

## Supplementary Information

### Determination of RNA polymerase binding surfaces of transcription factors by NMR spectroscopy

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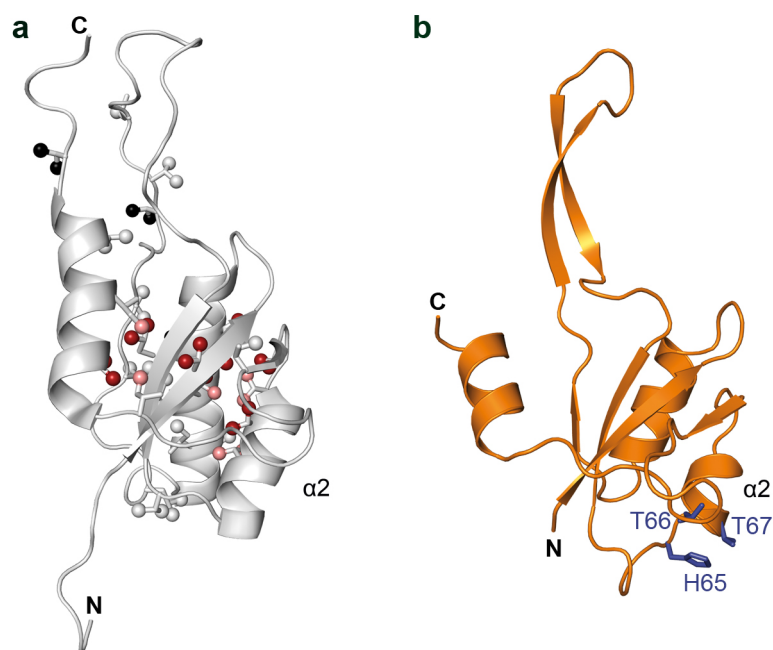
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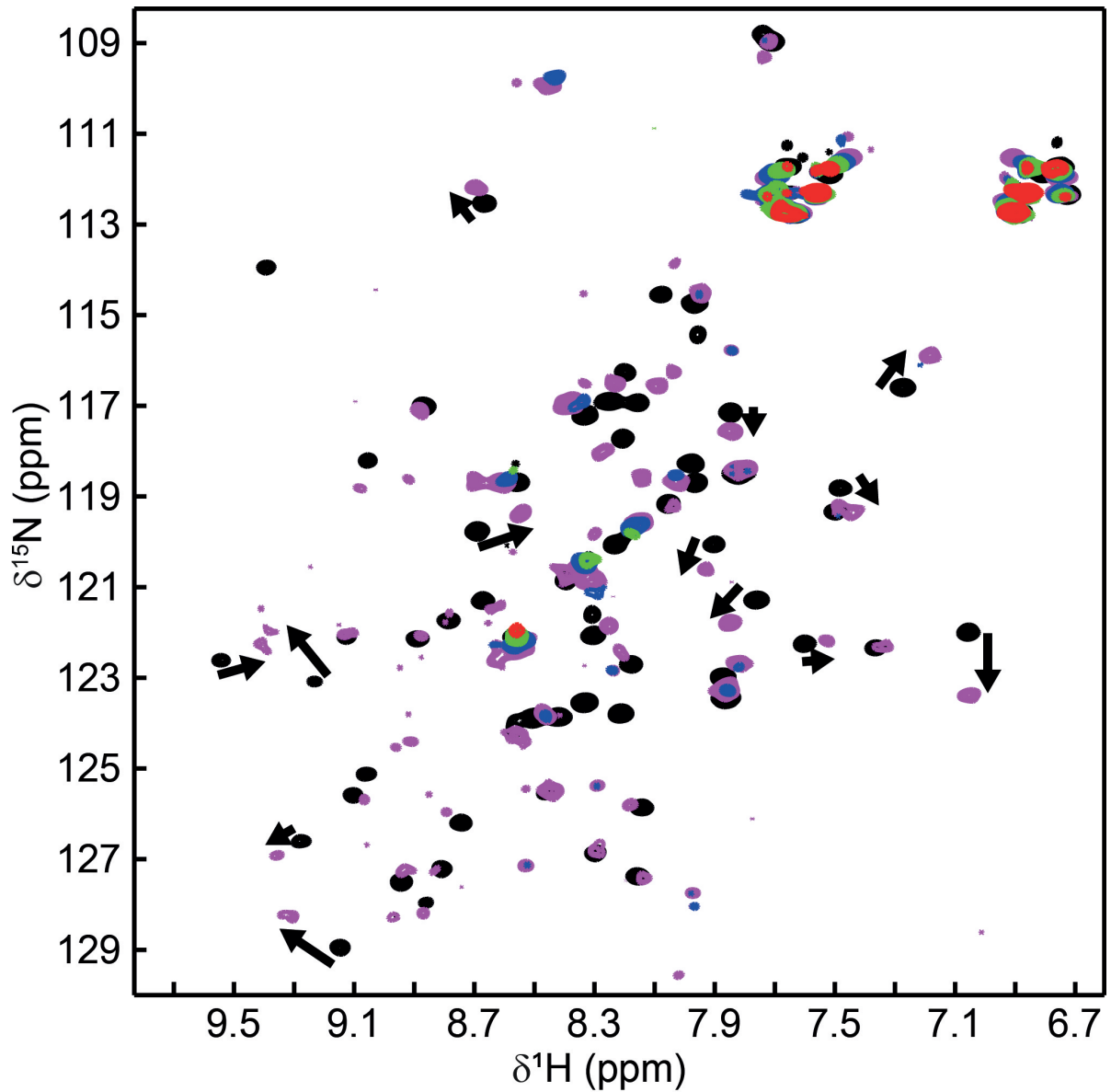
**Supplementary Table 1: Coordinates of the  $\beta$  flap tip helix in the modeled NusA-NTD<sup>A</sup>:*Tt*RNAP complex.** The table is an extract of the PDB file of elongating *Tt*RNAP (residues 767-781 of the  $\beta$  subunit; PDB ID: 2O5I) docked to NusA-NTD<sup>A</sup> as described in the Material and Methods section, giving the position of *Tt*RNAP relative to the deposited coordinates of NusA-NTD<sup>A</sup> (PDB ID: 2KWP).

ATOM	10777	N	PRO	C	767	3.453	-1.849	-42.571	1.00	90.52	N
ATOM	10778	CA	PRO	C	767	2.398	-2.073	-41.584	1.00	91.06	C
ATOM	10779	C	PRO	C	767	2.633	-1.165	-40.362	1.00	92.21	C
ATOM	10780	O	PRO	C	767	3.412	-0.213	-40.472	1.00	92.68	O
ATOM	10781	CB	PRO	C	767	2.524	-3.559	-41.274	1.00	90.38	C
ATOM	10782	CG	PRO	C	767	3.028	-4.129	-42.533	1.00	90.03	C
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ATOM	10784	N	THR	C	768	2.013	-1.418	-39.212	1.00	92.37	N
ATOM	10785	CA	THR	C	768	2.261	-0.517	-38.082	1.00	93.42	C
ATOM	10786	C	THR	C	768	2.739	-1.281	-36.849	1.00	94.34	C
ATOM	10787	O	THR	C	768	2.104	-2.254	-36.442	1.00	94.97	O
ATOM	10788	CB	THR	C	768	0.994	0.286	-37.704	1.00	92.74	C
ATOM	10789	OG1	THR	C	768	0.329	0.726	-38.894	1.00	92.51	O
