Complete dataset:

Individual data sheets for all the eighty human r-proteins showing the position of the r-protein on mature subunit (A), its impacts on pre-rRNA processing and mature rRNA accumulation (B), on nucleolar structure (C), and on the p53 steady-state level (D).

(A) 3-D models of human ribosomal subunits based on PDB entries 3J3D and 3J3A, for SSU r-proteins, and 3J3F and 3J3B, for LSU r-proteins. The positions of individual r-proteins on the mature subunits are highlighted. On small subunits, the 18S rRNA is shown in gray; on large subunits, the 5S, 5.8S, and 28S rRNAs are shown in red, blue, and gray, respectively. Left, interface view; right, solvent view. The main ribosomal features are indicated (see Supplementary Fig. 10).

(B) Effects of r-protein depletion on pre-rRNA processing and mature rRNA accumulation: northern blots and ethidium-bromide-stained denaturing agarose gels showing all the pre-rRNA intermediates and mature rRNAs detected. The 28S/18S rRNA ratio was calculated from electropherograms. A calibration set (described in Supplementary Figs S5, S6) is included for reference. Schematics representing the RNAs detected are shown to the left. Quantifications are available in Fig 4. and Supplementary Figs S5, S6.

(C) Effect of r-protein depletion on nucleolar structure: representative microscopic images (blue signal, DAPI; green signal, fibrillarin) obtained after treatment in duplicate screens (i and ii) performed with three different siRNAs (#1, #2, and #3). iNo values for each screen are indicated to the right and on a scaled bar at the bottom. The iNo value ranges between 0 (unperturbed nucleolus) and 0.2 (severely disrupted structure).

(D) Effect of r-protein depletion on the p53 steady-state level: fluorescent quantitative western blotting was performed in triplicate (i, ii, iii). The p53 signal was corrected for loading, using β-actin detection as a reference, and expressed with respect to the signal obtained in cells treated with a non-targeting (Scr) control (lane 2). The p53 signal was expressed as a mean of three independent experiments (see Fig. 6 for details). A calibration set (described in Fig. 6) is included for reference.

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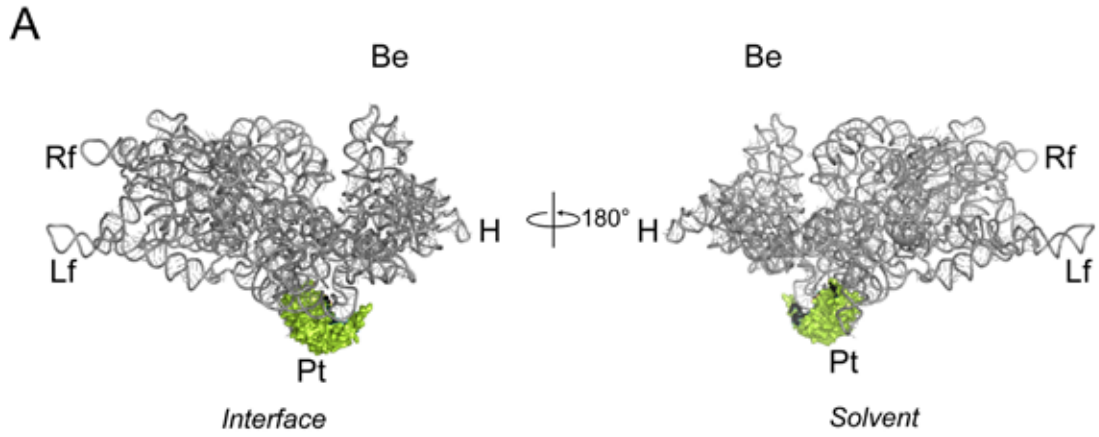
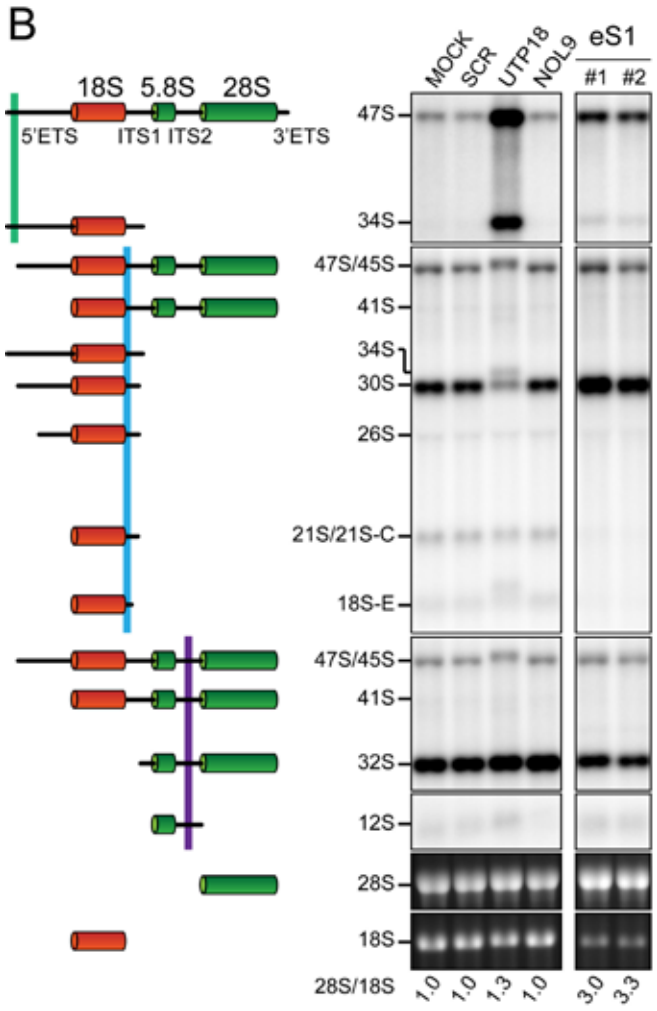
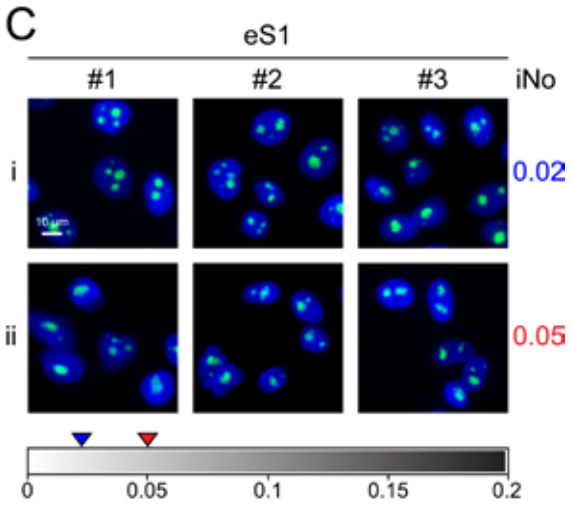
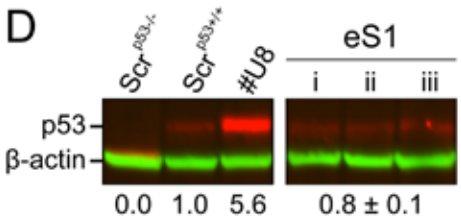
eS1 (RpS3a)









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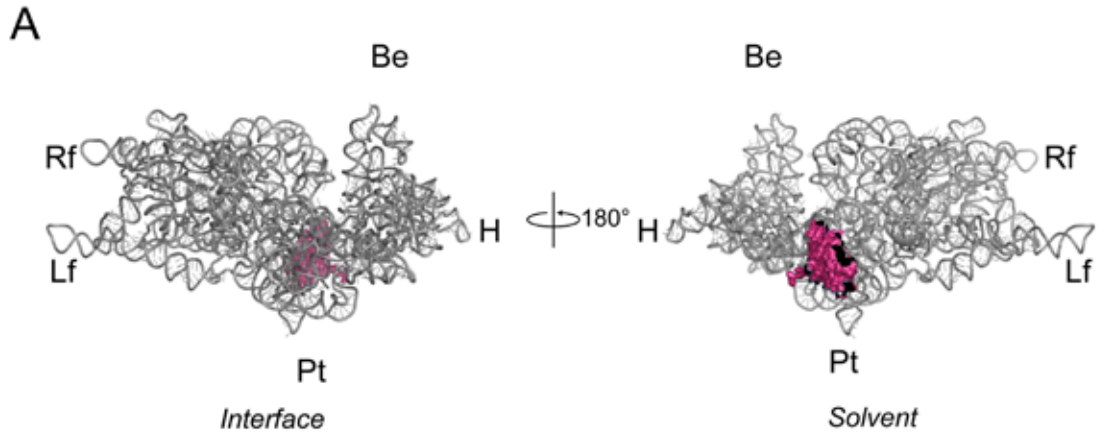
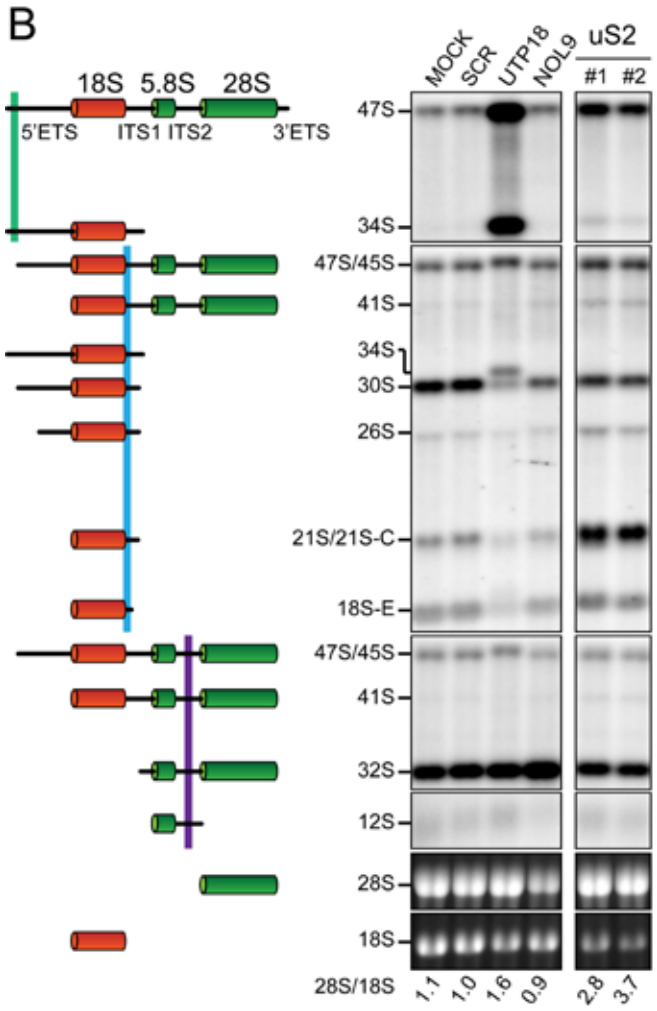
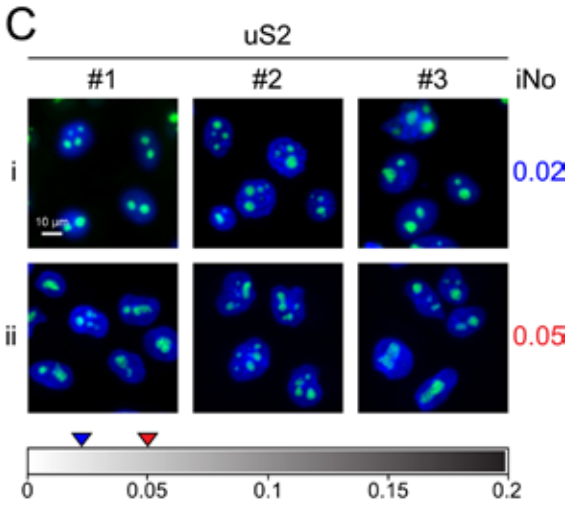
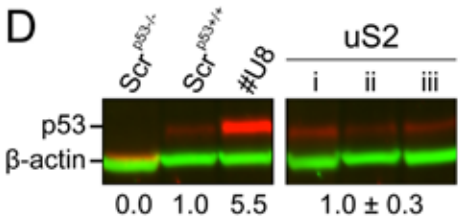
uS2 (RpSA)









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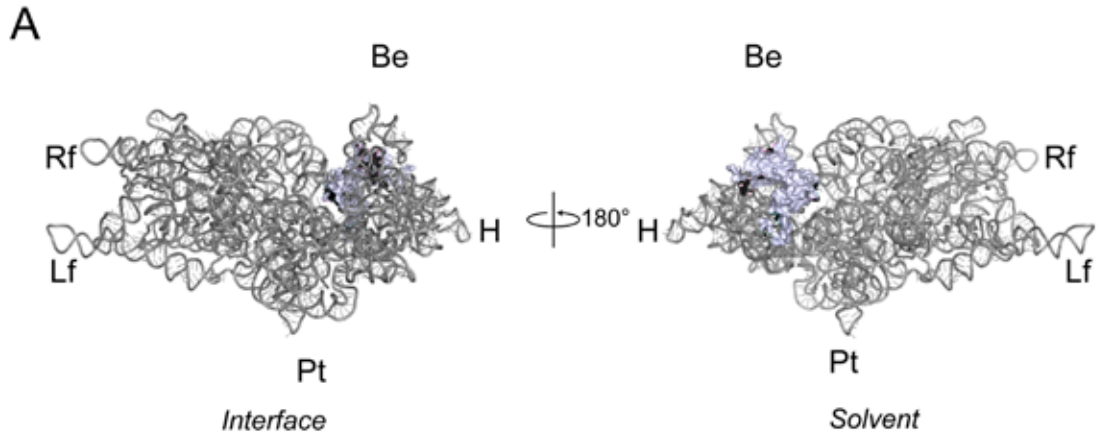
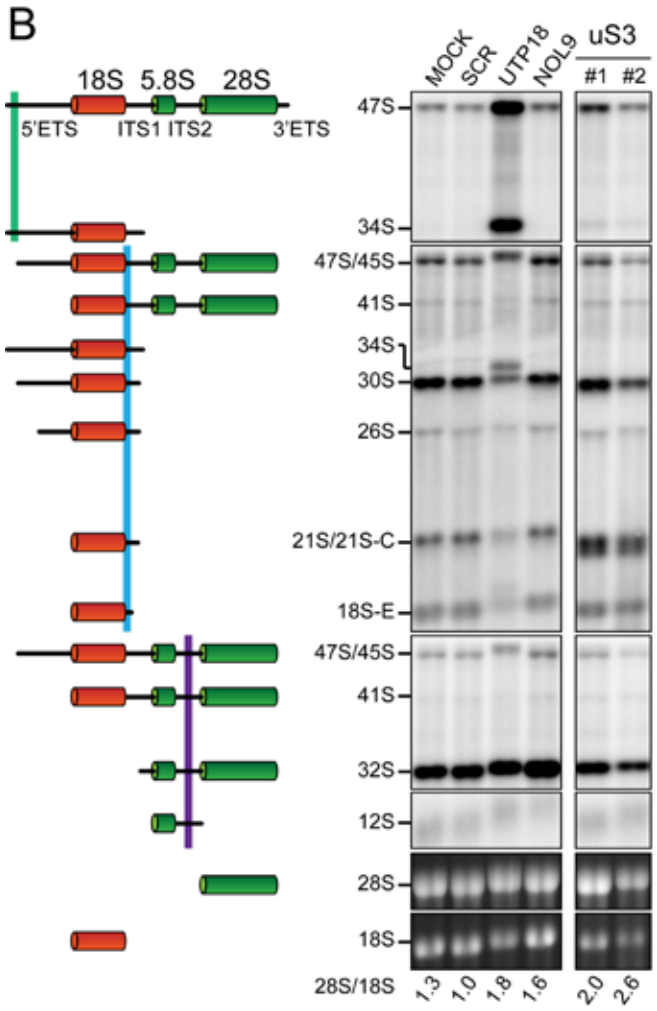
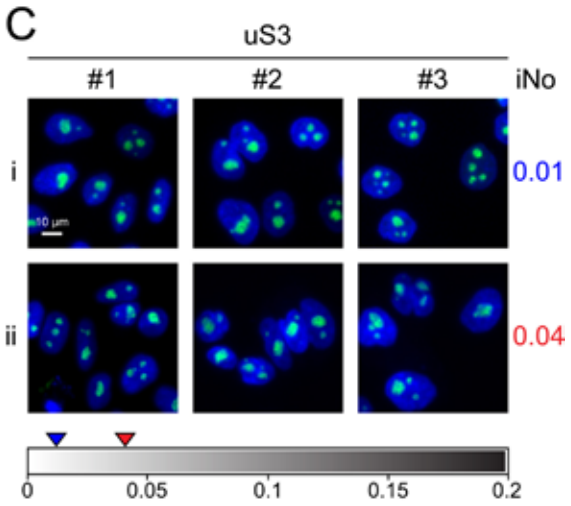
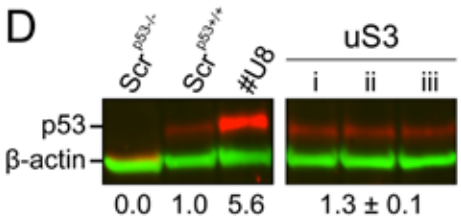
uS3 (RpS3)









