

# Supplementary Information

## Exploring RNA polymerase regulation by NMR spectroscopy

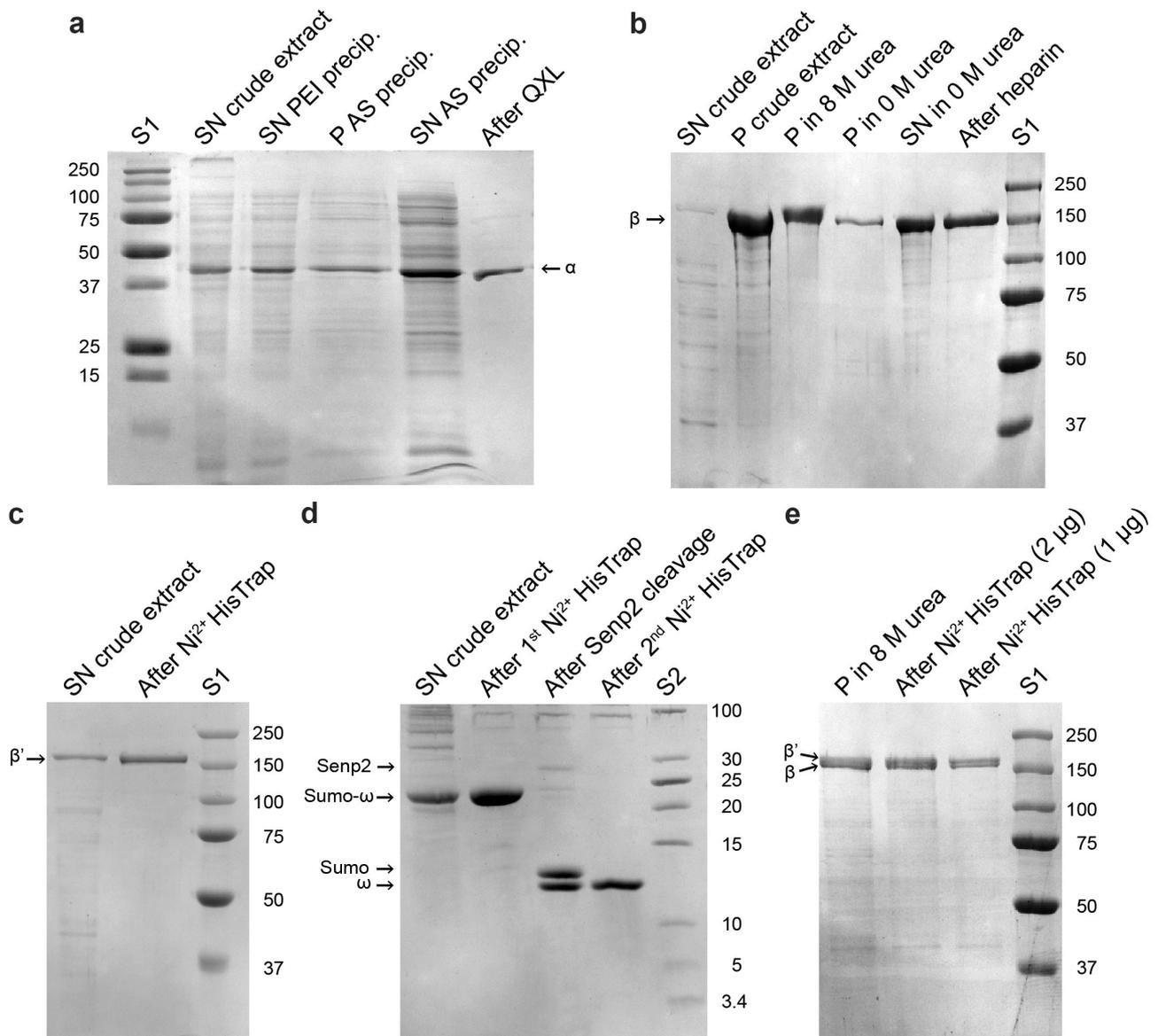
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