ATOM	10790	CG2	THR	C	768	1.369	1.533	-36.866	1.00	91.14	C
ATOM	10791	N	PRO	C	769	3.867	-0.844	-36.239	1.00	95.40	N
ATOM	10792	CA	PRO	C	769	4.475	-1.458	-35.040	1.00	95.44	C
ATOM	10793	C	PRO	C	769	3.577	-1.368	-33.769	1.00	95.51	C
ATOM	10794	O	PRO	C	769	3.583	-2.294	-32.943	1.00	95.59	O
ATOM	10795	CB	PRO	C	769	5.803	-0.706	-34.892	1.00	96.45	C
ATOM	10796	CG	PRO	C	769	6.147	-0.342	-36.332	1.00	95.78	C
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ATOM	10799	CA	GLU	C	770	1.962	-0.077	-32.434	1.00	93.34	C
ATOM	10800	C	GLU	C	770	0.563	-0.681	-32.666	1.00	93.16	C
ATOM	10801	O	GLU	C	770	-0.118	-1.081	-31.718	1.00	92.30	O
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ATOM	10803	CG	GLU	C	770	3.152	2.249	-32.385	1.00	90.19	C
ATOM	10804	CD	GLU	C	770	3.957	2.594	-31.128	1.00	88.39	C
ATOM	10805	OE1	GLU	C	770	4.437	1.679	-30.437	1.00	87.21	O
ATOM	10806	OE2	GLU	C	770	4.113	3.798	-30.832	1.00	87.50	O
ATOM	10807	N	GLU	C	771	0.159	-0.730	-33.938	1.00	93.66	N
ATOM	10808	CA	GLU	C	771	-1.116	-1.314	-34.376	1.00	95.22	C
ATOM	10809	C	GLU	C	771	-0.991	-2.838	-34.494	1.00	96.29	C
ATOM	10810	O	GLU	C	771	-1.993	-3.557	-34.560	1.00	96.81	O
ATOM	10811	CB	GLU	C	771	-1.531	-0.719	-35.743	1.00	95.59	C
ATOM	10812	CG	GLU	C	771	-2.798	-1.302	-36.423	1.00	95.80	C
ATOM	10813	CD	GLU	C	771	-2.986	-0.867	-37.893	1.00	96.05	C
ATOM	10814	OE1	GLU	C	771	-4.129	-0.944	-38.403	1.00	95.71	O
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ATOM	10816	N	ARG	C	772	0.255	-3.318	-34.526	1.00	95.94	N
