

# Redox controls RecA protein activity via reversible oxidation of its methionine residues

## General information

1. **Dataset for doi:** [10.7554/eLife.63747](https://doi.org/10.7554/eLife.63747)
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3. **Date of data collection (can be a single date, or a range) :** 2010 to 2020
4. **Information about geographic location of data collection :** Marseille France, Madison USA, Sevilla Spain, Brussels Belgium.
5. **Keywords used to describe the data topic :** ND
6. **Language information :** English
7. **Information about funding sources that supported the collection of the data :** ND

## Data and file overview

### 1. Short description for each filename :

**Fig S1A S2A raw data :** Excel Raw datas for Figure supplement 1A and Figure supplement 2A : Quantification analysis of datas from Figure 3C and 5A. EM quantitation analysis, DNA molecules observed by EM were manually counted. For each condition, 2 to 4 squares of 3 or 4 grids of the replicates were fully counted. RecA nucleofilament /DNA molecules were categorized into 6 groups: fully filamented circles, medium filamented circles, small filamented circles, very small filamented circles, linear (broken circles) and SSB/DNA (cssDNA SSB coated).

**Fig S1B S2B S3D Strand exchange quantification final :** Excel Raw datas for Figure supplement 1B and Figure supplement 2B : Quantification analysis from Figure 3E, 5C and 8C.

**Fig1a Raw Data :** Excel Raw datas for Fig1a, UV sensitivity of wild-type (WT) and mutant strains (BE152 ( $\Delta$ msrA  $\Delta$ msrB); BE007 375(Hpx-); BE080 (Hpx- $\Delta$ msrA  $\Delta$ msrB)) was tested by monitoring colony-forming units at different UV doses.

**Fig2a Raw Data :** Excel Raw datas for Fig2a, Transductant frequency of a lacZ-cat marker in different genetics backgrounds.

**Fig3a Raw Data mass spec:** Excel Raw datas for Fig3a, the relative percentage of Met-O in the various forms of RecA (native, oxidized (RecAox) and repaired (RecArep)) was determined by mass spectrometry analysis.

**Fig3b gel uncropped 3b :** Uncropped scanned image of the anti-RecA western blot shown in Fig. 3B

**Fig3D 5B 8B raw data ATPase data :** Excel Raw datas for Fig3D, Fig 5B and Fig 8B, on ATP hydrolysis rate.

**Fig4D Raw data :** (PDF) Uncropped microscopic image shown in Fig. 4D. LL1594 ( $\Delta$ recA) cells expressing in trans the different RecA variants were imaged in stationary phase by phase-contrast microscopy.

**Fig4F raw data lacZ :** Excel Raw data of Fig4F . SOS induction after 2h exposure to MMC in a  $\Delta$ recA strain expressing in trans the different recA alleles was monitored by *sfiA::lacZ* expression.

**Fig4F raw uncropped WB:** PDF, Uncropped scanned image of the anti-RecA and anti-LexA western blot shown in Fig. 4F.

**Fig6B raw Data anti LexA :** (.tif) Uncropped scanned image of the anti-LexA western blot shown in Fig. 6B.

**Fig6B raw Data anti RecA :** (.jpg) Uncropped scanned image of the anti-RecA western blot shown in Fig. 6B.

**Fig7ab Raw Data :** Excel Raw data of Fig 7A and 7B. Competition assay in aerobic (A) and anaerobic (B) conditions.

**Fig8a Raw Data :** Excel Raw data of Fig 8A. Size measurement of cssDNA-RecA and cssDNA-RecAM164Q filament observed by electron microscopy in the absence or in the presence of SSB.

2. **Date that the file was created :** from 2010 and 2020
3. **Date(s) that the file(s) was updated (versioned) and the nature of the update(s),**  
if applicable : 12/22/2021