



	Experiment title: Structural study of RadA in complex with ds DNA	Experiment number: MX2261
Beamline: CM01	Date of experiment: from: 31/11/2020 to: 01/12/2020	Date of report: 20/02/2021 <i>Received at ESRF:</i>
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Report:

Supported by robust biochemical and microbiology data, our team aimed to uncover the structural mechanisms behind the function of the helicase RadA, which plays an essential role in natural transformation in *Streptococcus pneumoniae*. Using an optimized DNA substrate and a non-hydrolysable ATP analogue, we succeeded to compensate for the protein's high degree of flexibility and lock it in an active conformation. On the ESRF session from 30-11-2020 to 02-12-2020, raw movies of RadA were collected, leading to the extraction of high-quality particles, used for Single-Particle Analysis. The high-quality of the data allowed us to isolate a group of particles leading to a 3.15 Å density map. The highly asymmetrical ATPase domains and ATP binding sites, as well as the DNA substrate and adjacent contact loops were well resolved, revealing a continuous translocation mode composed

of heterogeneous energetic states arranged in a staircase shape. The resulting molecular model is in the last stages of validation before deposition and the interpretation of this map under the light of the collected biochemical data points to a promising publication submission on a high impact journal (IF>10) over the next six months.