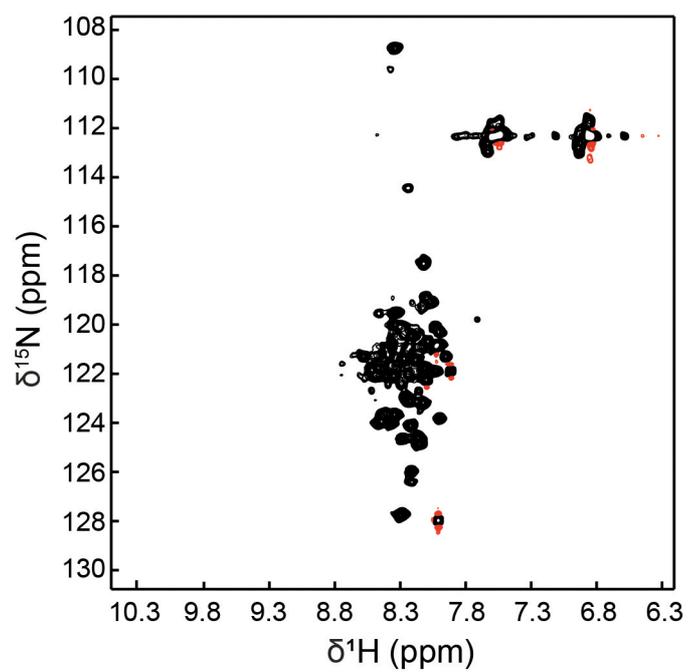
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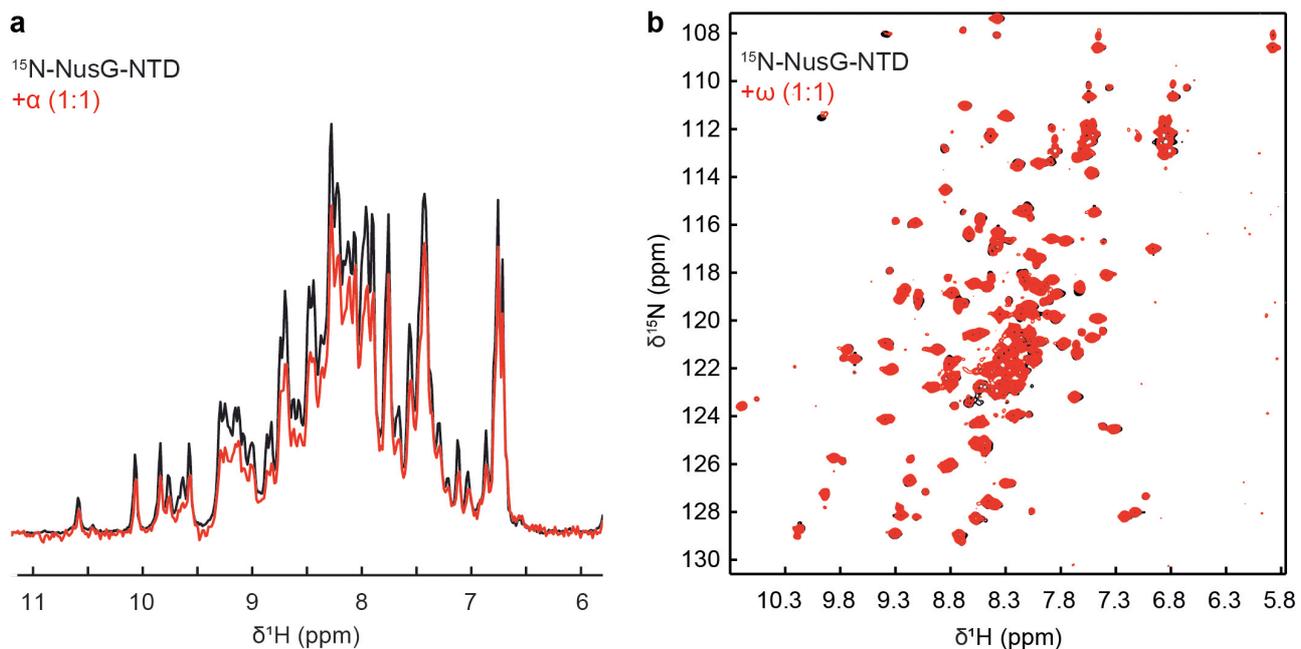