ATOM	10817	CA	ARG	C	772	0.562	-4.755	-34.598	1.00	96.21	C
ATOM	10818	C	ARG	C	772	0.310	-5.431	-33.247	1.00	97.11	C
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ATOM	10821	CG	ARG	C	772	2.497	-6.441	-35.071	1.00	92.48	C
ATOM	10822	CD	ARG	C	772	1.926	-7.149	-36.290	1.00	91.56	C
ATOM	10823	NE	ARG	C	772	1.943	-6.309	-37.490	1.00	90.45	N
ATOM	10824	CZ	ARG	C	772	1.929	-6.773	-38.739	1.00	90.61	C
ATOM	10825	NH1	ARG	C	772	1.906	-8.079	-38.978	1.00	91.27	N
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ATOM	10827	N	LEU	C	773	0.629	-4.710	-32.164	1.00	97.02	N
ATOM	10828	CA	LEU	C	773	0.423	-5.199	-30.800	1.00	97.16	C
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ATOM	10830	O	LEU	C	773	-1.557	-6.174	-29.874	1.00	97.78	O
ATOM	10831	CB	LEU	C	773	1.212	-4.334	-29.791	1.00	96.99	C
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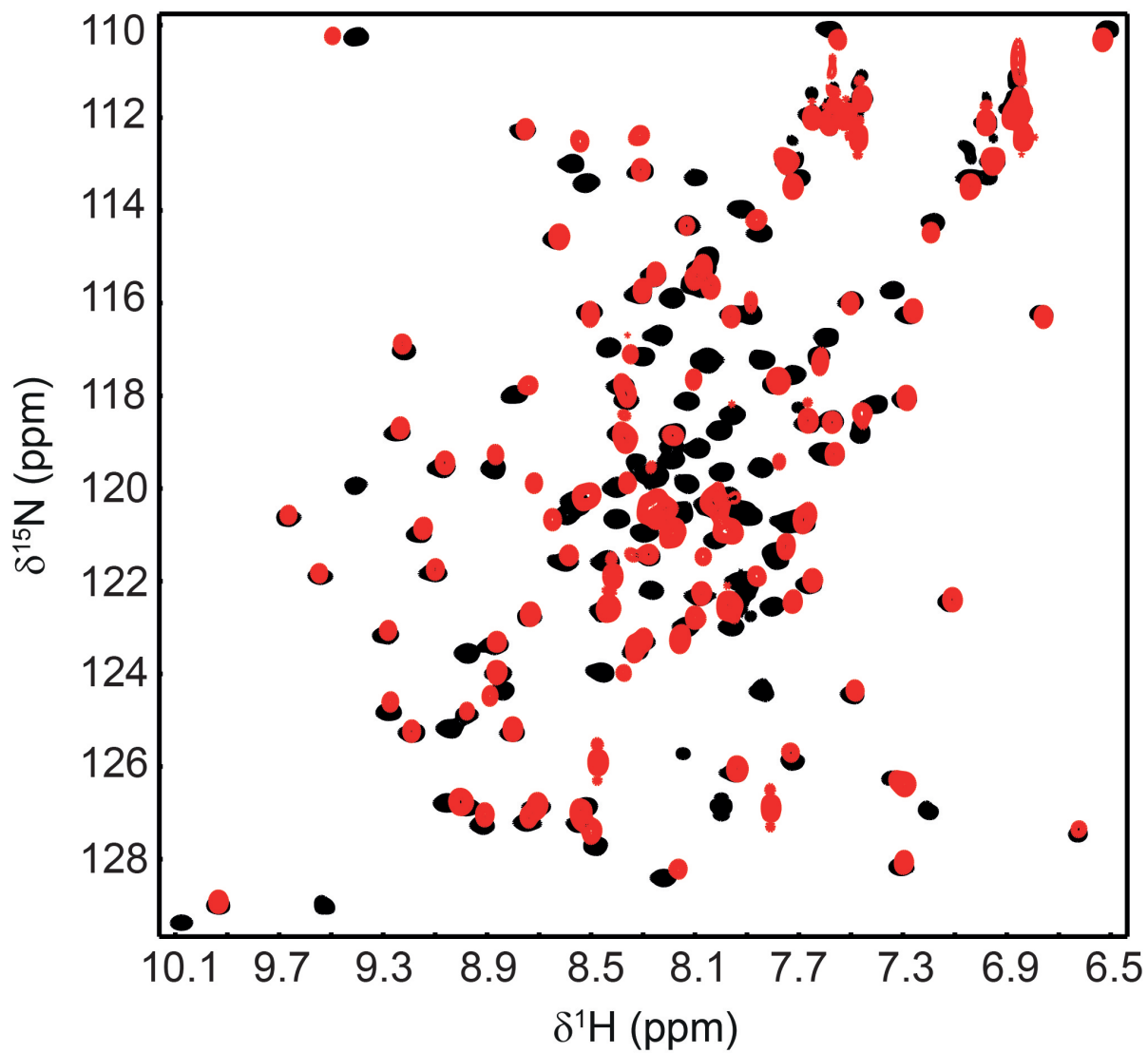
ATOM	10833	CD1	LEU	C	773	3.329	-3.401	-28.800	1.00	96.92	C
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ATOM	10844	CA	ARG	C	775	-4.402	-6.381	-33.208	1.00	94.68	C
ATOM	10845	C	ARG	C	775	-4.209	-7.740	-32.520	1.00	94.67	C
ATOM	10846	O	ARG	C	775	-5.184	-8.404	-32.214	1.00	94.44	O
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ATOM	10850	NE	ARG	C	775	-6.342	-4.568	-36.888	1.00	89.53	N
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ATOM	10858	CB	SER	C	776	-1.021	-9.512	-31.521	1.00	94.77	C
ATOM	10859	OG	SER	C	776	-0.360	-9.645	-32.780	1.00	94.97	O
