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Crystal Structure of the SeqA-N Fiber: Implications for DNA Replication and *oriC* Sequestration. Alba Guarné^{1,2}, Therese Brendler³, Qinghai Zhao², Rodolfo Ghirlando², Stuart Austin³, Wei Yang², ¹McMaster Univ., HSC-4N16, Hamilton, Canada; ²LMB, NIDDK, Bethesda, USA, ³GRCBL, NCI-Frederick, Frederick, USA.

In *Escherichia coli* initiation of DNA replication is a precisely regulated event that occurs only once and at a precise moment during the cell cycle. Although many proteins regulate DNA replication, only one negative modulator has been identified thus far, the SeqA protein. First, SeqA regulates timing of replication initiation by counteracting the DnaA protein. Second, SeqA sequesters newly replicated origins by binding to clusters of transiently hemimethylated GATC sites, thus preventing premature re-initiation events. SeqA has two independent functional domains, SeqA-N and SeqA-C. Our previous studies revealed how SeqA-C, the C-terminal domain of SeqA, interacts with DNA (Guarné *et al.*, 02). Here we present the crystal structure of SeqA-N, the SeqA oligomerization domain. Our structure reveals that SeqA-N is a dimer with the ability to form long protein fibers maintained through hydrophobic interactions. Based on our *in vitro* and *in vivo* data, fiber formation is essential for SeqA function. Altogether, our results support a model showing how SeqA organizes DNA at the replication fork.

Guarné A, Zhao Q, Ghirlando R & Yang W (2002). *Nat. Str. Biol.* 9, 839-43.