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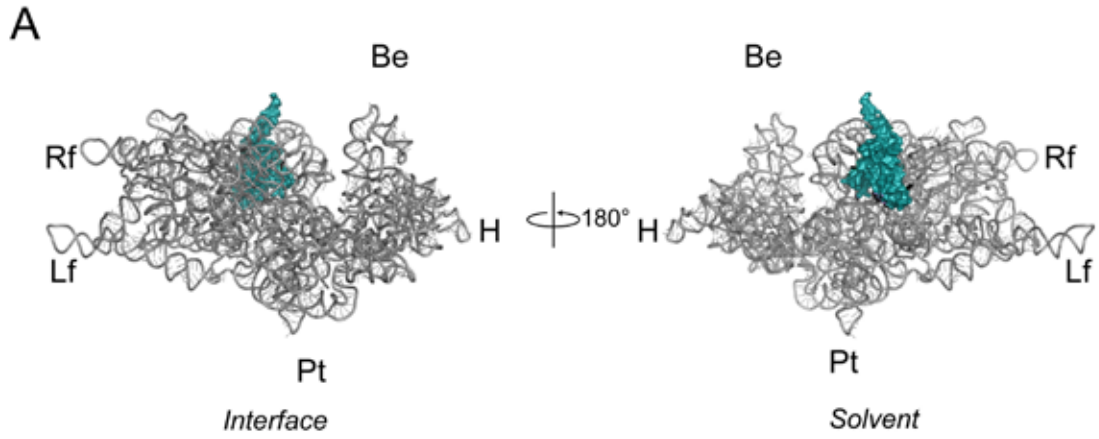
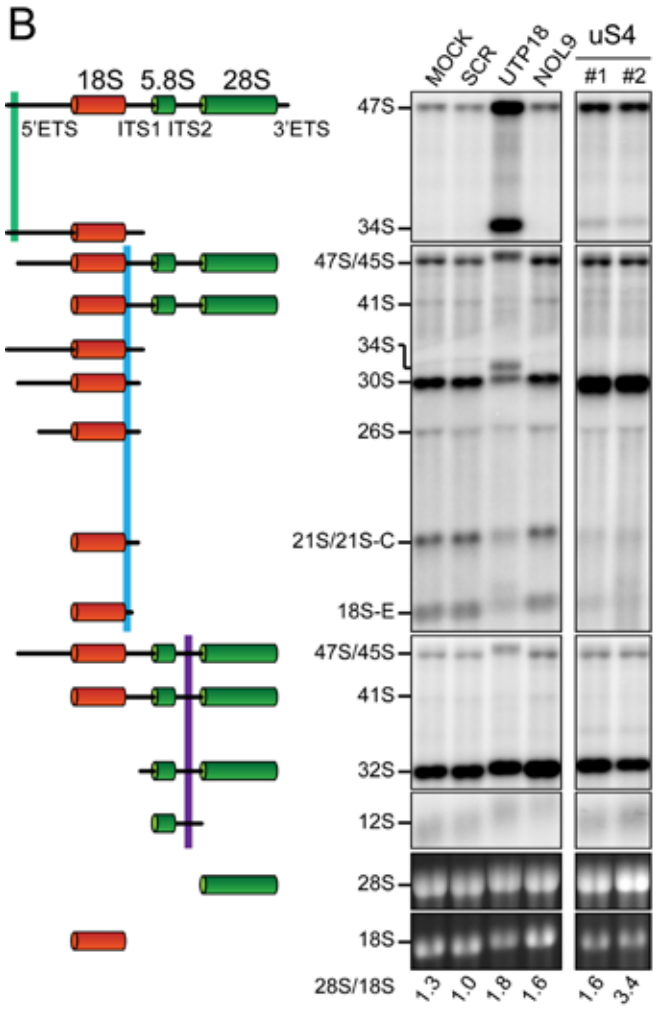
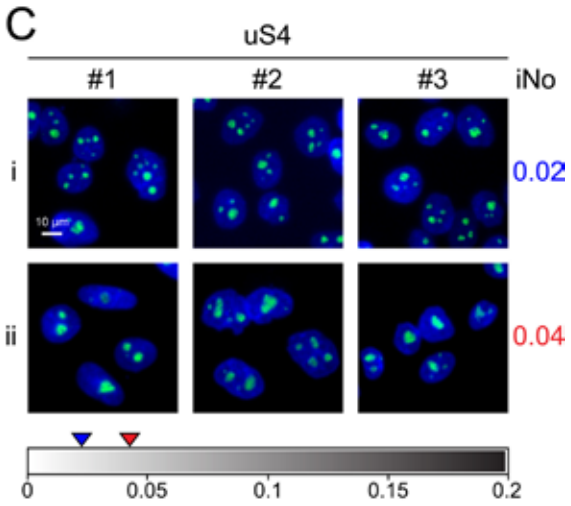
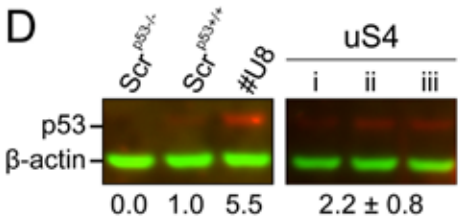
uS4 (RpS9)









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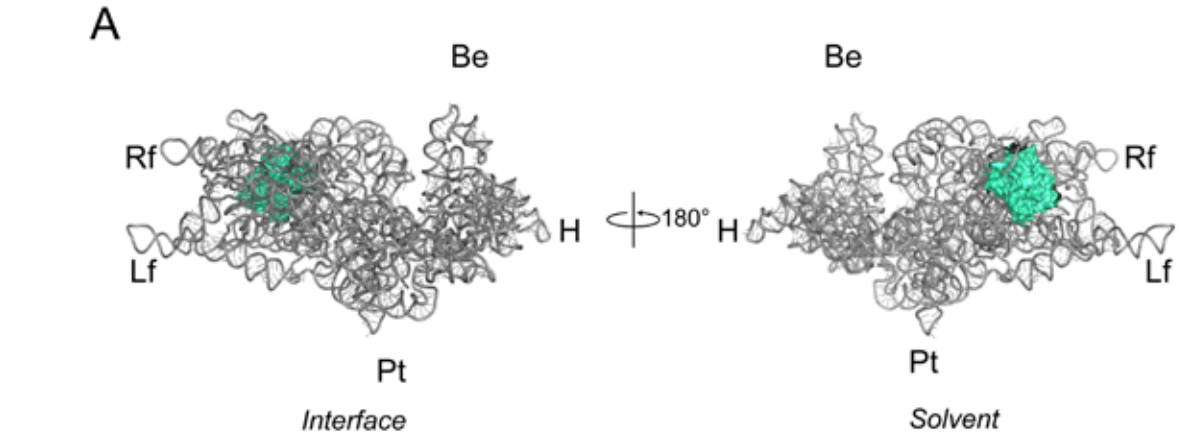
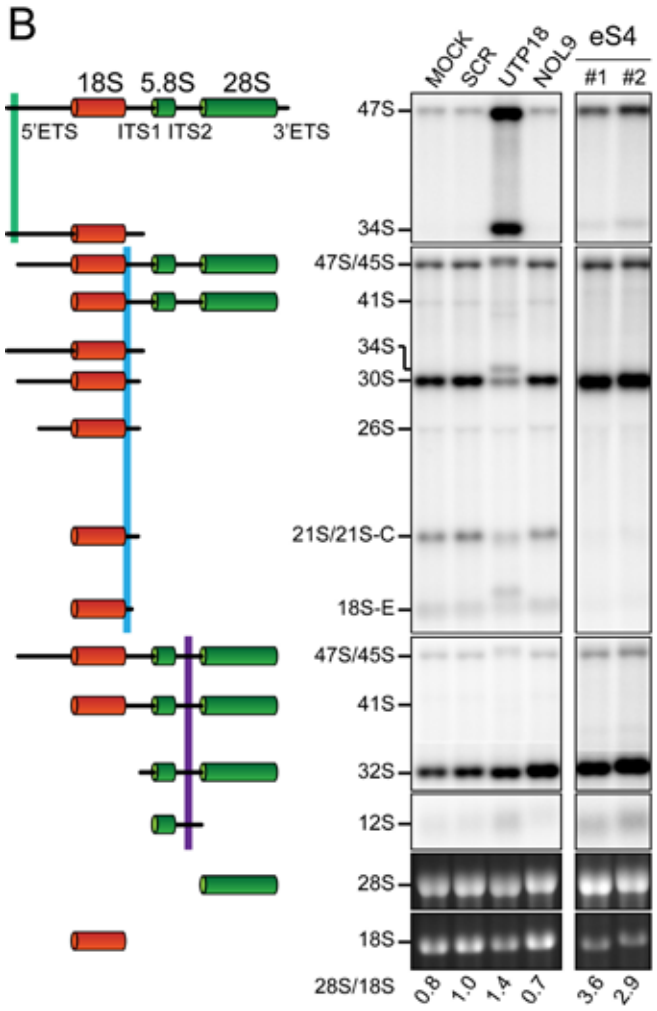
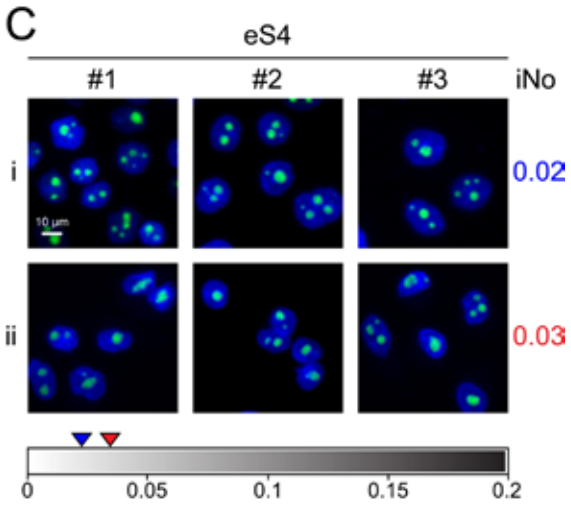
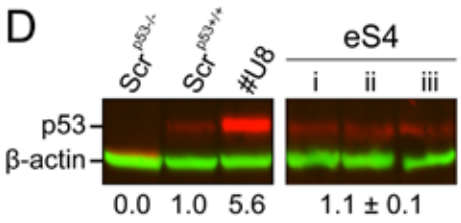
eS4 (RpS4)









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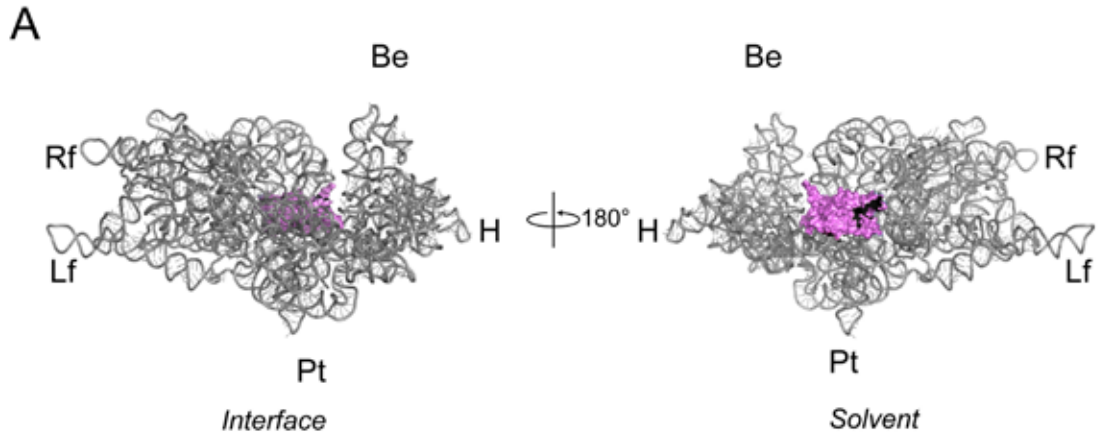
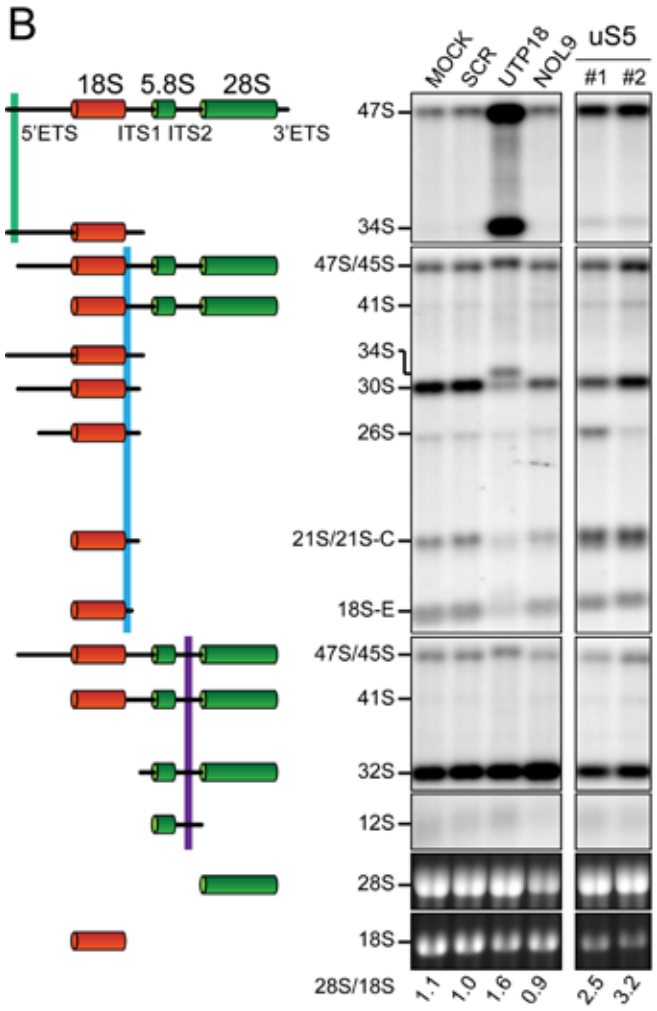
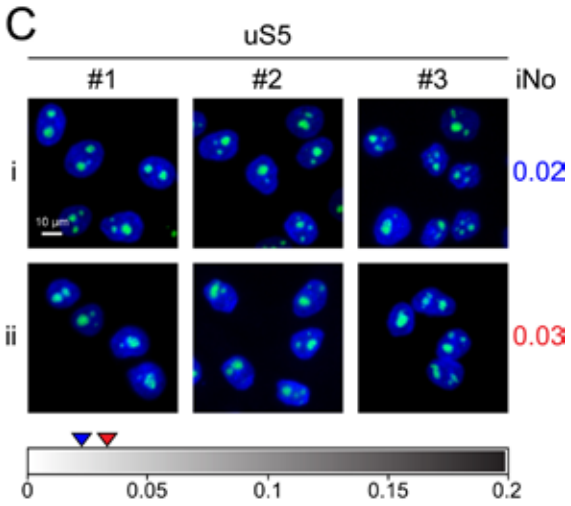
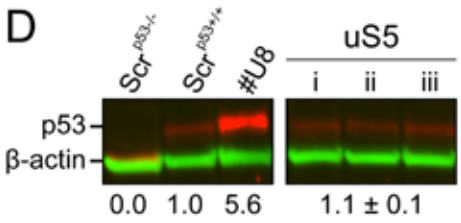
uS5 (RpS2)