**Supplementary Figure 1: Purification of individual RNAP subunits.** 2  $\mu\text{g}$  protein were applied to each lane. S1, Precision Plus Protein Standard (BioRad, Munich, Germany); S2, PageRuler Low Range Protein Ladder (Thermo Scientific, Schwerte, Germany); SN, supernatant; P, pellet; PEI, polyethylenimine, AS, ammonium sulfate (**a**) 19 % (w/v) SDS-polyacrylamide gel of aliquots taken from the fractions during  $\alpha$  subunit purification after staining with Coomassie Blue. (**b**) 10 % (w/v) SDS-polyacrylamide gel of aliquots taken from the fractions during  $\beta$  subunit purification after staining with Coomassie Blue. (**c**) 10 % (w/v) SDS-polyacrylamide gel of aliquots taken from the fractions during  $\beta'$  subunit purification after staining with Coomassie Blue. (**d**) Schagger-Jagow gel<sup>1</sup> of aliquots taken from the fractions during  $\omega$  subunit purification after staining with Coomassie

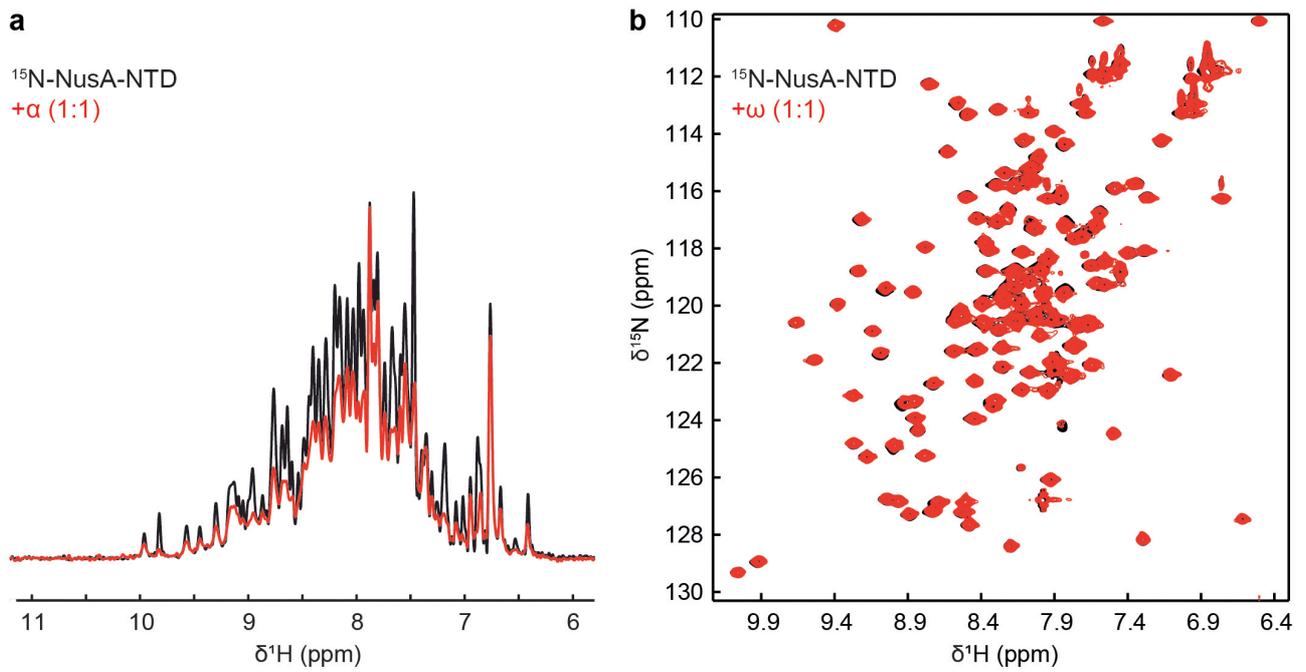
Blue. (e) 10 % (w/v) polyacrylamide gel of aliquots taken from the fractions during  $\beta\beta'$  complex purification after staining with Coomassie Blue.



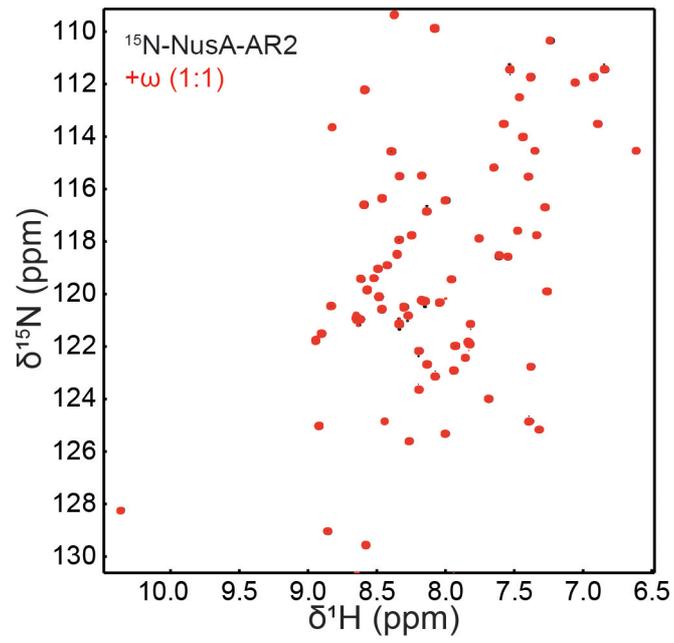
**Supplementary Figure 2:** [ $^1\text{H}, ^{15}\text{N}$ ]-HSQC spectrum of 300  $\mu\text{M}$   $^{15}\text{N}$ - $\omega$ . Positive and negative signals are colored in black and red, respectively.