ATOM	10860	N	ILE	C	777	-3.334	-8.580	-29.415	1.00	93.70	N
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ATOM	10864	CB	ILE	C	777	-3.896	-7.308	-27.305	1.00	92.10	C
ATOM	10865	CG1	ILE	C	777	-2.455	-6.821	-27.095	1.00	91.21	C
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ATOM	10867	CD1	ILE	C	777	-2.357	-5.456	-26.433	1.00	90.12	C
ATOM	10868	N	PHE	C	778	-6.256	-8.615	-28.820	1.00	93.48	N
ATOM	10869	CA	PHE	C	778	-7.673	-9.029	-28.887	1.00	93.33	C
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ATOM	10871	O	PHE	C	778	-8.818	-10.872	-29.934	1.00	93.84	O
ATOM	10872	CB	PHE	C	778	-8.583	-7.804	-29.105	1.00	92.40	C
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ATOM	10874	CD1	PHE	C	778	-7.540	-6.454	-27.198	1.00	91.29	C
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ATOM	10876	CE1	PHE	C	778	-7.638	-5.546	-26.104	1.00	90.92	C
ATOM	10877	CE2	PHE	C	778	-10.067	-5.440	-26.441	1.00	91.24	C
ATOM	10878	CZ	PHE	C	778	-8.906	-5.037	-25.723	1.00	90.85	C
ATOM	10879	N	GLY	C	779	-7.153	-9.925	-31.108	1.00	95.41	N
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ATOM	10881	C	GLY	C	779	-6.406	-10.473	-33.421	1.00	97.94	C
ATOM	10882	O	GLY	C	779	-6.809	-9.697	-34.309	1.00	98.21	O
ATOM	10883	N	GLU	C	780	-5.190	-11.038	-33.414	1.00	98.62	N
ATOM	10884	CA	GLU	C	780	-4.154	-10.817	-34.448	1.00	98.20	C
ATOM	10885	C	GLU	C	780	-4.735	-10.916	-35.859	1.00	97.77	C
ATOM	10886	O	GLU	C	780	-4.483	-10.050	-36.707	1.00	97.44	O
ATOM	10887	CB	GLU	C	780	-3.002	-11.842	-34.299	1.00	98.74	C