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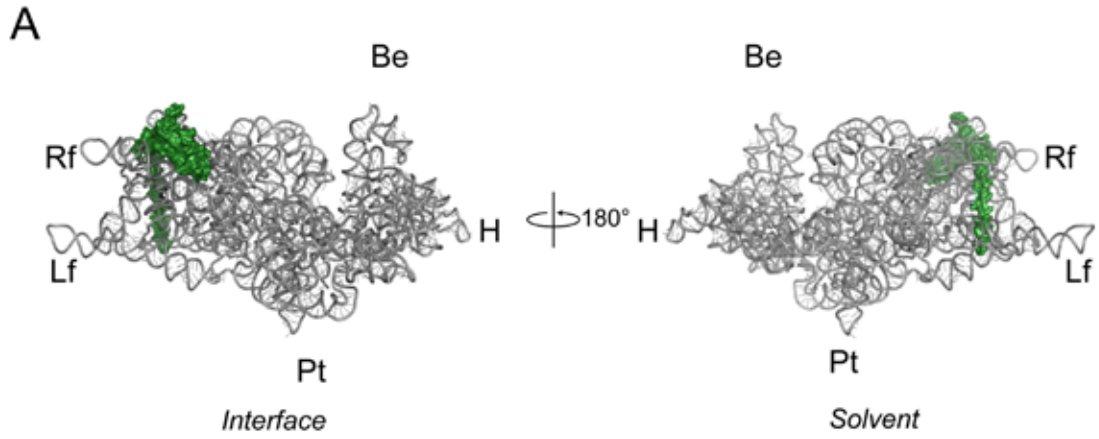
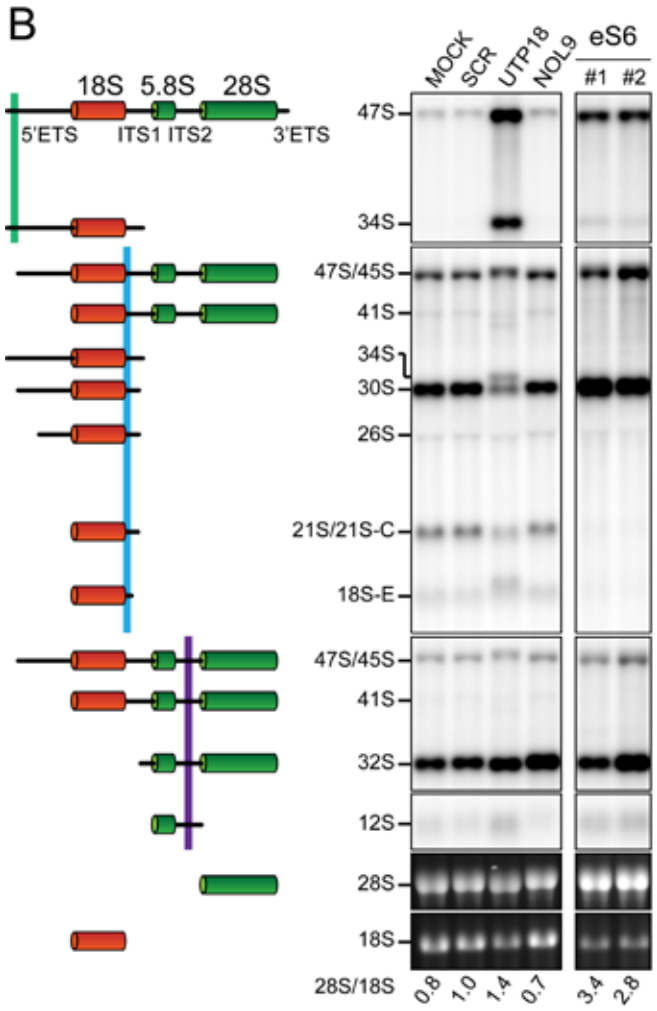
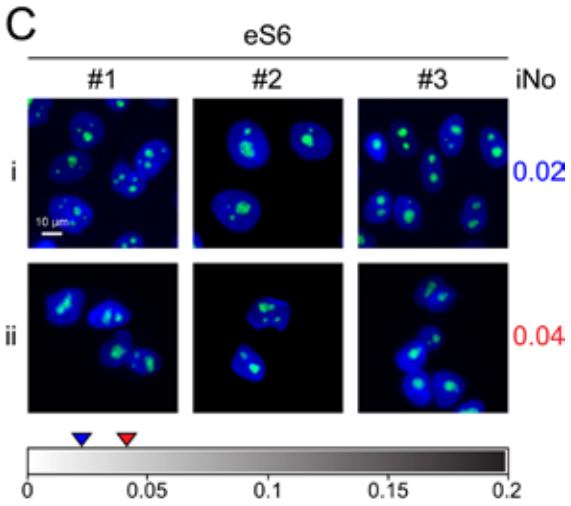
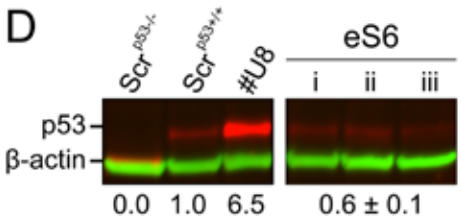
eS6 (RpS6)









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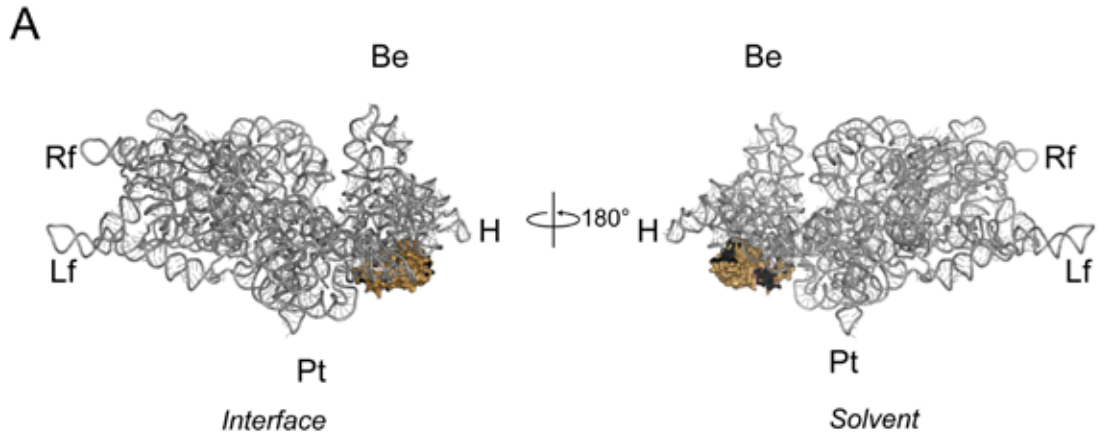
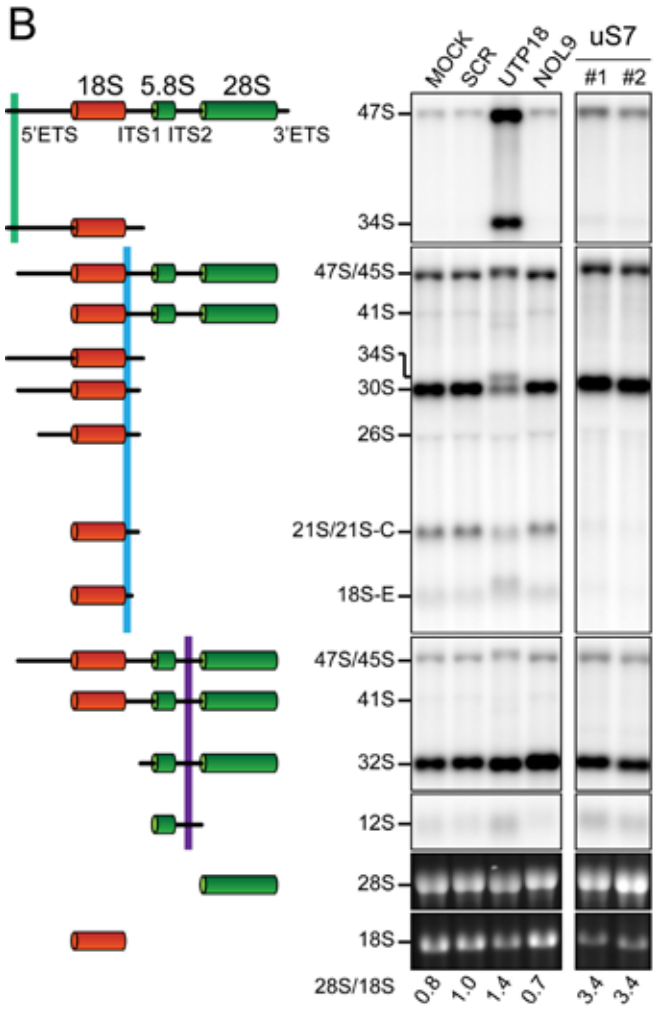
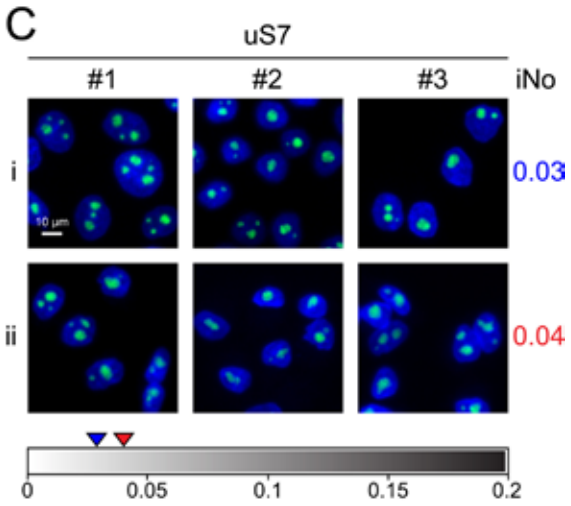
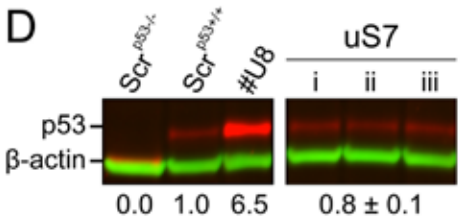
uS7 (RpS5)









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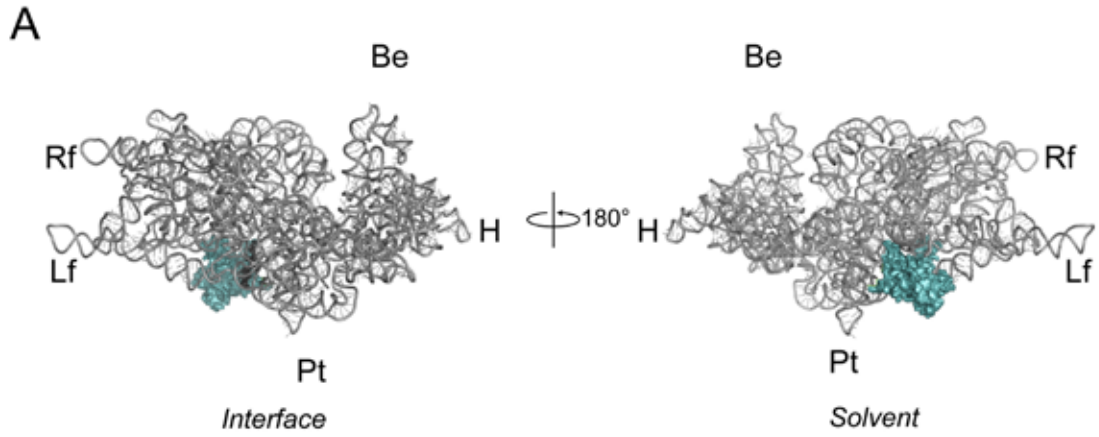
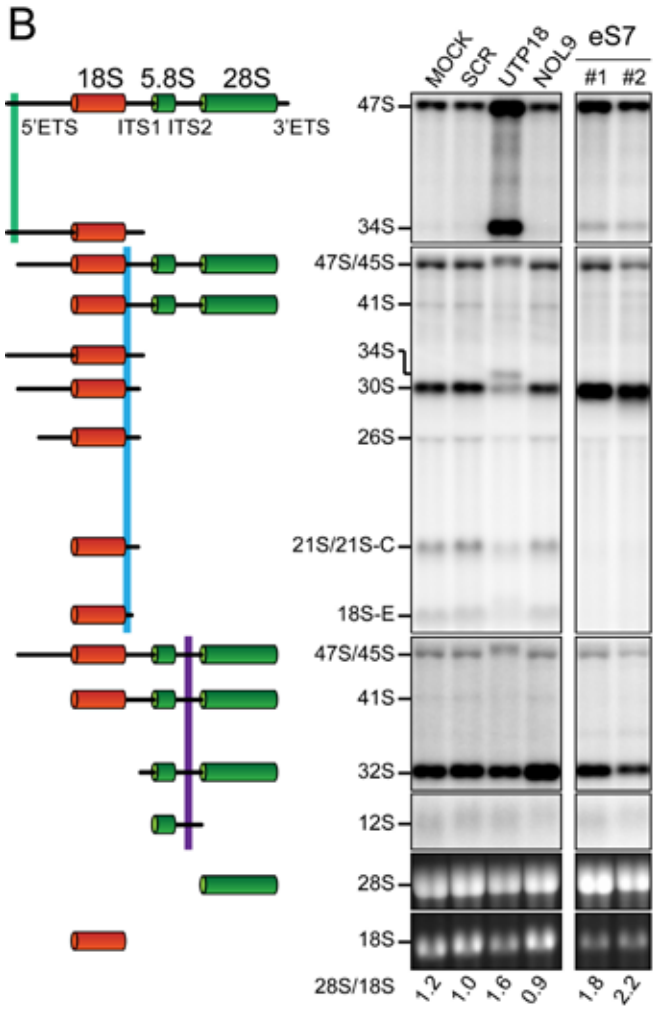
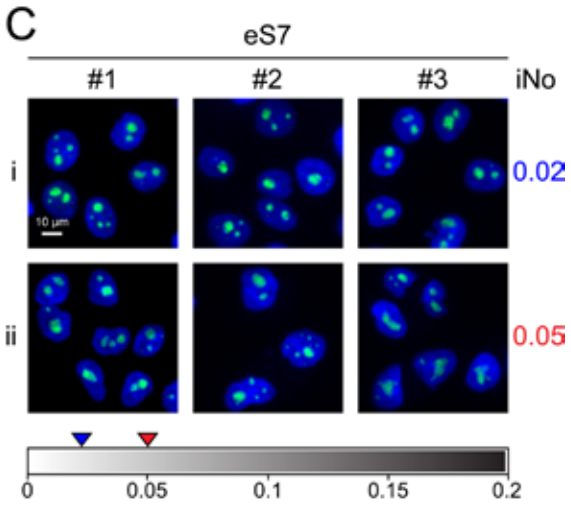
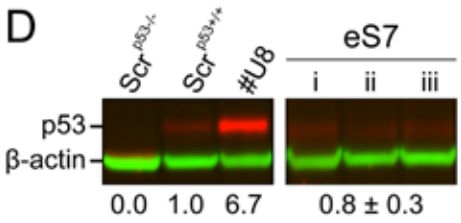
eS7 (RpS7)