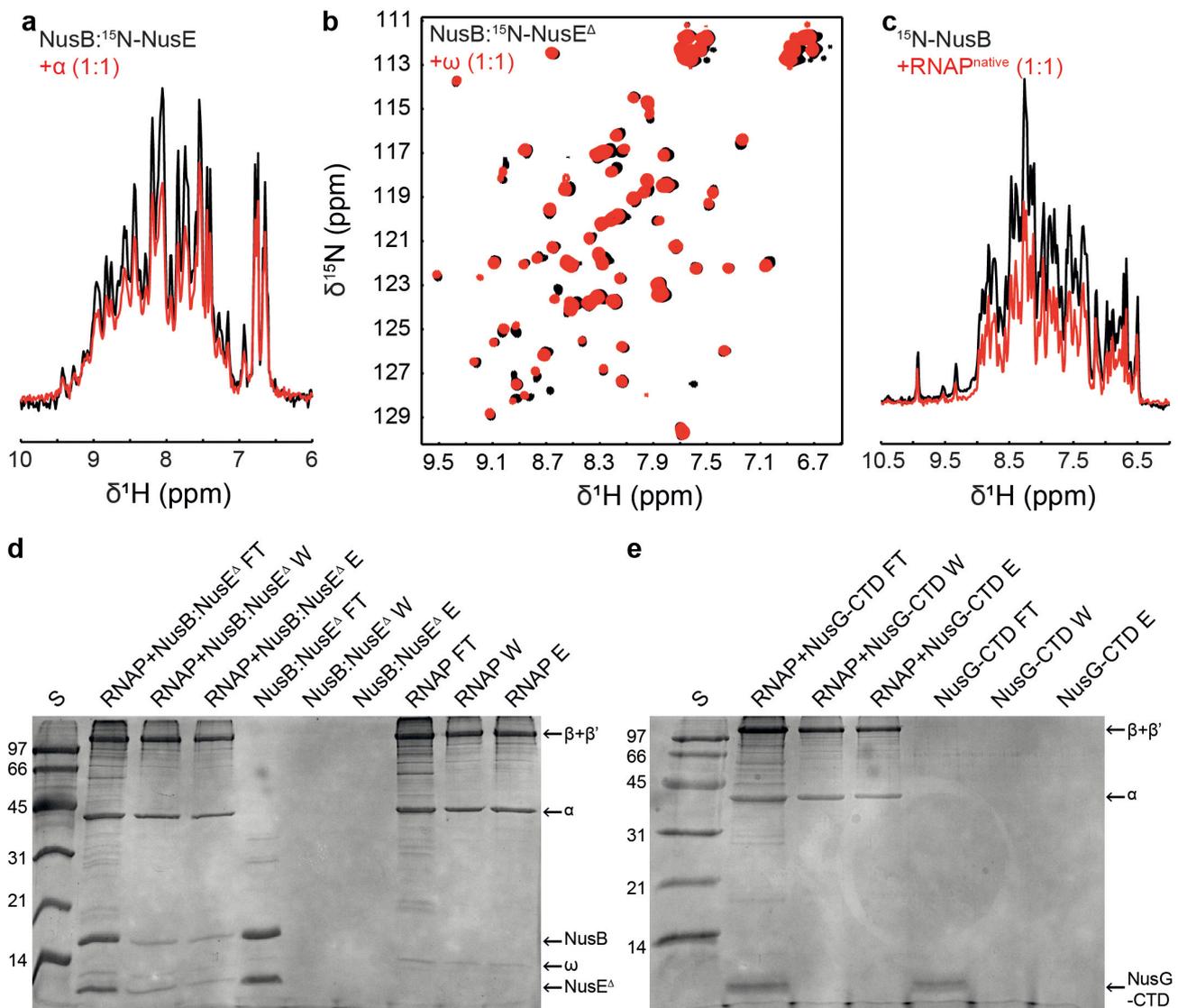
**Supplementary Figure 3: NusG-NTD does not interact with isolated  $\alpha$  or  $\omega$ .** (a) 1D [ $^1\text{H}$ ,  $^{15}\text{N}$ ]-HSQC spectra of 30  $\mu\text{M}$  NusG-NTD in the absence, black, and in the presence, red, of an equimolar concentration of  $\alpha$ . (b) 2D [ $^1\text{H}$ ,  $^{15}\text{N}$ ]-HSQC spectra of 100  $\mu\text{M}$  NusG-NTD in the absence, black, and in the presence, red, of an equimolar concentration of  $\omega$ .



**Supplementary Figure 4: NusA-NTD does not interact with isolated  $\alpha$  or  $\omega$ .** (a) 1D [<sup>1</sup>H, <sup>15</sup>N]-HSQC spectra of 30  $\mu\text{M}$  NusA-NTD in the absence, black, and in the presence, red, of an equimolar concentration of  $\alpha$ . (b) 2D [<sup>1</sup>H, <sup>15</sup>N]-HSQC spectra of 100  $\mu\text{M}$  NusA-NTD in the absence, black, and in the presence, red, of an equimolar concentration of  $\omega$ .

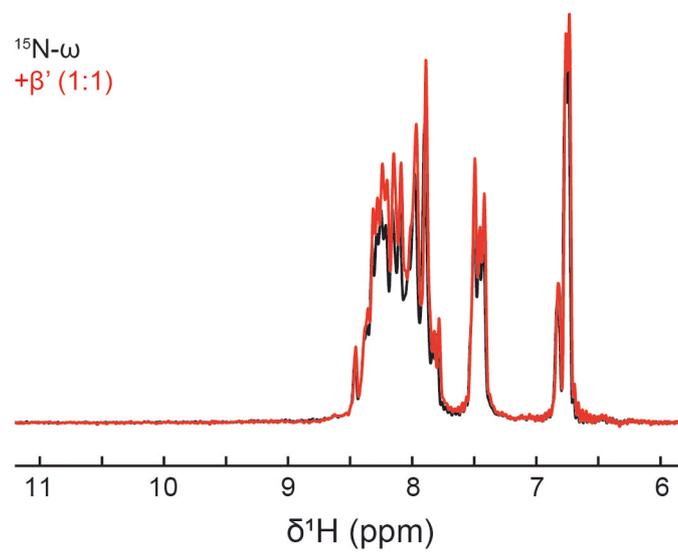


**Supplementary Figure 5: NusA-AR2 does not interact with isolated  $\omega$ .** 2D [ $^1\text{H}$ ,  $^{15}\text{N}$ ]-HSQC spectra of 30  $\mu\text{M}$  NusA-AR2 in the absence, black, and in the presence, red, of an equimolar concentration of  $\omega$ .