ATOM	10888	CG	GLU	C	780	-3.479	-13.315	-34.185	1.00	98.09	C
ATOM	10889	CD	GLU	C	780	-2.821	-14.257	-35.186	1.00	97.77	C
ATOM	10890	OE1	GLU	C	780	-3.289	-15.415	-35.292	1.00	97.28	O
ATOM	10891	OE2	GLU	C	780	-1.848	-13.846	-35.859	1.00	97.54	O
ATOM	10892	N	LYS	C	781	-5.507	-11.978	-36.099	1.00	97.33	N
ATOM	10893	CA	LYS	C	781	-6.147	-12.202	-37.392	1.00	96.31	C
ATOM	10894	C	LYS	C	781	-7.292	-11.208	-37.620	1.00	95.87	C
ATOM	10895	O	LYS	C	781	-8.485	-11.533	-37.511	1.00	96.54	O
ATOM	10896	CB	LYS	C	781	-6.675	-13.642	-37.491	1.00	95.28	C
ATOM	10897	CG	LYS	C	781	-7.331	-14.173	-36.226	1.00	93.86	C
ATOM	10898	CD	LYS	C	781	-8.176	-15.409	-36.492	1.00	93.01	C
ATOM	10899	CE	LYS	C	781	-7.389	-16.500	-37.197	1.00	92.99	C
ATOM	10900	NZ	LYS	C	781	-6.056	-16.712	-36.568	1.00	93.33	N



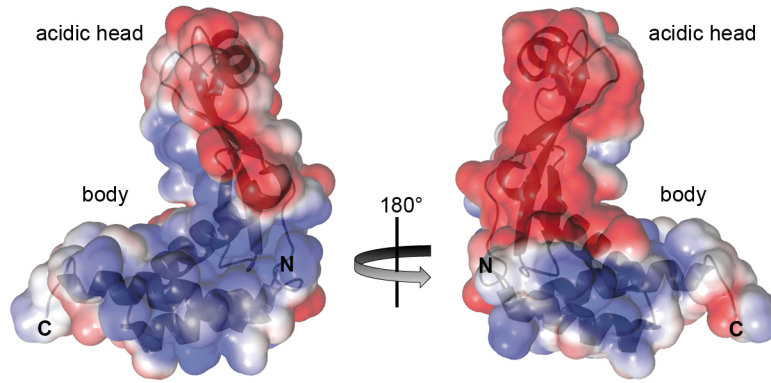
**Supplementary Figure 1: Structures of NusG-NTD and RfaH-NTD.** (a) RNAP binding site of NusG-NTD. Structure of NusG-NTD (PDB ID: 2K06) in cartoon representation, grey. Ile, Leu, and Val residues are shown as sticks with the carbon atoms of their methyl groups represented as spheres. Strongly affected methyl groups, dark red; slightly affected methyl groups, light red; unaffected methyl groups, grey; unassigned methyl groups, black. (b)  $\beta$ GL binding motif of RfaH-NTD. Structure of RfaH-NTD (PDB ID: 2OUG) in cartoon representation, orange. Residues involved in  $\beta$ GL binding are shown as blue sticks and labeled.