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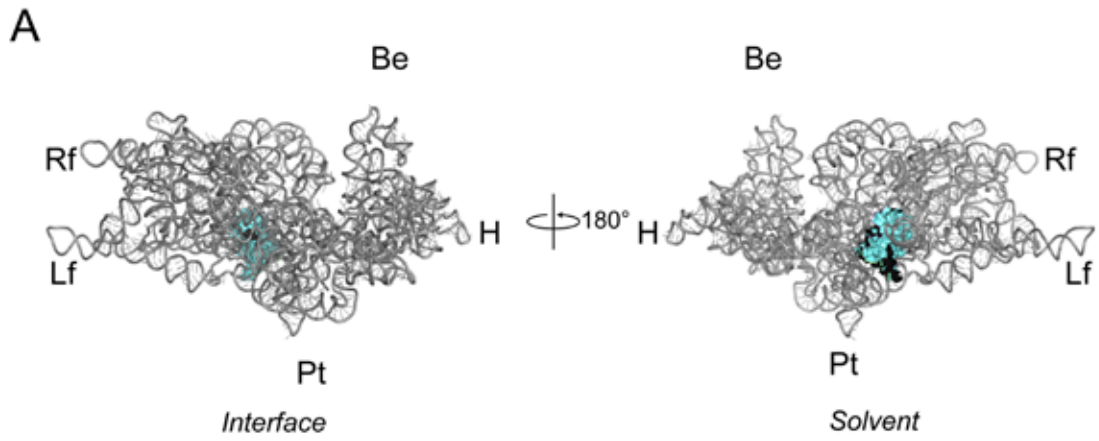
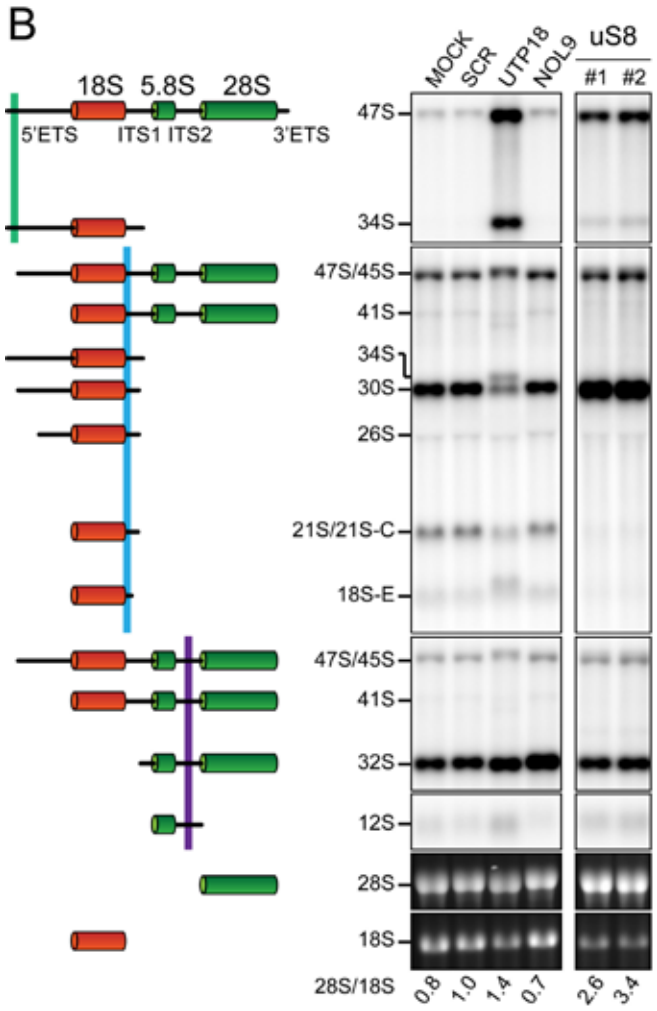
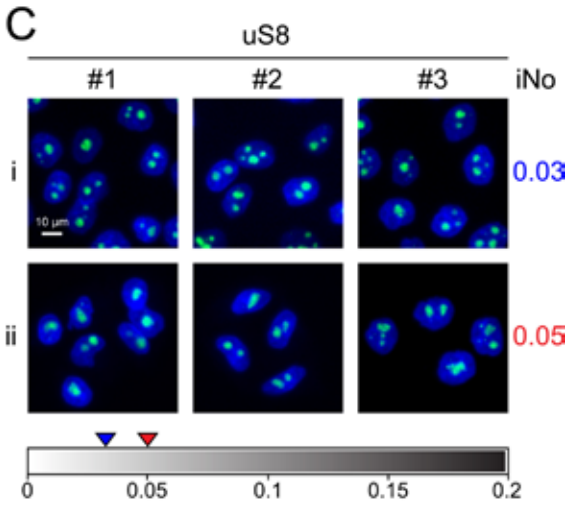
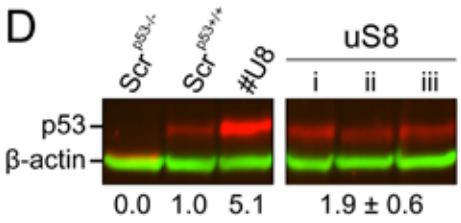
uS8 (RpS15a)









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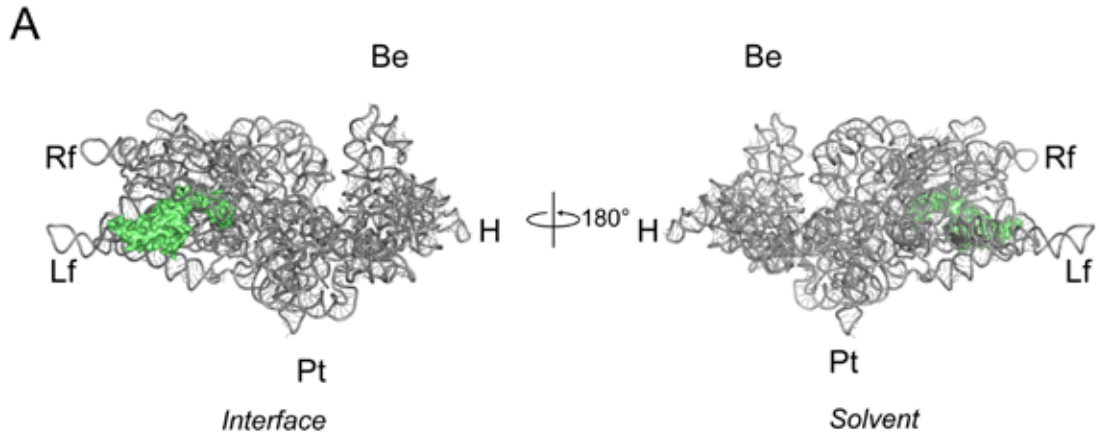
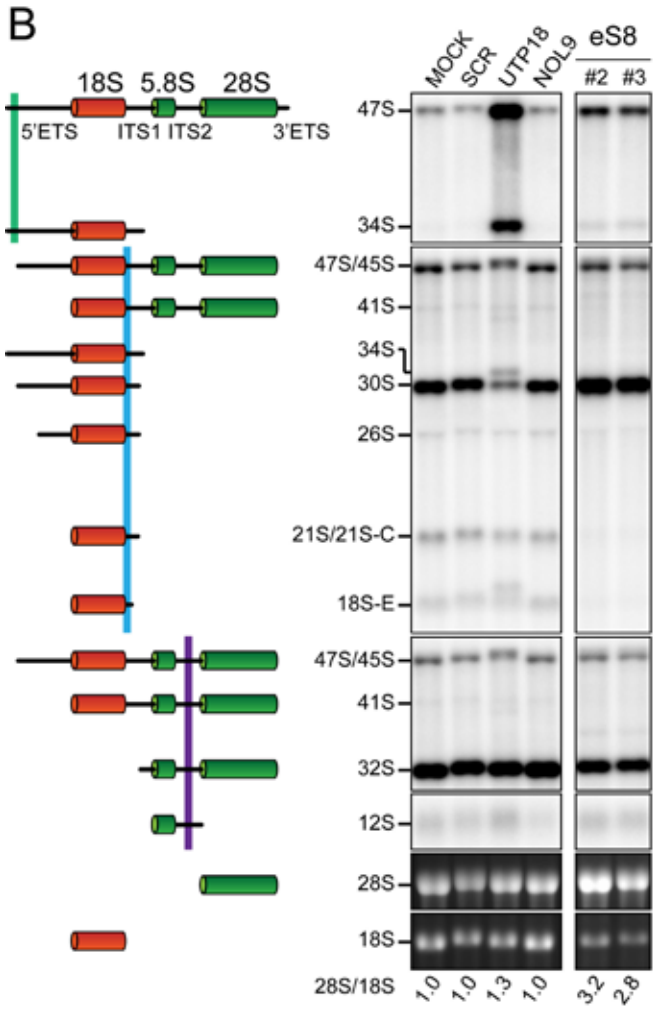
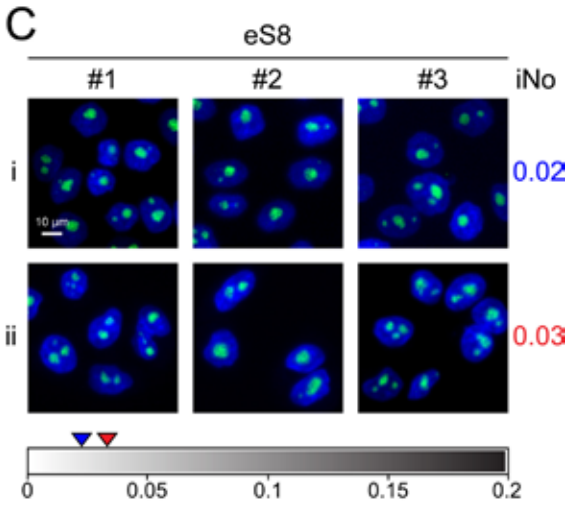
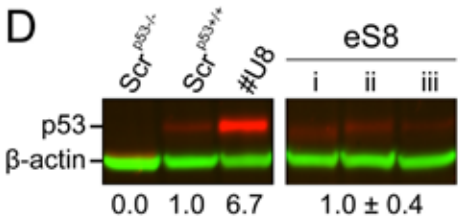
eS8 (RpS8)









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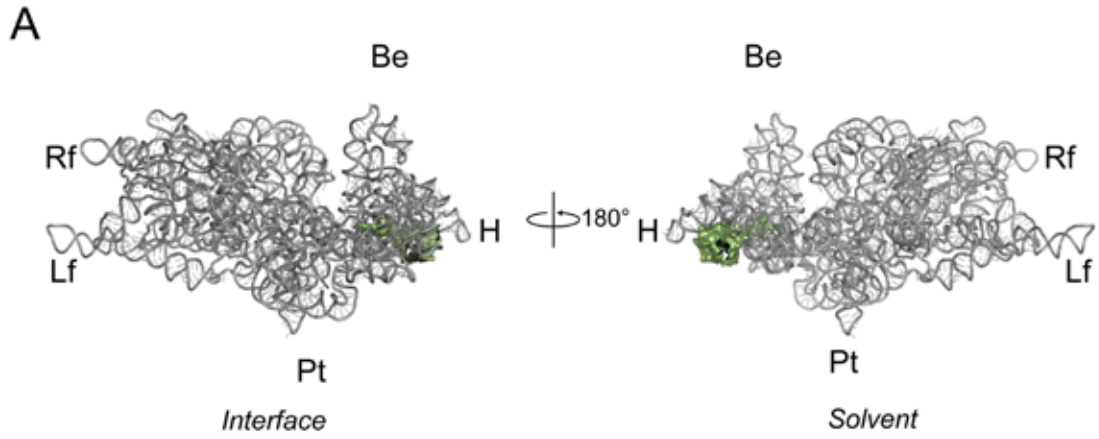
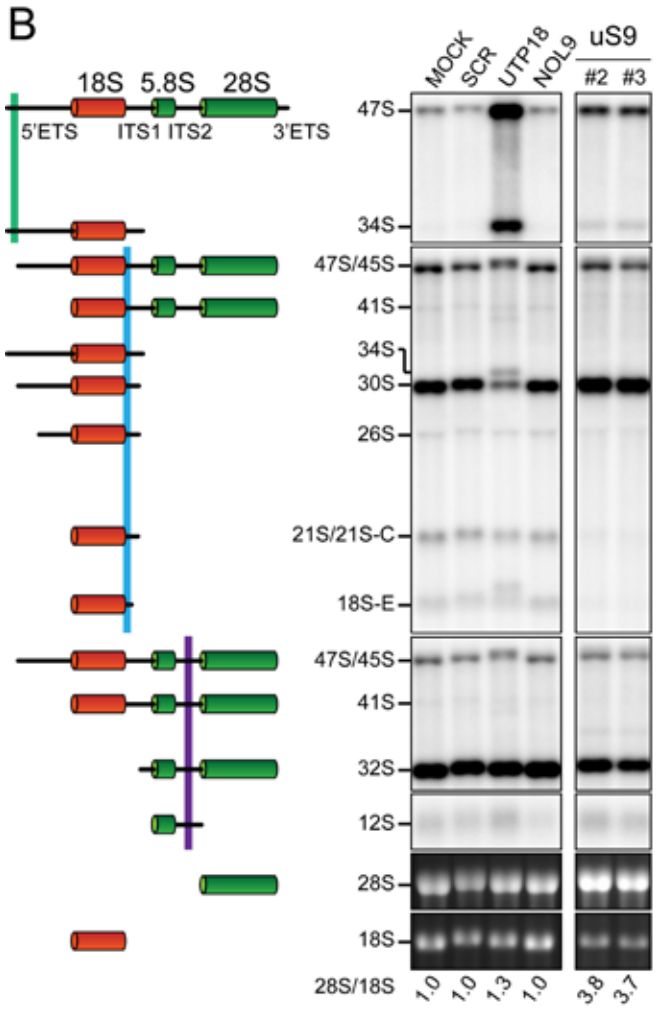
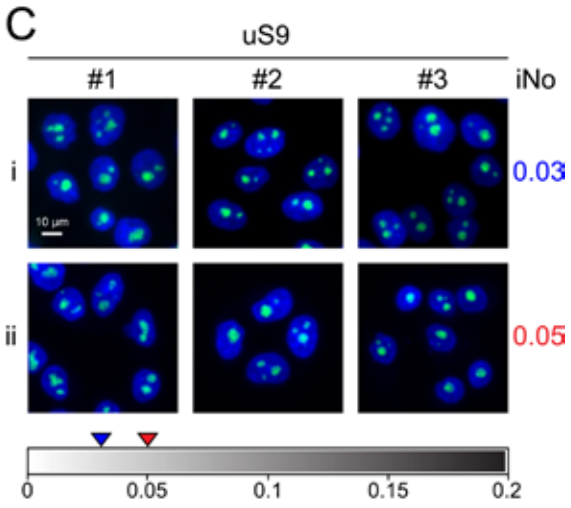
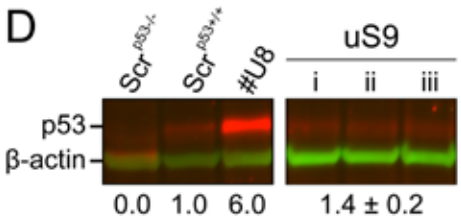
uS9 (RpS16)









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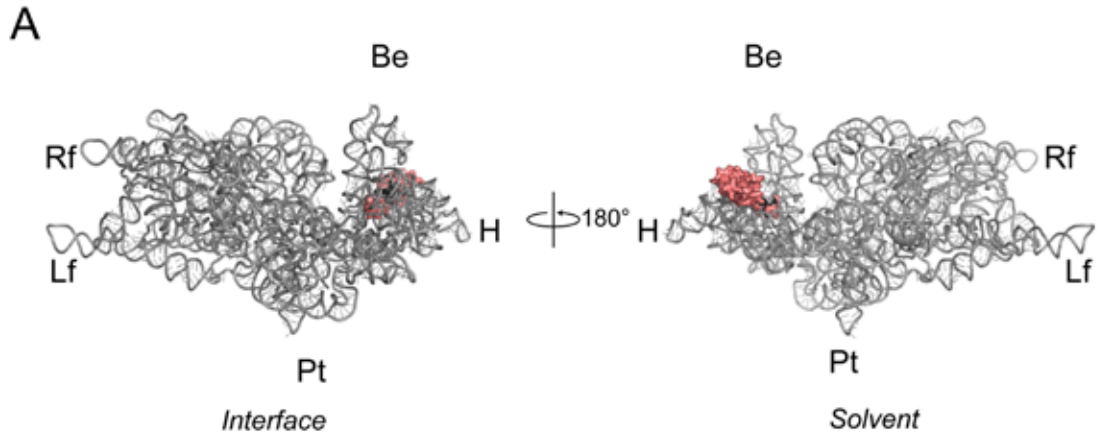
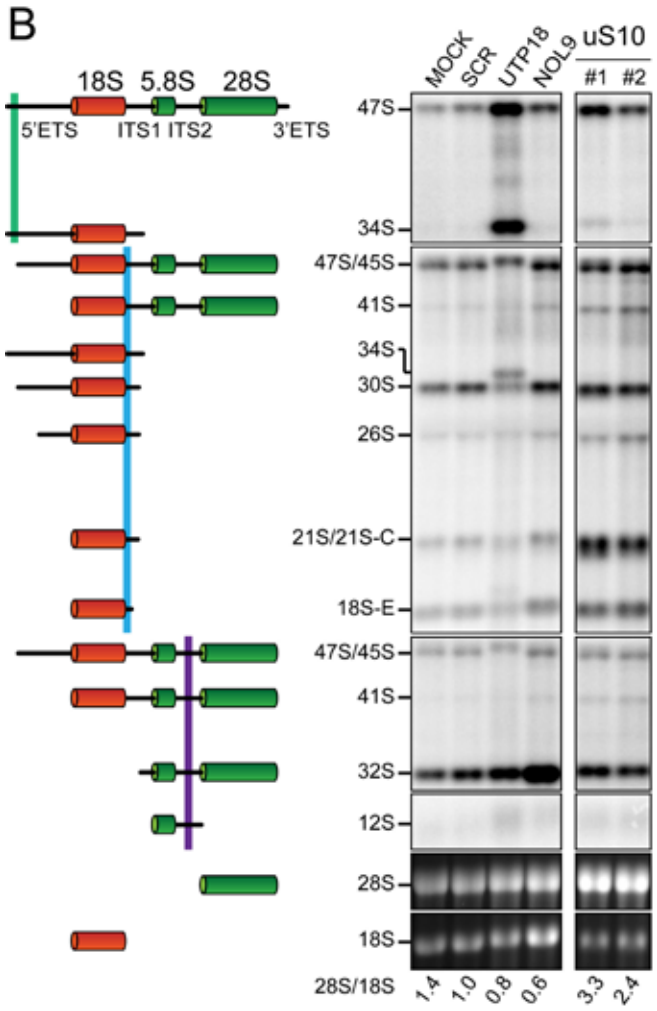
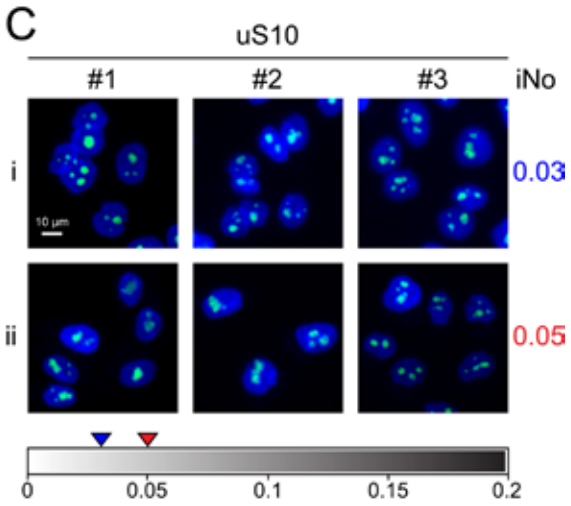
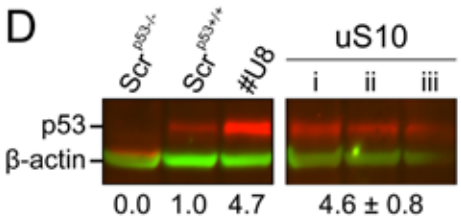
uS10 (RpS20)