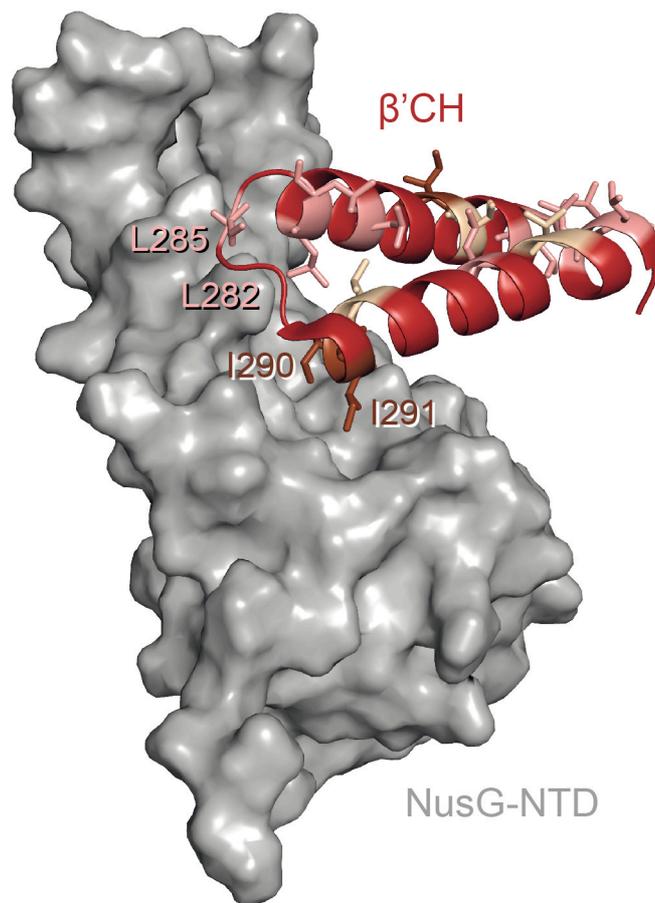


**Supplementary Figure 6: Interaction studies of NusB and NusB:NusE<sup>Δ</sup> with RNAP, isolated  $\alpha$  and  $\omega$ .** (a) 1D [<sup>1</sup>H,<sup>15</sup>N]-HSQC spectra of 30  $\mu$ M NusB:<sup>15</sup>N-NusE<sup>Δ</sup> in the absence, black, and in the presence, red, of an equimolar concentration of  $\alpha$ . (b) 2D [<sup>1</sup>H,<sup>15</sup>N]-HSQC spectrum of 100  $\mu$ M NusB:<sup>15</sup>N-NusE<sup>Δ</sup> in the absence, black, and in the presence, red, of an equimolar concentration of  $\omega$ . (c) 1D [<sup>1</sup>H,<sup>15</sup>N]-HSQC spectra of 30  $\mu$ M <sup>15</sup>N-NusB in the absence, black, and in the presence, red, of an equimolar concentration of RNAP<sup>native</sup>. (d,e) Crosslinking of RNAP and NusB:NusE<sup>Δ</sup>. 19 % (w/v) SDS-polyacrylamide gel after Ni<sup>2+</sup> affinity chromatography and staining with Coomassie Blue. Crosslinking of RNAP and NusG-CTD was used as negative control. S: BioRad low range SDS-PAGE Standard (BioRad, Munich, Germany), FT: flow through, W: fraction of the

last washing step with 5 mM imidazole, E: eluate.



**Supplementary Figure 7: The  $\omega$  subunit does not interact with the  $\beta'$  subunit.** 1D [ $^1\text{H},^{15}\text{N}$ ]-HSQC spectra of the amide region of 30  $\mu\text{M}$   $^{15}\text{N}-\omega$  subunit in the absence, black, and in the presence of an equimolar concentration of  $\beta'$ , red.



**Supplementary Figure 8: Model of NusG-NTD binding to the  $\beta'$ CH.** The NusG-NTD:  $\beta'$ CH complex (PDB code: 2K06, NusG-NTD, surface representation; PDB code: 4KMU,  $\beta'$  clamp helices, ribbon representation) was modeled based on the crystal structure of *Pyrococcus furiosus* Spt4/5 binding to the RNAP clamp domain<sup>2</sup>. Ile (brown), Leu (pink) and Val (beige) residues in the  $\beta'$  clamp helices are represented as sticks.

## Supplementary Methods

**Cloning.** Plasmids containing the genes *rpoA*, *rpoB*, *rpoC* and *rpoZ* were kindly provided by Irina Artsimovitch. *rpoB* was cloned from pIA942 into pET29b (Novagen, Madison, WI, USA) via *Bam*HI and *Nde*I. *rpoC* was cloned from pIA661 into pET29b via *Nde*I and *Hind*III restriction sites allowing the expression of *rpoC* with a hexahistidine tag at the C-terminus. For tagless production of *rpoZ* the gene was excised from pIA839 with its ribosome binding site via *Xba*I and *Hind*III and cloned into pET32a (Novagen, Madison, WI, USA). For expression of *rpoZ* with an N-terminal SUMO tag the *rpoZ* gene was cloned into pET28 derivative harboring the small ubiquitin-like modifier (SUMO) 1 gene via *Bam*HI and *Xho*I restriction sites.