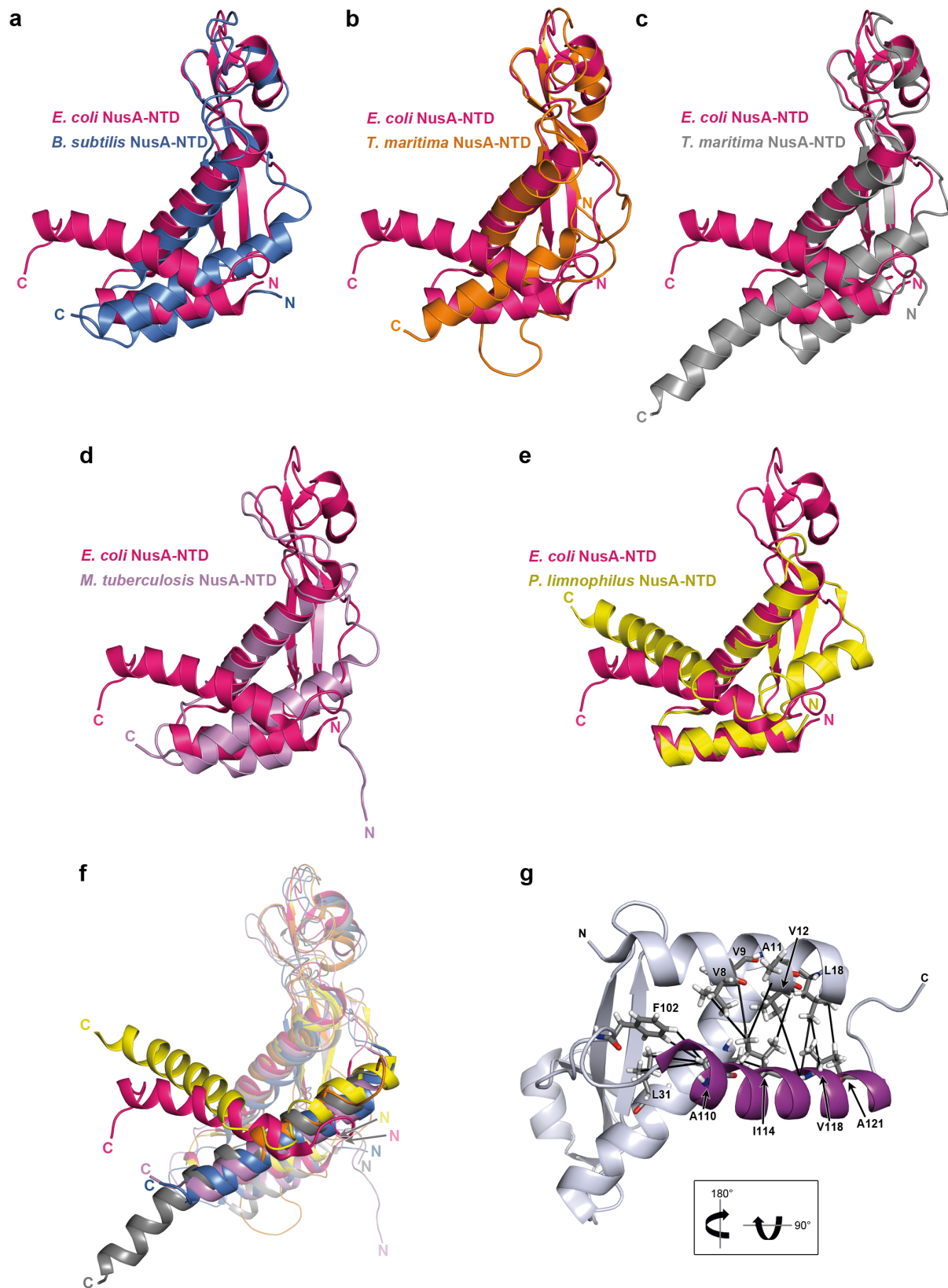
**Supplementary Figure 2: Displacement of RNAP from NusE $^{\Delta}$  by NusG-CTD.** 2D [ $^1\text{H}$ ,  $^{15}\text{N}$ ]-HSQC spectra of free NusB:[ $^{15}\text{N}$ ]-NusE $^{\Delta}$ , black, NusB:[ $^{15}\text{N}$ ]-NusE $^{\Delta}$  in the presence of RNAP in equimolar concentration, red, and NusB:[ $^{15}\text{N}$ ]-NusE $^{\Delta}$  in the presence of RNAP and NusG-CTD (molar ratio 1:1:1, green; 1:1:3, blue; 1:1:10, purple). Black arrows indicate the chemical shift changes that occur upon complex formation of NusG-CTD and NusB:[ $^{15}\text{N}$ ]-NusE $^{\Delta}$ .



**Supplementary Figure 3: Superposition of the  $[^1\text{H},^{15}\text{N}]$ -HSQC spectra of  $[^{15}\text{N}]$ -NusA-NTD(1-137), red, and  $[^{15}\text{N}]$ -NusA-NTD<sup>A</sup>, black. The protein concentration was 400  $\mu\text{M}$  in each sample.**



**Supplementary Figure 4: Electrostatic potential molecular surface of NusA-NTD<sup>Δ</sup>.** NusA-NTD<sup>Δ</sup> in cartoon and surface representation. The electrostatic surface potential is colored from -2 kT/e, red, to +2 kT/e, blue.



**Supplementary Figure 5: Comparison of NusA-NTD structures.