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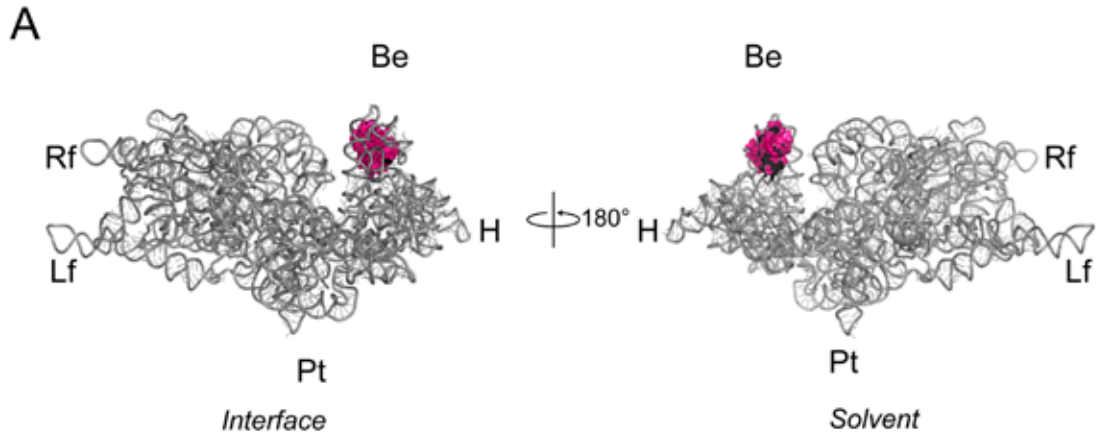
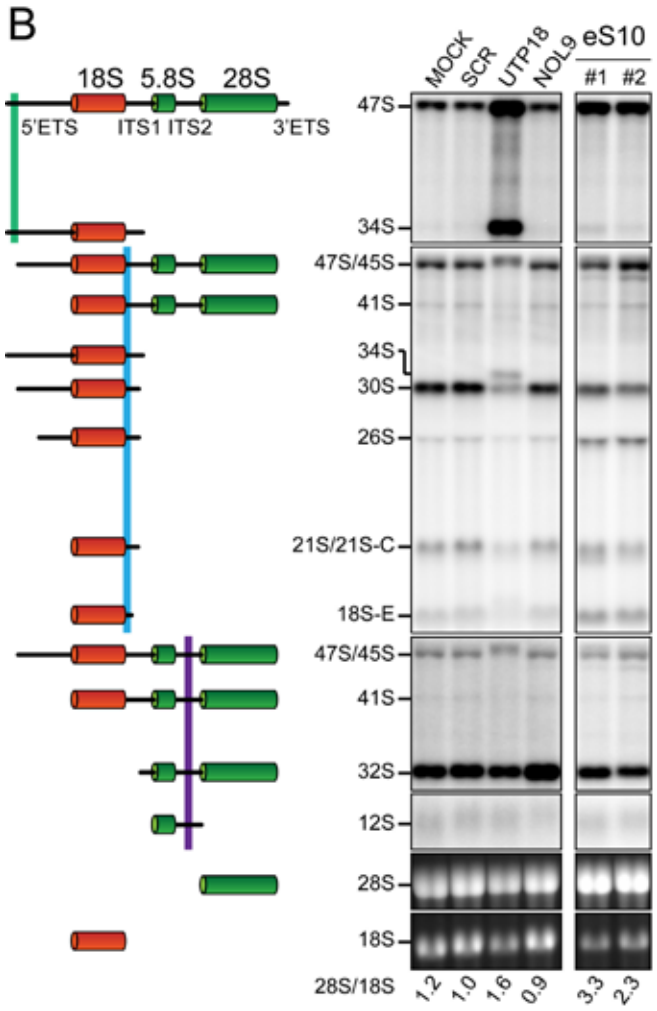
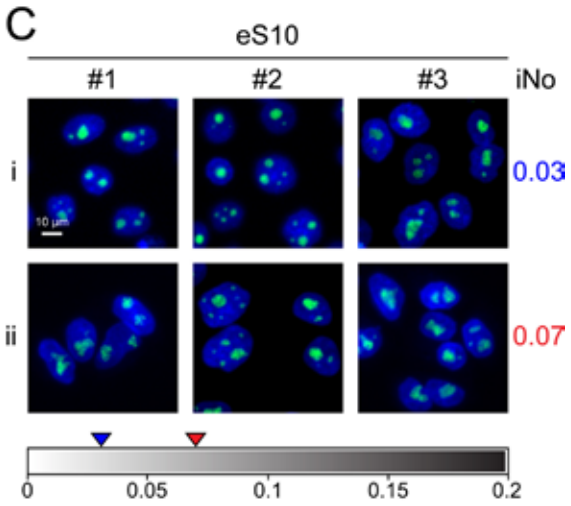
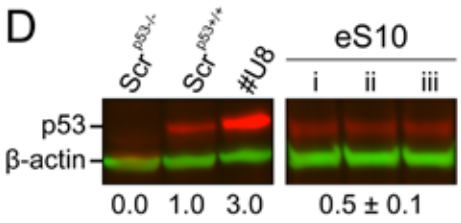
eS10 (RpS10)









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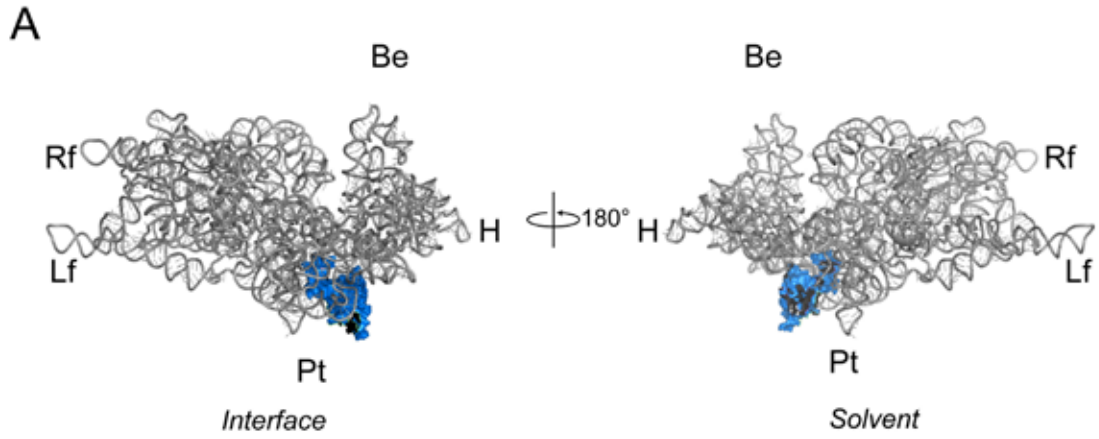
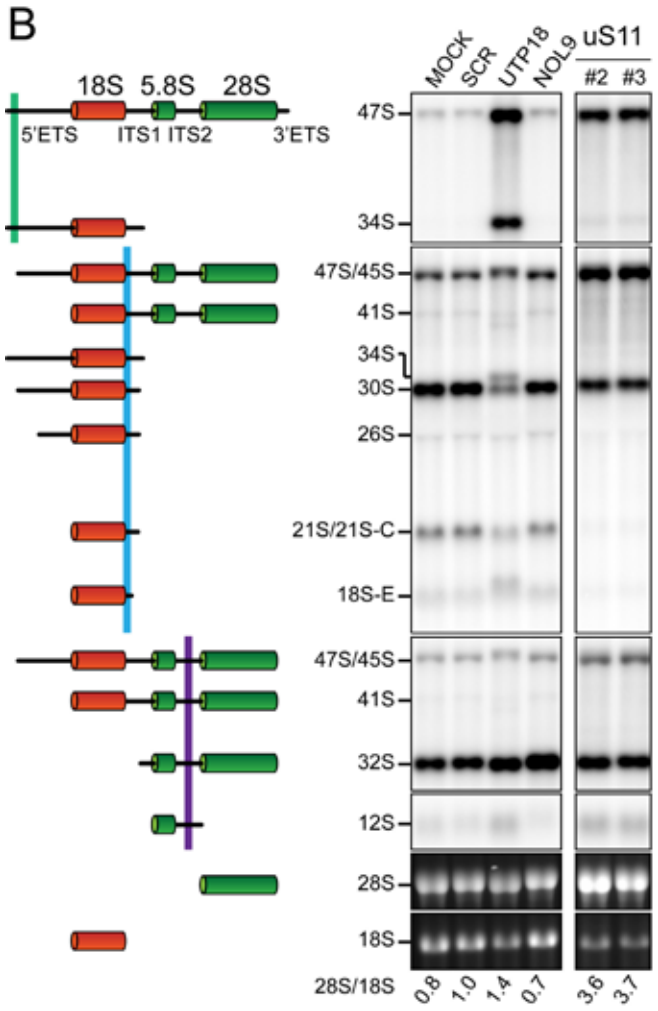
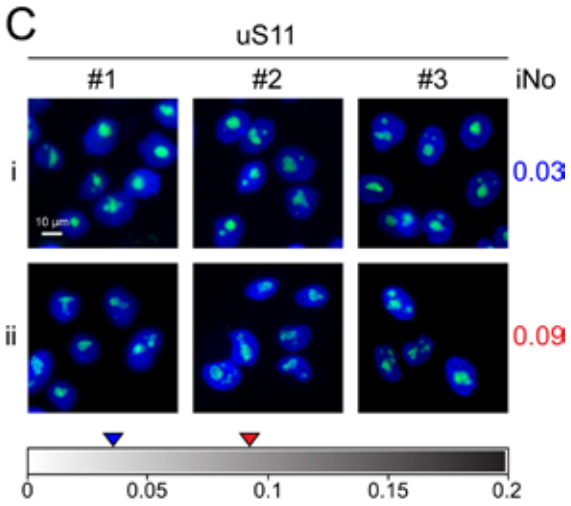
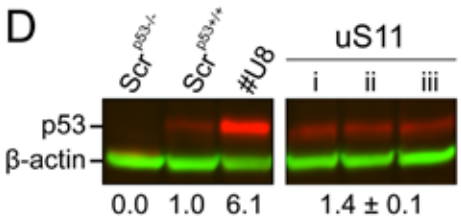
uS11 (RpS14)









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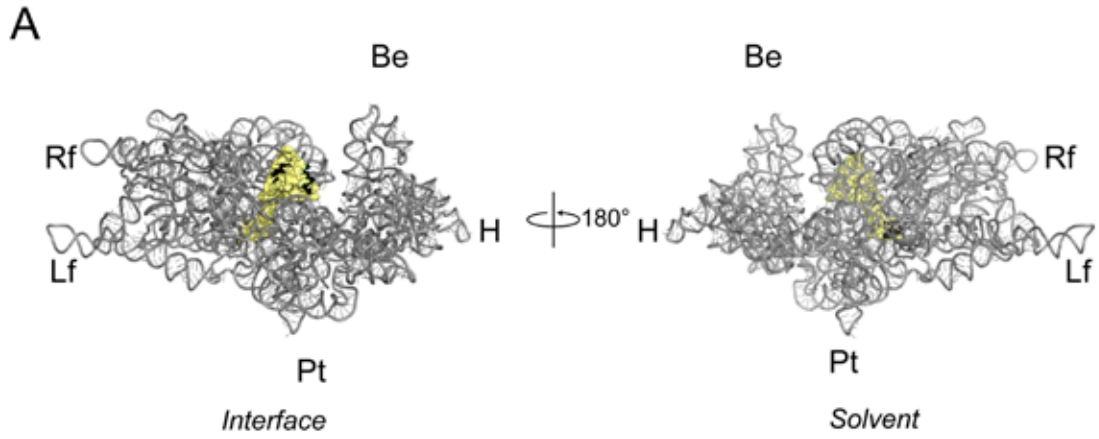
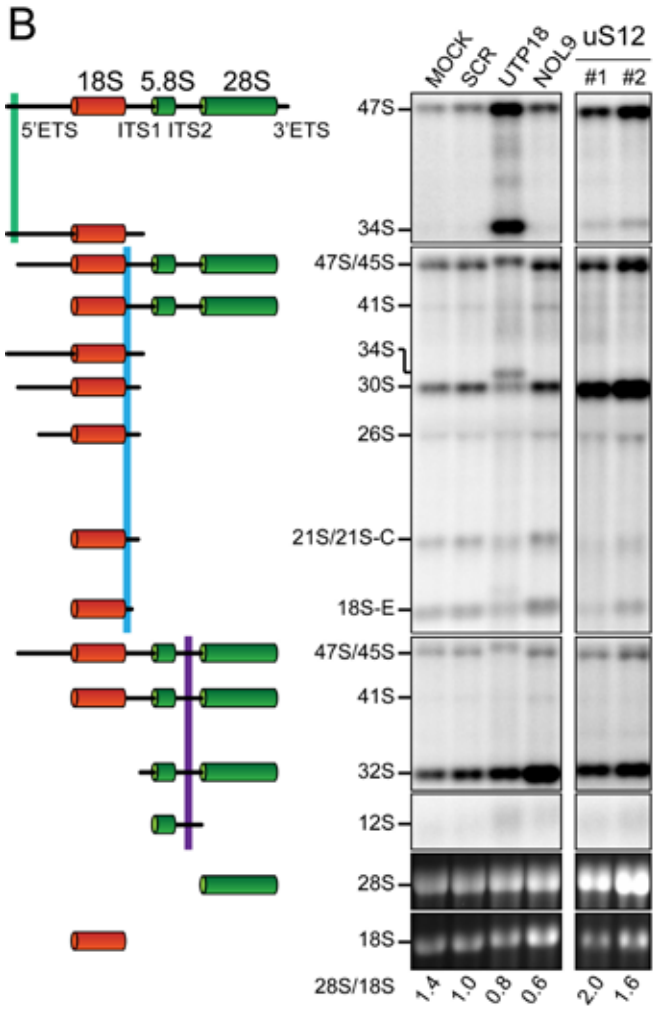
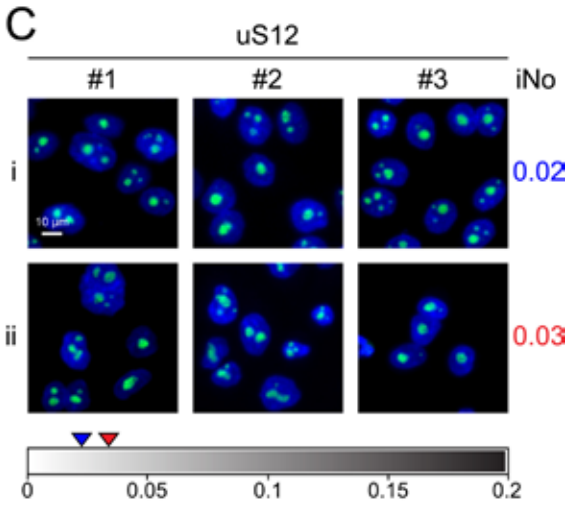
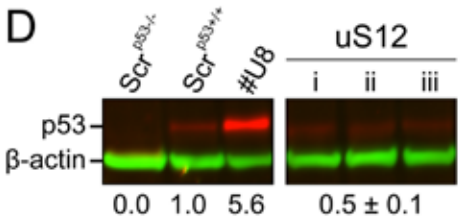
uS12 (RpS23)