The gene for NusA-NTD (1-125) was cloned using the Champion™ pET101 Directional TOPO® Expression Kit (Invitrogen, Carlsbad, CA, USA) with the following primers: Fwd-primer: 5'-CAC CAT GAA CAA AGA AAT TTT GGC-3'; Rev-primer: 5'-AGA ACC ACG CGG AAC CAG CAT CGC ACG TTC GGC TTC ACG-3'. The resulting *E. coli* expression vector pET101\_NusA-NTD contains a C-terminal hexa-histidine tag and a thrombin cleavage site between NusA-NTD and the histidine tag.

**Gene expression and protein purification.** *rpoA* was expressed in *E. coli* BL21 (DE3) (Novagen, Madison, WI, USA) harboring the plasmid pIA287. Cells were grown in M9 minimal medium<sup>3,4</sup> containing 100 µg/ml ampicillin at 37 °C. At an optical density of 600 nm (*OD*<sub>600</sub>) of ~ 0.7 expression was induced by 0.1 mM isopropyl-thiogalactoside (IPTG). Cells were harvested after 3 h (9,000 x g, 15 min, 4°C), resuspended in 50 mM Tris/HCl (pH 8.0) containing 500 mM NaCl and disrupted by a microfluidizer (Microfluidics, Newton, MA, USA). Nucleic acids were precipitated by addition of 0.6 % (v/v) polyethylenimine and removed by centrifugation (12,000 x g, 30 min, 4 °C). Subsequently, an ammonium sulfate precipitation (60 % (w/v)) was performed with the supernatant. After centrifugation (12,000 x g, 4 °C, 30 min) the supernatant was dialyzed against 20 mM Tris/HCl (pH 8.0) overnight at 4 °C and applied to a HiTrap QXL column (GE Healthcare,

Munich, Germany). After washing with 20 mM Tris/HCl (pH 8.0) elution was performed using a step gradient with increasing NaCl concentrations (0.25-1 M NaCl in 20 mM Tris/HCl (pH 8.0)). Fractions containing the target protein were combined, dialyzed against the required buffer, concentrated by ultrafiltration (VivaSpin units, molecular weight cut-off (MWCO) = 3.5 kDa, Sartorius Stedim Biotech GmbH, Göttingen, Germany) and stored at -80 °C after freezing with liquid nitrogen. 67 mg protein were obtained from a one liter culture.

*rpoB* was expressed in *E. coli* BL21 (DE3) harboring the pET29b/*rpoB* plasmid. Cells were grown in M9 minimal medium<sup>3,4</sup> containing 30 µg/ml kanamycin at 37 °C. At an  $OD_{600}$  of ~ 0.7 expression was induced by 1 mM IPTG. Cells were harvested 4 h after induction and lysed as described for *rpoA* using a buffer containing 50 mM Tris/HCl (pH 8.0), 500 mM NaCl, 5 % (v/v) glycerol, 1 mM DTT. After centrifugation (30 min, 4 °C, 12,000 x g) the pellet was resolved in 1 mM EDTA (pH 8.0), 1 mg/ml deoxycholic acid sodium salt, 20 mM DTT and lysozyme (0.2 mg/ml) and again centrifuged for 30 min at 12,000 x g and 4 °C. The pellet was then washed three times with the same buffer, subsequently three times with 50 mM Tris/HCl (pH 8.0), 50 mM NaCl, 10 mM EDTA, 5 mM DTT and once with H<sub>2</sub>O. Finally, the pellet was resuspended in 50 mM Tris/HCl (pH 7.2), 8 M Urea, 500 mM NaCl and stirred for 1 h at room temperature. Urea was removed by dialysis against 50 mM Tris/HCl (pH 7.2), 5 % (v/v) glycerol, 500 mM NaCl, 0.5 mM EDTA, 1 mM DTT at 4 °C for 3 h followed by overnight dialysis using the same buffer without NaCl. The dialysate was centrifuged (30 min, 4 °C, 12,000 x g) and the supernatant was applied to a HiTrap Heparin HP column (GE Healthcare, Munich, Germany). After washing with 50 mM Tris/HCl (pH 7.2), 5 % (v/v) glycerol, 0.5 mM EDTA, 1 mM DTT elution was performed using a constant NaCl gradient up to 1 M in 50 mM Tris/HCl (pH 7.2), 5 % (v/v) glycerol, 0.5 mM EDTA, 1 mM DTT. Fractions containing pure  $\beta$  were combined and dialyzed against the required buffer before the protein solution was concentrated by ultrafiltration (MWCO = 10 kDa) and stored at -80 °C after freezing with liquid nitrogen. The yield was 53 mg protein per l culture.

*rpoC* was expressed in *E. coli* Rosetta (DE3) pLysS (Novagen, Madison, WI, USA). The recombinant protein harbored a seven amino acid linker followed by a hexahistidine tag (His<sub>6</sub>) at the C-terminus. Cells were grown in M9 minimal medium<sup>3,4</sup> containing 30 µg/ml kanamycin and 34 µg/ml chloramphenicol at 37 °C. When an *OD*<sub>600</sub> of ~ 0.5 was reached the temperature was lowered to 16 °C and gene expression was induced with 1 mM IPTG at an *OD*<sub>600</sub> of 0.6-0.8. Cells were harvested 6 h after induction, resuspended and lysed as described above using buffer A (50 mM Tris/HCl (pH 7.5), 500 mM NaCl, 5 % (v/v) glycerol, 10 mM MgCl<sub>2</sub>, 10 µM ZnCl<sub>2</sub>, 10 mM imidazole). After centrifugation (30 min, 12,000 x *g*, 4 °C) the supernatant was applied to a HisTrap HP column (GE Healthcare, Munich, Germany). After washing with buffer A, elution was carried out using a step gradient with increasing imidazole concentrations (10-500 mM in buffer A). Fractions containing β' were combined. Following dialysis against the required buffer the protein solution was concentrated by ultrafiltration (MWCO = 10 kDa) and stored at -80 °C after shock freezing in liquid nitrogen. One liter culture yielded 15 mg protein.

