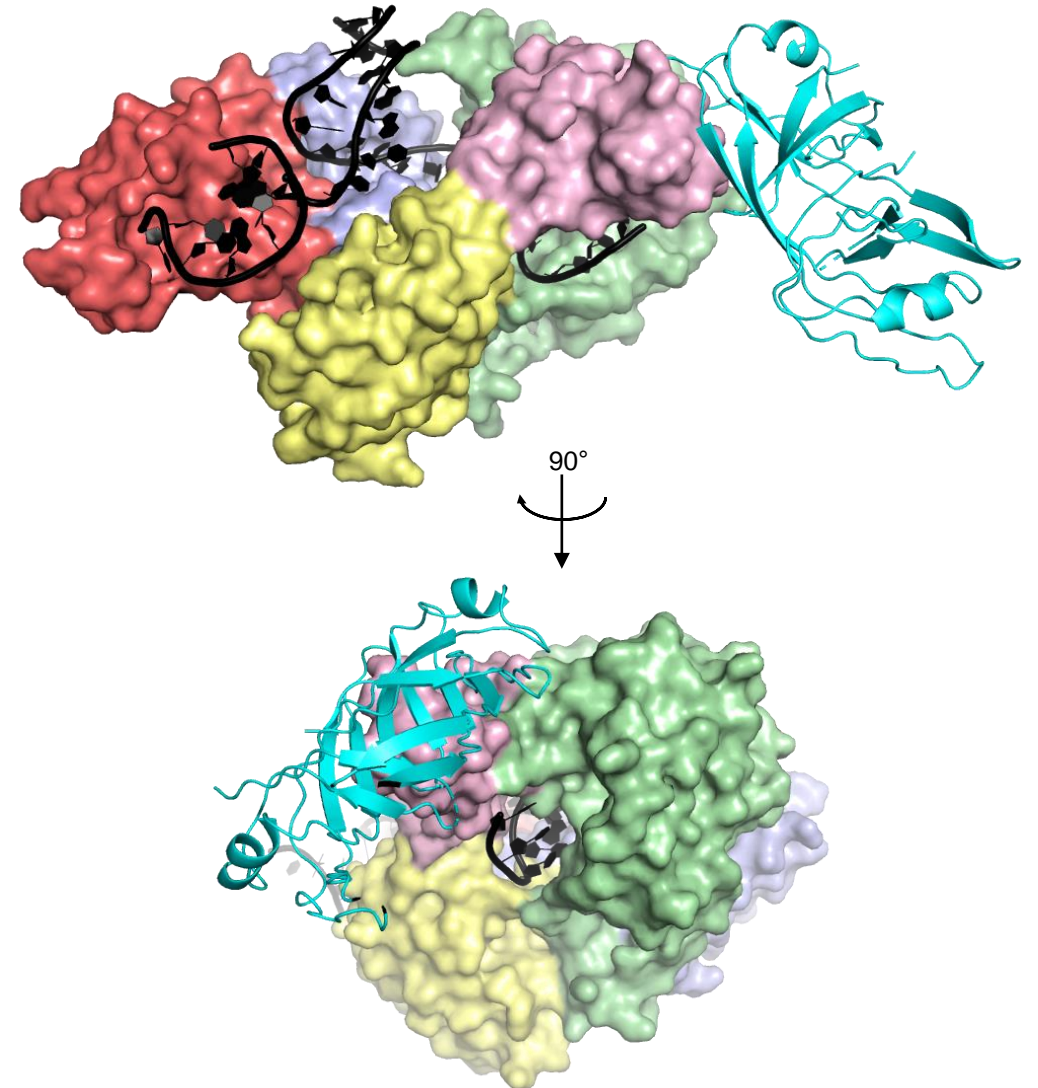


PriA's cysteine-rich region (CRR) undergoes large conformational change to form pore for ssDNA



apo PriA
Windgassen et al.
(2018), *PNAS*.
PDB: 6DCR

PriA/PriB/fork Cryo-EM structure



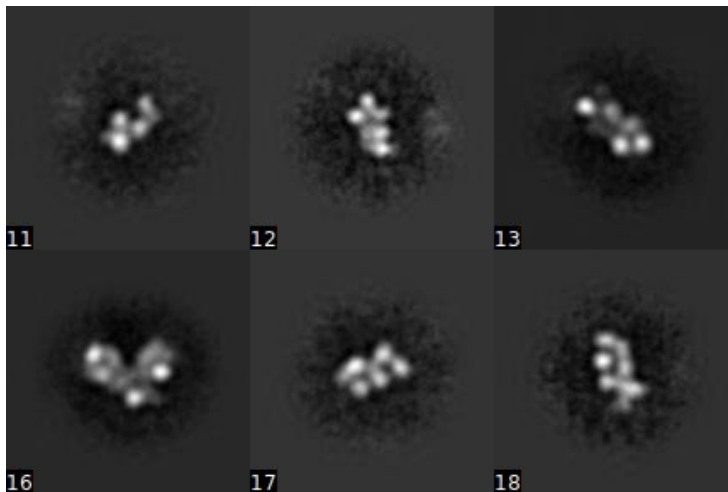
Conclusions, future directions, and acknowledgements

Conclusions:

- Solved a 3.2 Å Cryo-EM structure of PriA/PriB/DNA fork
 - PriB bound to PriA CRR
 - ssDNA resolved in pore formed by CRR conformational change

Future Directions:

- *In vitro/In vivo* validation of the structure
- Add DnaT to the complex:



Negative Stain-EM images of PriA/PriB/DnaT/DNA fork

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Questions?

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