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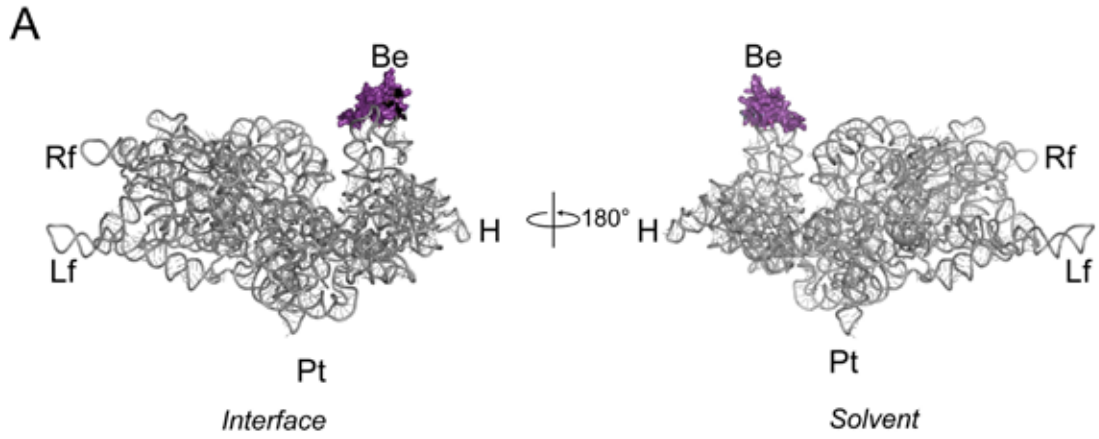
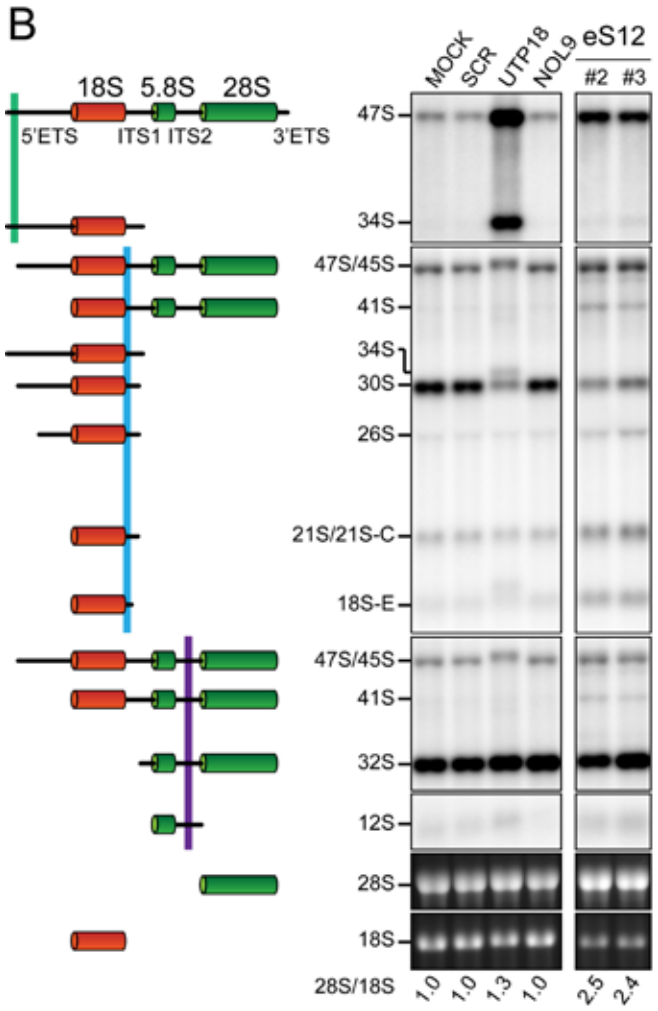
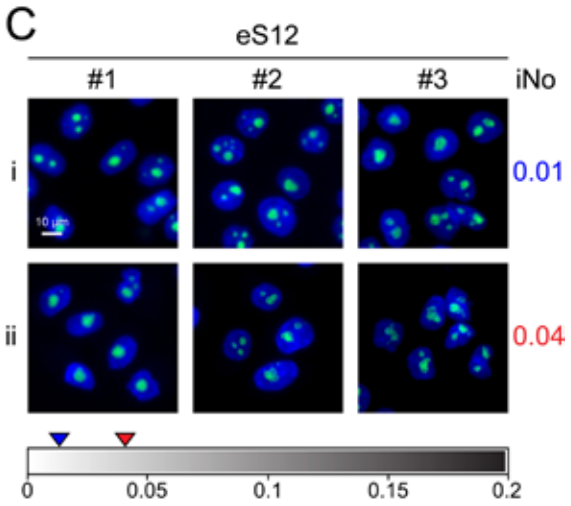
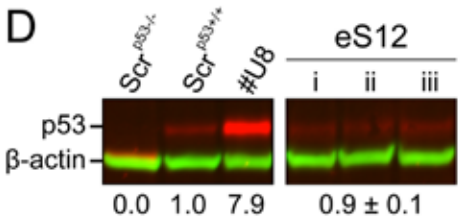
eS12 (RpS12)









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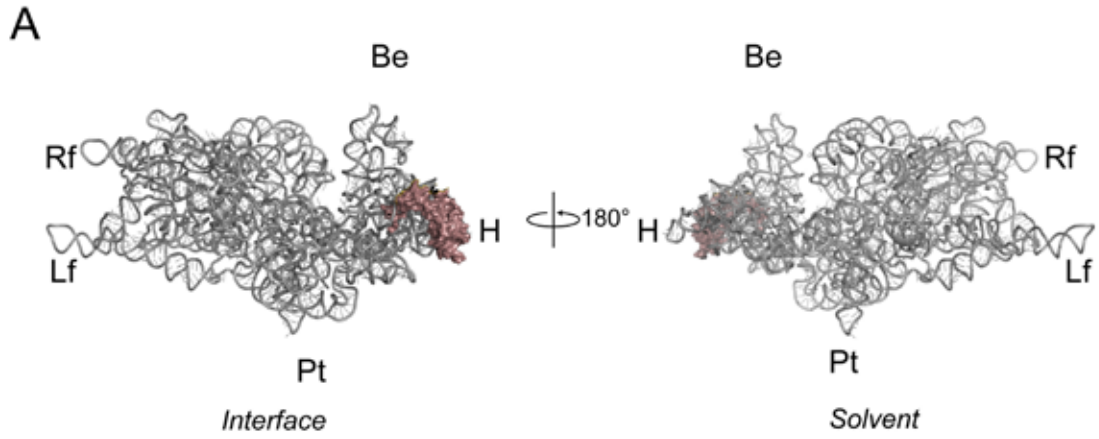
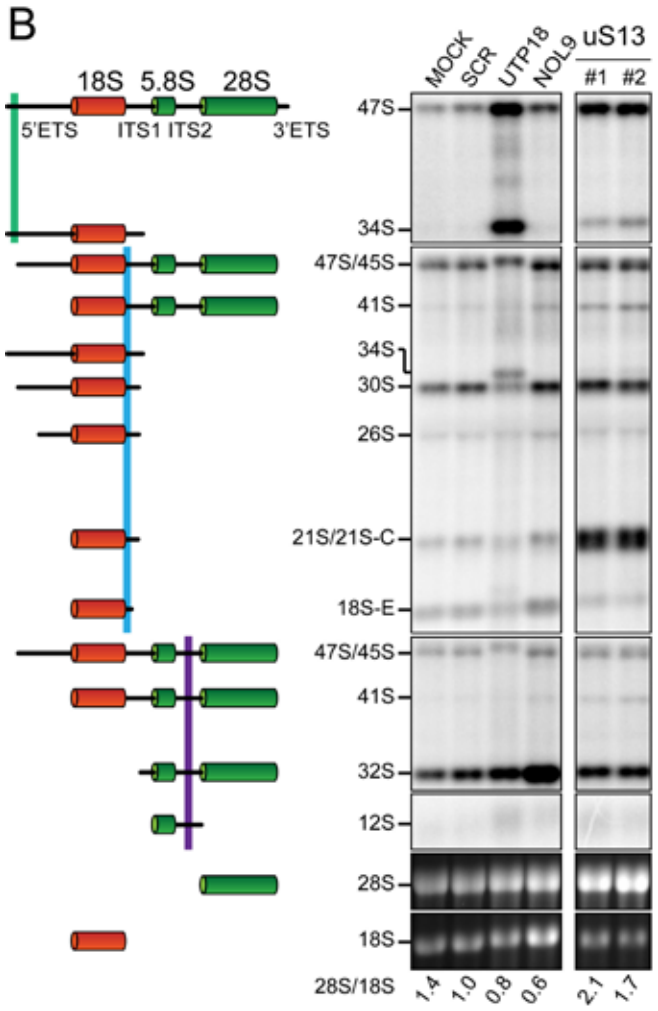
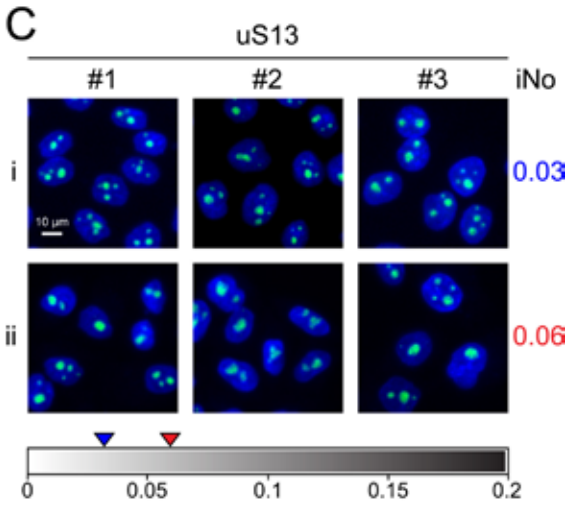
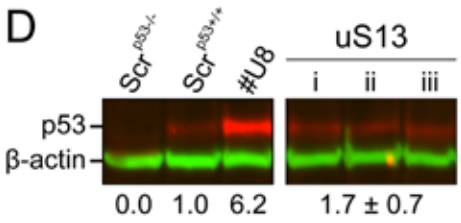
uS13 (RpS18)









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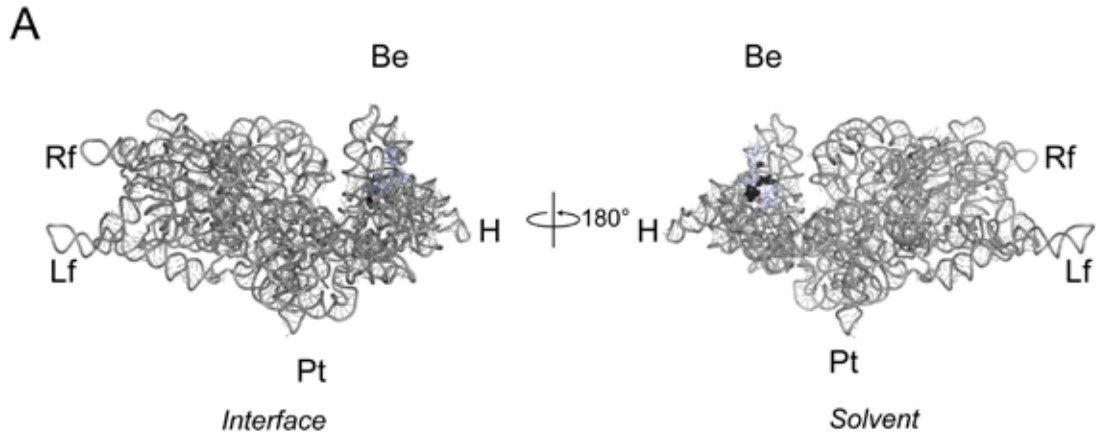
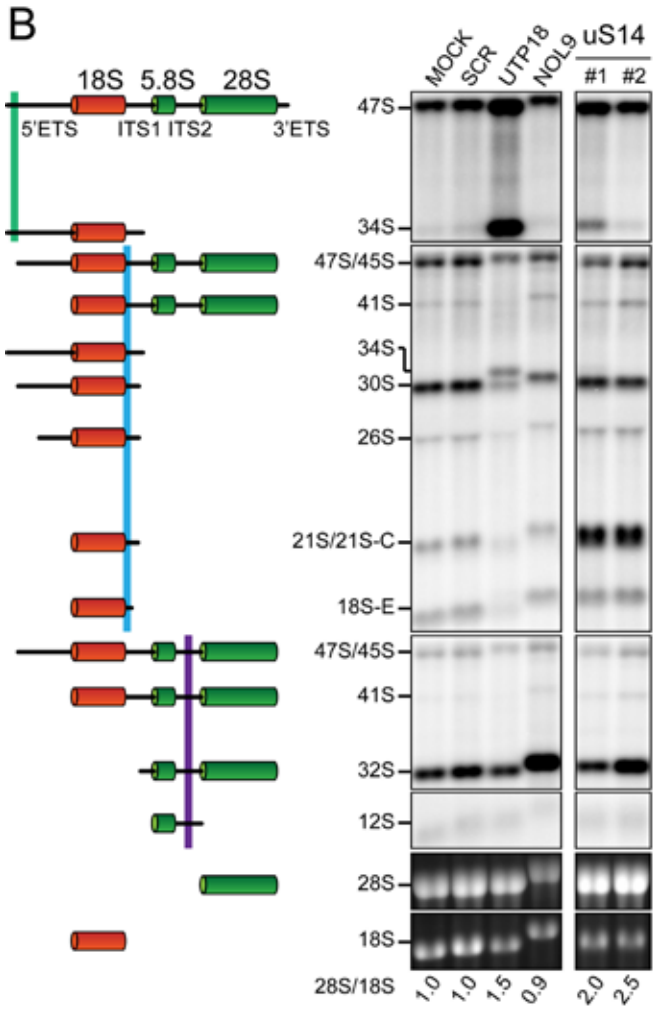
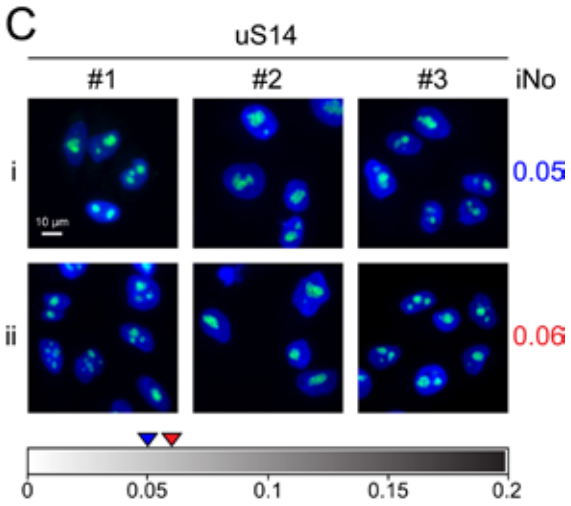
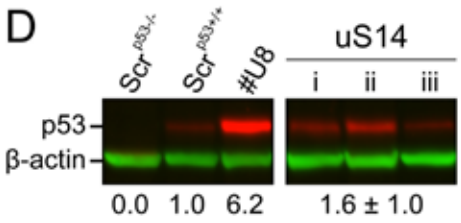
uS14 (RpS29)