The ω subunit with N-terminal His<sub>6</sub>-SUMO tag was produced in *E. coli* Rosetta (DE3) pLysS harboring pET28M-SUMO1/*rpoZ*. Cells were grown in M9 minimal medium<sup>3,4</sup> in the presence of 30 µg/ml kanamycin and 34 µg/ml chloramphenicol at 37 °C until an *OD*<sub>600</sub> of 0.4 was reached. The temperature was lowered to 25 °C and at an *OD*<sub>600</sub> of 0.6-0.8 expression was induced with 1 mM IPTG. Cells were harvested after 4 h, resuspended and lysed as described above. In this case 25 mM Tris/HCl (pH 7.5), 300 mM NaCl, 10 mM imidazole was used for resuspension. After centrifugation (12,000 x *g*, 30 min, 4 °C), the supernatant was applied to a HisTrap HP column. After washing with 25 mM Tris/HCl (pH 7.5), 300 mM NaCl, 10 mM imidazole, elution was performed using a step gradient with increasing imidazole concentrations (10-500 mM in resuspension buffer). Fractions containing His<sub>6</sub>-SUMO-ω were combined and cleaved during dialysis overnight against 25 mM Tris/HCl (pH 7.5), 300 mM NaCl by Senp2, a protease that cleaves directly after SUMO protein. The protein solution was reapplied to the HisTrap HP column.

Pure  $\omega$  was found in the flow through, dialyzed against the required buffer, concentrated by ultrafiltration (MWCO = 3 kDa) and stored at -80 °C after freezing with liquid nitrogen with a yield of 3 mg protein per liter culture.

Tagless  $\omega$  was used for *in vitro* assembly of RNAP and produced in *E. coli* Rosetta (DE3) pLysS containing pET32a/*rpoZ*. Cells were grown in M9 minimal medium<sup>3,4</sup> containing 100  $\mu$ g/ml ampicillin and 34  $\mu$ g/ml chloramphenicol at 37 °C. After induction with 0.1 mM IPTG at an  $OD_{600}$  of 0.6-0.8 cells were grown for another 3 h before harvesting (9,000 x g, 15 min).

NusA-NTD contained amino acids 1-125 and was produced in *E. coli* BL21 Star (DE3) (Invitrogen, Darmstadt, Germany) harboring pET101\_NusA-NTD. Cells were grown at 37 °C in LB medium containing ampicillin (100  $\mu$ g/ml) until an  $OD_{600}$  of 0.6 was reached. Then the temperature was lowered to 20 °C. After 30 min overexpression was induced by 1 mM IPTG. Cells were harvested after overnight growth, resuspended and lysed as described for *rpoA* using a buffer containing 20 mM Tris/HCl (pH 7.5), 150 mM NaCl, 10 % (v/v) glycerol, 20 mM imidazole. After centrifugation at 12,000 x g and 4 °C for 30 min, the supernatant was applied to a Ni<sup>2+</sup>-NTA HiTrap column (GE Healthcare, Munich, Germany). After washing with 20 mM Tris/HCl (pH 7.5), 150 mM NaCl, 10 % (v/v) glycerol, 20 mM imidazole elution was performed *via* a step gradient with increasing imidazole concentrations (20 mM – 1 M imidazole in 20 mM Tris/HCl (pH 7.5), 150 mM NaCl, 10 % (v/v) glycerol, 20 mM imidazole). The fractions containing the NusA-NTD-His<sub>6</sub> fusion protein were combined and the protein was cleaved by thrombin (Novagen, Madison, WI, USA), during dialysis against 20 mM Tris/HCl (pH 7.5) at room temperature overnight. The protein solution was applied to a HiTrap QXL column which was subsequently washed with 20 mM Tris/HCl (pH 7.5) before elution was carried out *via* a step gradient with increasing NaCl concentrations (0 M-1 M NaCl in 20 mM Tris/HCl (pH 7.5)). The fractions containing NusA-NTD were combined and dialyzed against the required buffer. Finally, the protein solution was

concentrated by ultrafiltration (MWCO = 3 kDa), frozen in liquid nitrogen and stored at -80 °C.