** (a-e) Superposition of NusA-NTD<sup>A</sup> (pink) with (a) *Bs*NusA-NTD (blue, PDB ID: 2MT4, root mean square deviation



(r.m.s.d.) 1.8 Å), **(b)** *Tm*NusA-NTD (orange, PDB ID: 1HH2, r.m.s.d. 1.9 Å) **(c)** *Tm*NusA-NTD (grey, PDB ID: 1L2F, r.m.s.d. 1.7 Å), **(d)** *Mt*NusA-NTD (violet, PDB ID: 1K0R, r.m.s.d. 1.8 Å), and **(e)** *Pl*NusA-NTD (yellow, PDB ID: 4MTN, r.m.s.d. 1.4 Å). The linker helix was not used for the superpositions. **(f)** Superposition of NusA-NTD structures shown in **(a-e)**. The linker helix is shown in bright colors. **(g)** NOE network fixing the position of the linker helix in NusA-NTD<sup>Δ</sup> (cartoon representation, grey; the linker helix is highlighted in purple). The inset indicates how the molecule is rotated in respect to **(a)**. Residues participating in the NOE network are labeled and shown as sticks (carbon atoms, dark grey; nitrogen atoms, blue; oxygen atoms, red; hydrogen atoms, white). Unambiguously identified NOEs are shown as black lines. For clarity only one NOE is displayed per methyl group (using the corresponding methyl carbon atom as center).

## Supplementary References

1. Burmann, B. M. *et al.* A NusE:NusG Complex Links Transcription and Translation. *Science* **328**, 501-504 (2010).