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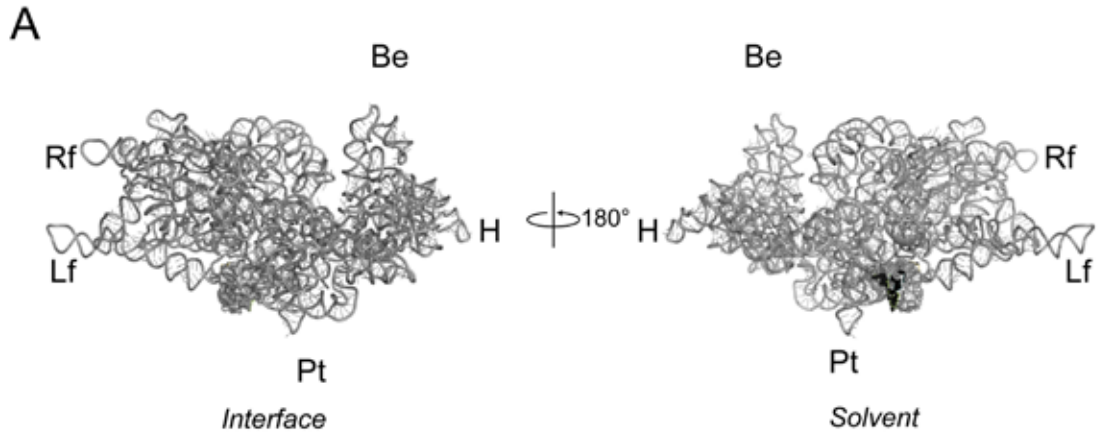
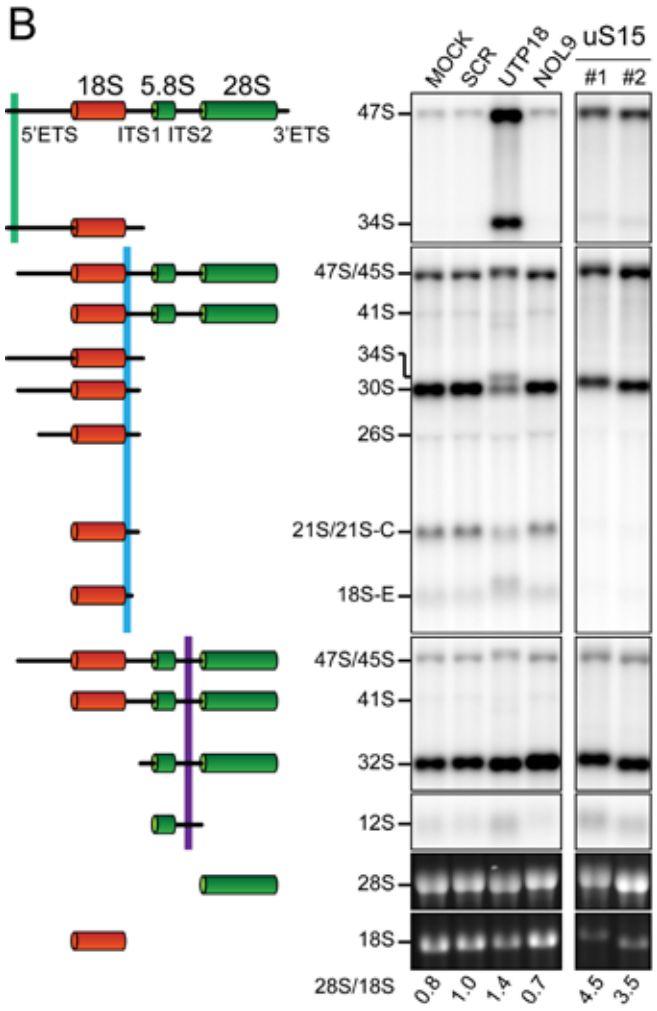
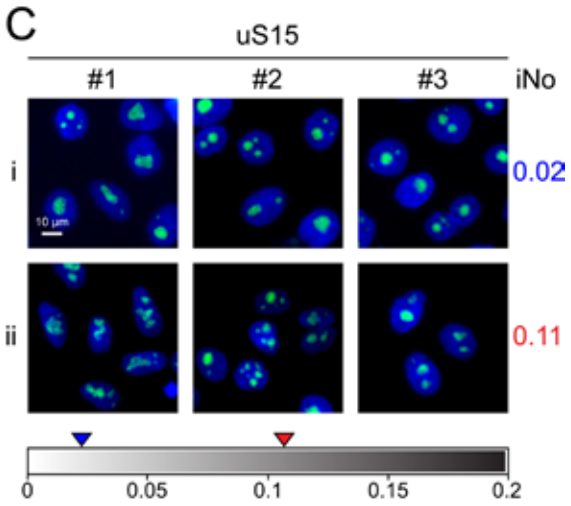
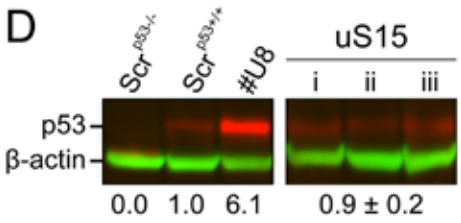
uS15 (RpS13)









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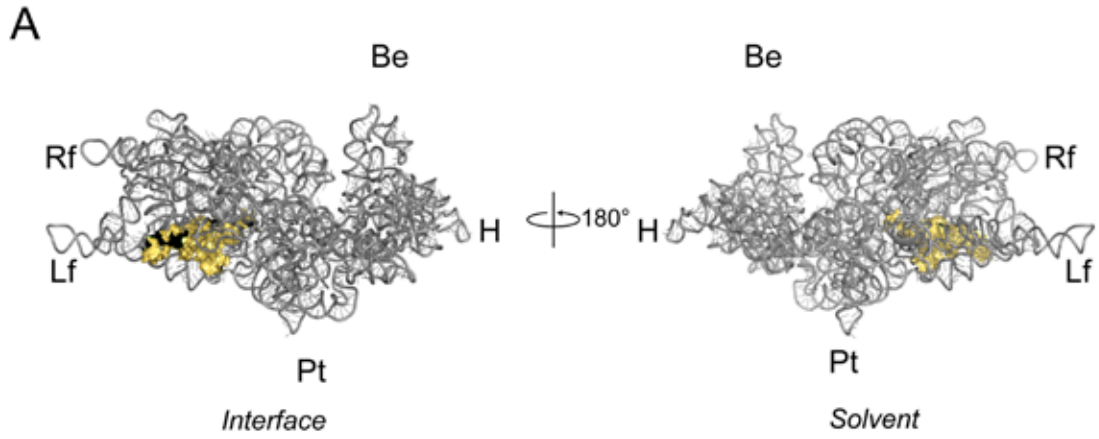
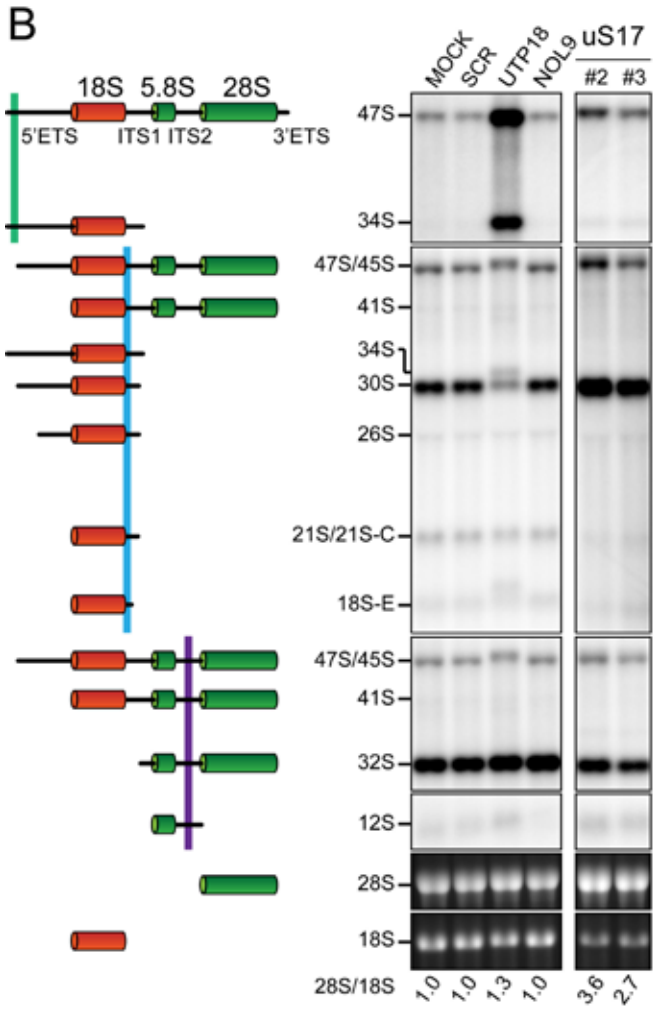
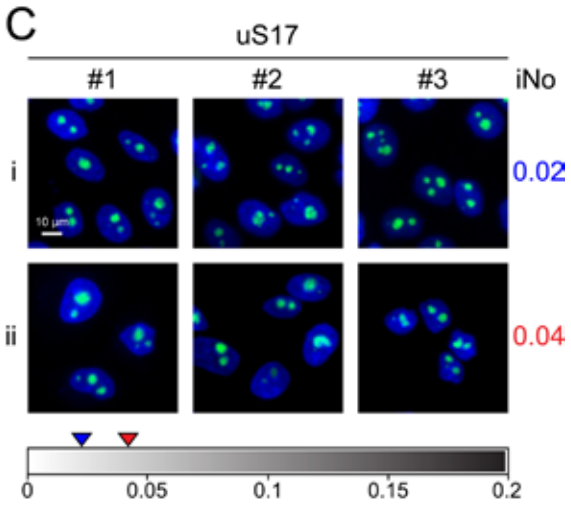
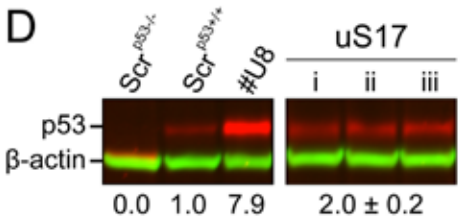
uS17 (RpS11)









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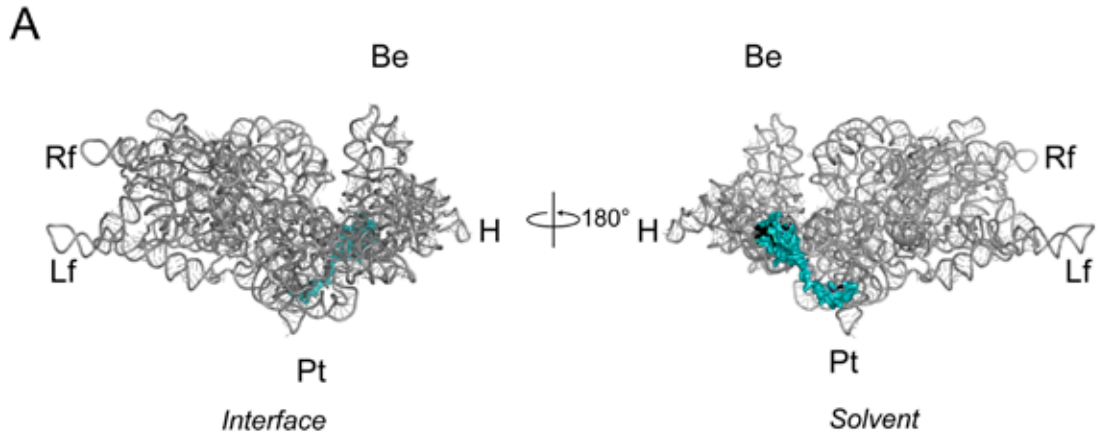
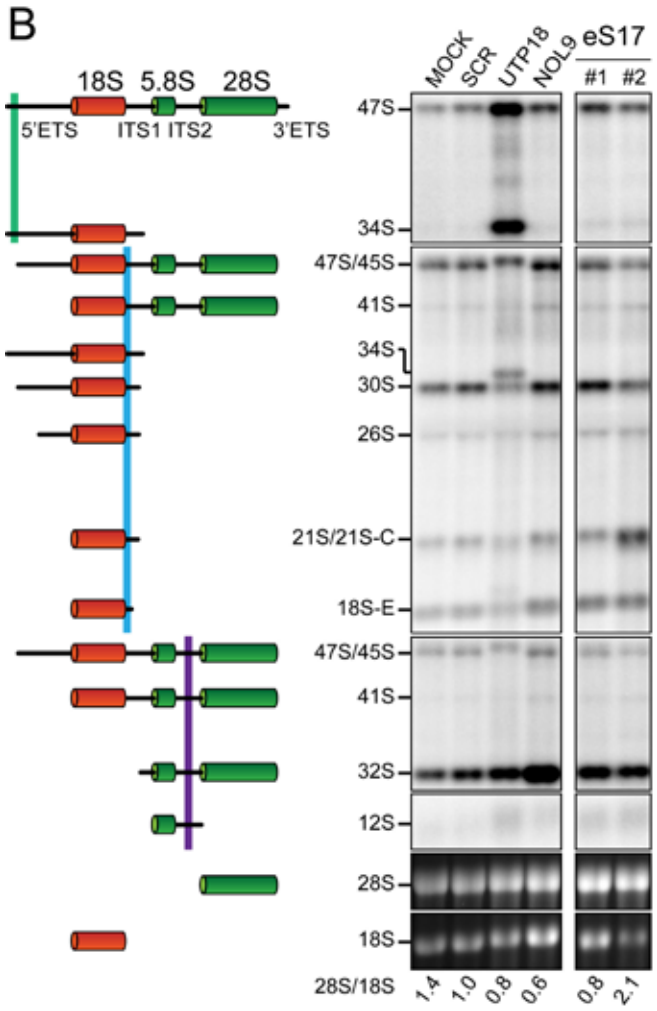
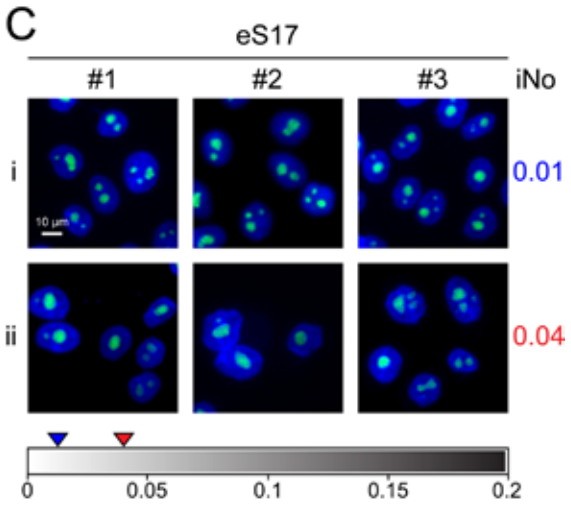
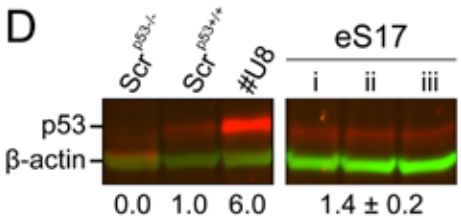
eS17 (RpS17)