The gene of the SUMO protease SENP2 was expressed in *E. coli* Rosetta (DE3) (Novagen, Madison, WI, USA) harboring the plasmid pET28b-senp2. Cells were grown in LB medium containing 30 µg/ml kanamycin and 34 µg/ml chloramphenicol at 37 °C. At  $OD_{600} \sim 0.7$  expression was induced by 1 mM IPTG. Cells were harvested after 4 h (9,000 x g, 15 min, 4°C), resuspended in 40 mM Tris/HCl (pH 7.5) containing 500 mM NaCl, 10 mM imidazole and 5 mM DTT and disrupted by a microfluidizer. The supernatant was applied to a HisTrap HP column. Elution was performed using a step gradient with increasing imidazole concentrations (10-500 mM in resuspension buffer). The fractions containing SENP2 were combined, dialyzed against 5 mM Tris/HCl (pH 7.5), 250 mM NaCl, 10 mM DTT, 0.1 mM EDTA and concentrated by ultrafiltration (MWCO = 10 kDa). Finally the glycerol concentration was adjusted to 20 %, aliquots were frozen in liquid nitrogen and stored at -80 °C.

The production and purification of NusB:NusE<sup>Δ</sup>, NusB, RNAP  $\alpha$ -CTD, NusG-NTD, NusG-CTD and NusA-AR2 were carried out as described previously (Refs. <sup>5-7</sup> for NusB:NusE<sup>Δ</sup> and NusB, Ref. <sup>8</sup> for  $\alpha$ CTD, Ref. <sup>9</sup> for NusG-NTD, Ref. <sup>6</sup> for NusG-CTD, Ref. <sup>8</sup> for NusA-AR2).

**Formaldehyde crosslink.** The crosslinking of RNAP and NusB:NusE<sup>Δ</sup> was based on the SPINE method<sup>10</sup>. 7.7 nmol RNAP were mixed with 15.4 nmol NusB:NusE<sup>Δ</sup> in 25 mM HEPES (pH 7.5), 100 mM NaCl and a 4 % (w/v) paraformaldehyde solution in the same buffer was added to a final concentration of 0.6 % (w/v). For the crosslink, the mixture was incubated at 37 °C for 20 min. 0.7 ml of Ni<sup>2+</sup> chelating sepharose (50 % (w/v), GE Healthcare, Munich, Germany), equilibrated with 25 mM HEPES (pH 7.5), 100 mM NaCl, were added and incubated for 20 min at room temperature. Afterwards the mixture was transferred to a 2.5 ml gravity flow column and the flow trough was collected. The column was washed ten times with 1 ml of 25 mM HEPES (pH 7.5),

100 mM NaCl and seven times with 1 ml of the same buffer containing 5 mM imidazole. Bound protein was eluted with 25 mM HEPES (pH 7.5), 100 mM NaCl, 500 mM imidazole. The protein contained in 200  $\mu$ l in the flow through, the last washing step and the eluate was precipitated with 50  $\mu$ l 50 % (v/v) trichloroacetic acid (TCA) by incubation for 20 min on ice and subsequent centrifugation for 10 min at 15,000 x g. The pellet was dissolved in 50  $\mu$ l 2x Roti (Roth, Karlsruhe, Germany). The crosslink was broken by boiling the solution for 20 min and the samples were analyzed by SDS-PAGE. The isolated RNAP, the isolated NusB:NusE<sup>3</sup> complex as well as NusG-CTD in the absence and presence of RNAP as negative control were treated accordingly.

**Programs.** All structures were visualized using PyMOL<sup>11</sup>.

## Supplementary References

1. Schägger, H. & von Jagow, G. Tricine Sodium Dodecyl-Sulfate Polyacrylamide-Gel Electrophoresis for the Separation of Proteins in the Range from 1-Kda to 100-Kda. *Anal. Biochem.* **166**, 368-379 (1987).
2. Martinez-Rucobo, F. W., Sainsbury, S., Cheung, A. C. & Cramer, P. Architecture of the RNA polymerase-Spt4/5 complex and basis of universal transcription processivity. *EMBO J.* **30**, 1302-1310 (2011).
3. Meyer, O. & Schlegel, H. G. Biology of aerobic carbon monoxide-oxidizing bacteria. *Annu. Rev. Microbiol.* **37**, 277-310 (1983).
4. Sambrook, J., Fritsch, E. F. & Maniatis, T. in *Molecular Cloning - A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1994).
5. Burmann, B. M., Luo, X., Wahl, M. C., Rösch, P. & Gottesman, M. E. Fine tuning of the *E. coli* NusB:NusE complex affinity to *BoxA* RNA is required for processive antitermination. *Nucleic Acids Res.* **38**, 314-326 (2010).
6. Burmann, B. M. *et al.* A NusE:NusG complex links transcription and translation. *Science* **328**, 501-504 (2010).
7. Luo, X. *et al.* Structural and functional analysis of the *E. coli* NusB-S10 transcription antitermination complex. *Mol. Cell* **32**, 791-802 (2008).
8. Schweimer, K. *et al.* NusA interaction with the  $\alpha$ -subunit of *E. coli* RNA polymerase is via the UP-element site and releases autoinhibition. *Structure* **19**, 945-954 (2011).
9. Burmann, B. M., Schweimer, K., Scheckenhofer, U. & Rösch, P. Domain interactions of the transcription:translation coupling factor *E.coli* NusG are intermolecular and transient. *Biochem. J.* **435**, 783-789 (2011).
10. Herzberg, C. *et al.* SPINE: a method for the rapid detection and analysis of protein-protein interactions *in vivo*. *Proteomics* **7**, 4032-4035 (2007).

11. Schrödinger L. The PyMOL molecular graphics system, version 1.3. *Schrödinger, LLC, Mannheim, Germany* (2010).