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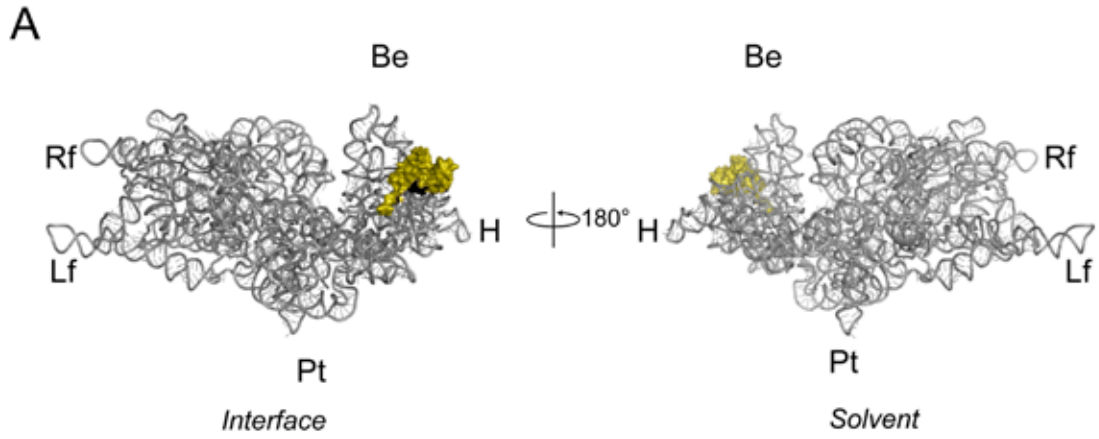
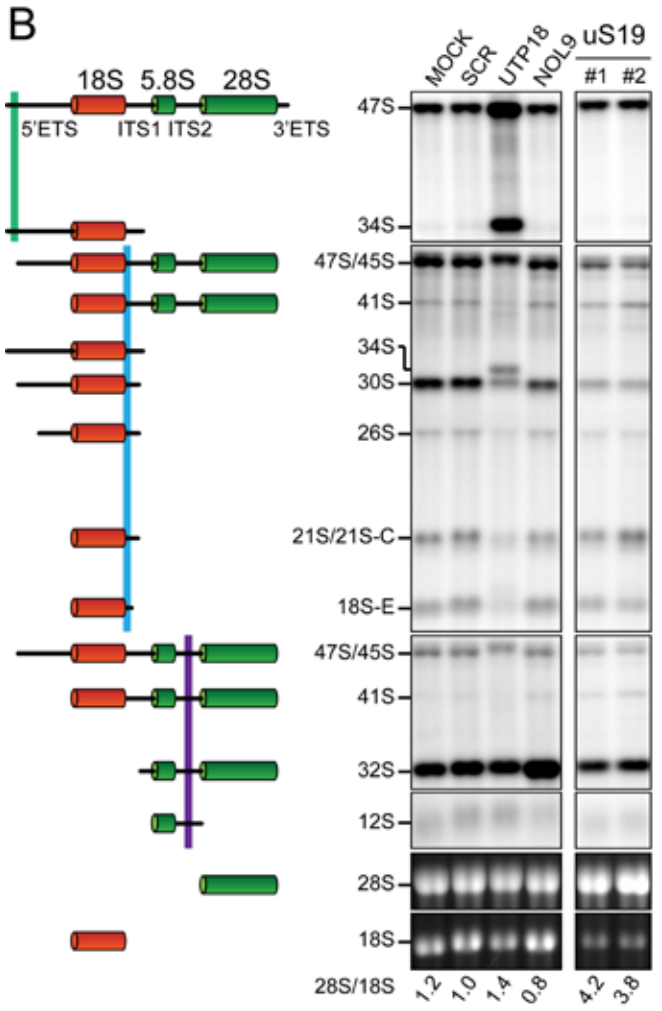
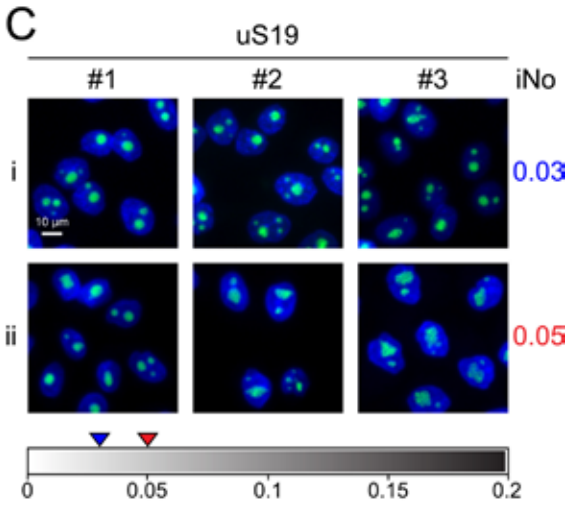
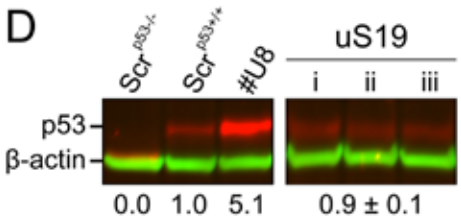
uS19 (RpS15)









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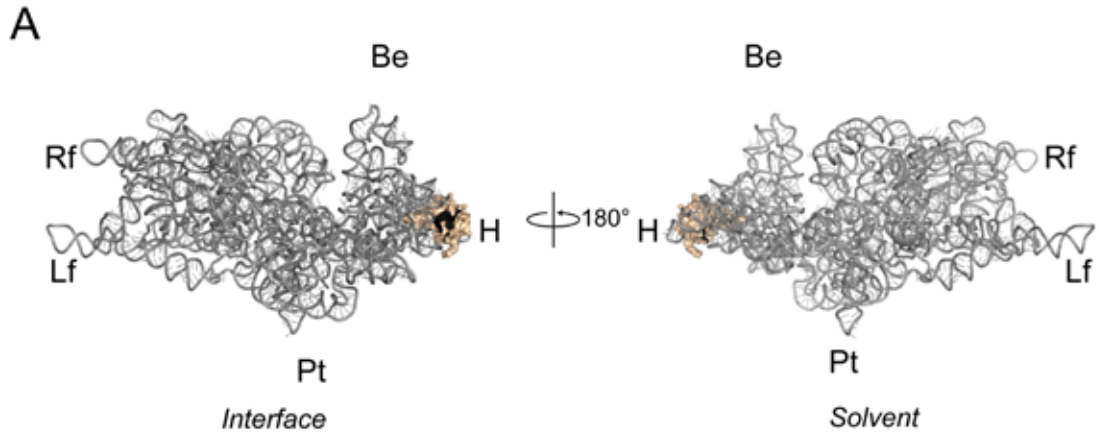
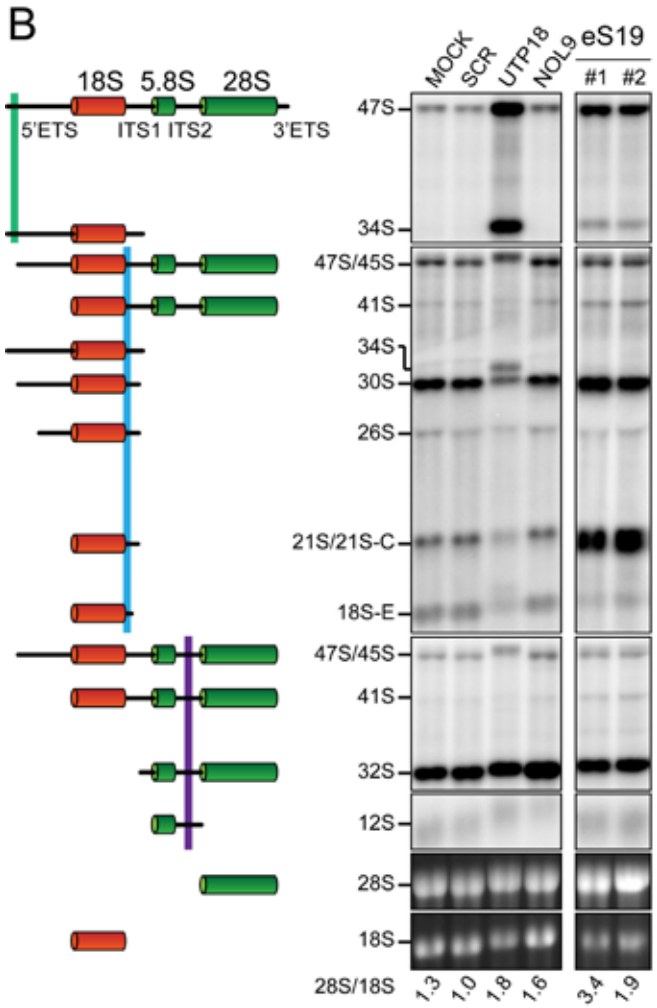
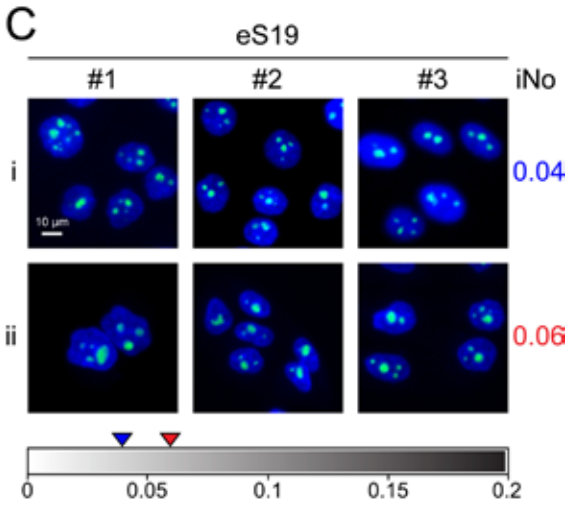
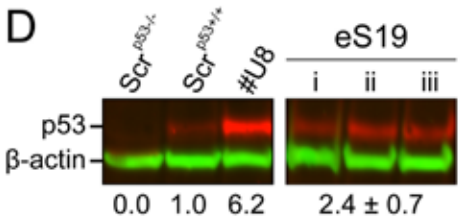
eS19 (RpS19)









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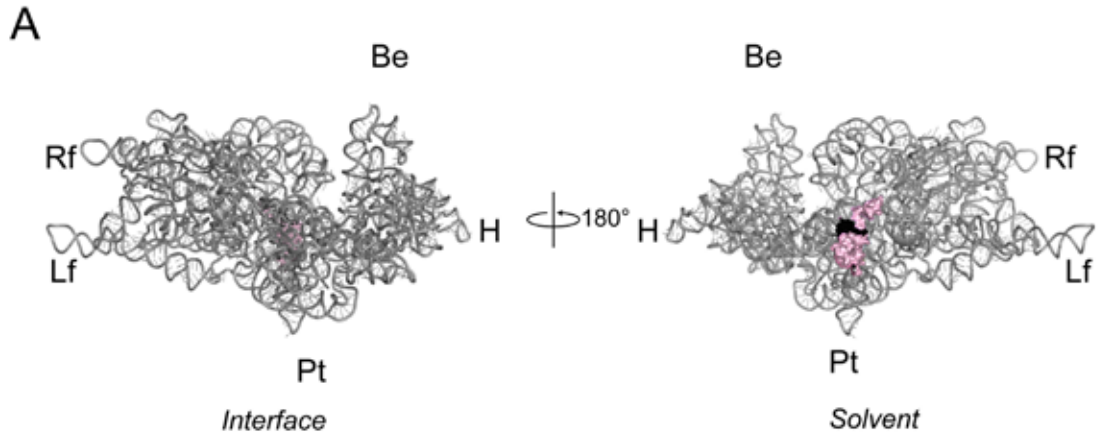
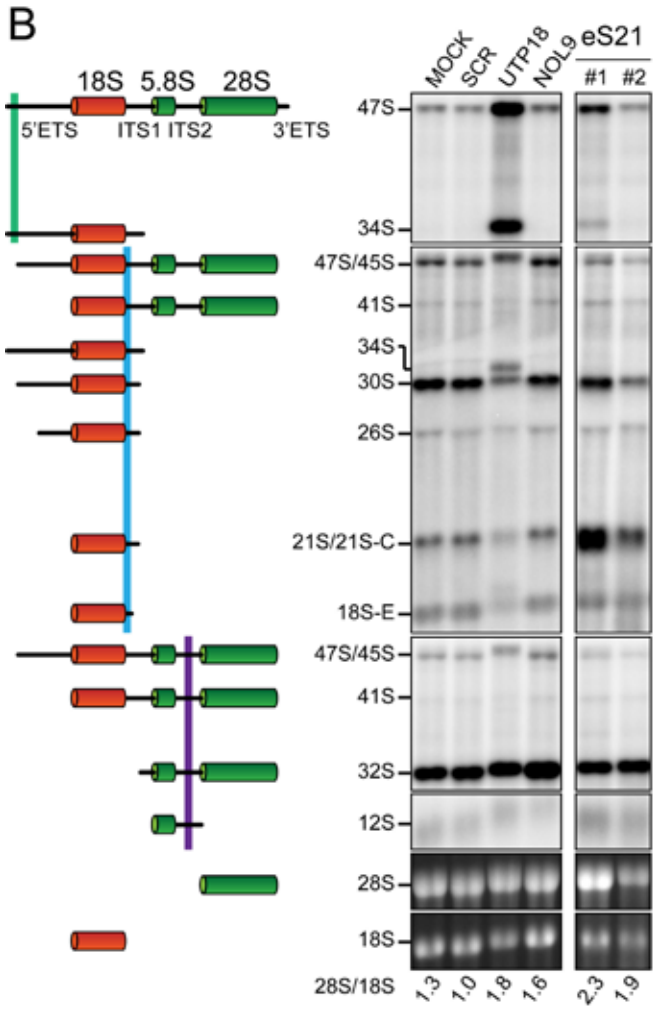
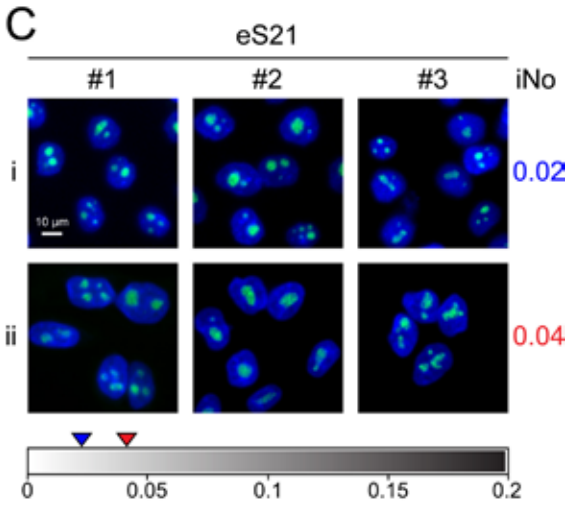
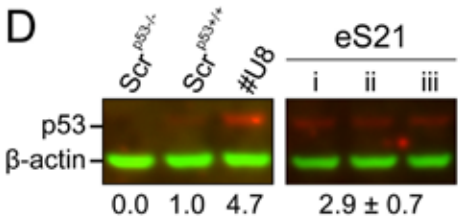
eS21 (RpS21)









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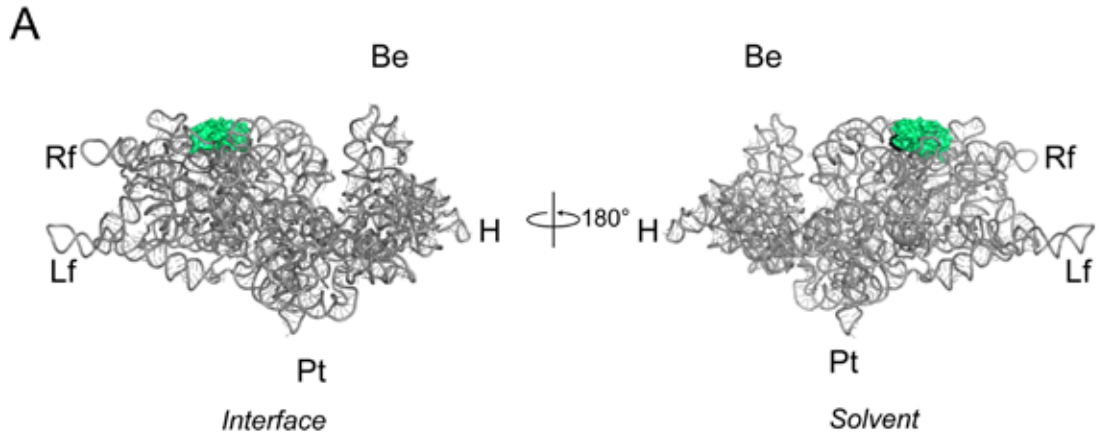
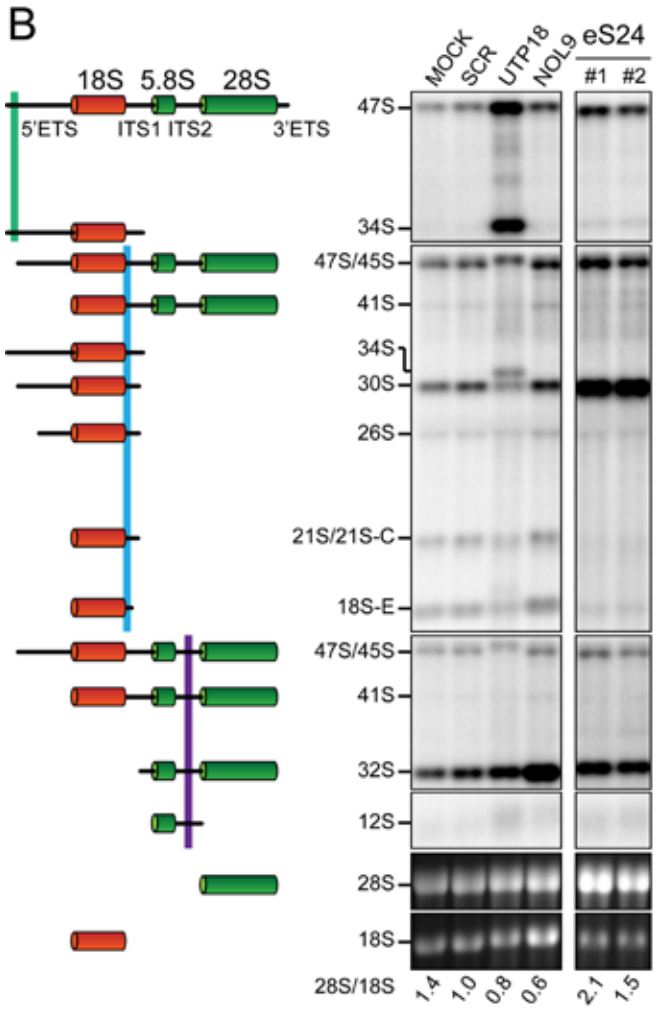
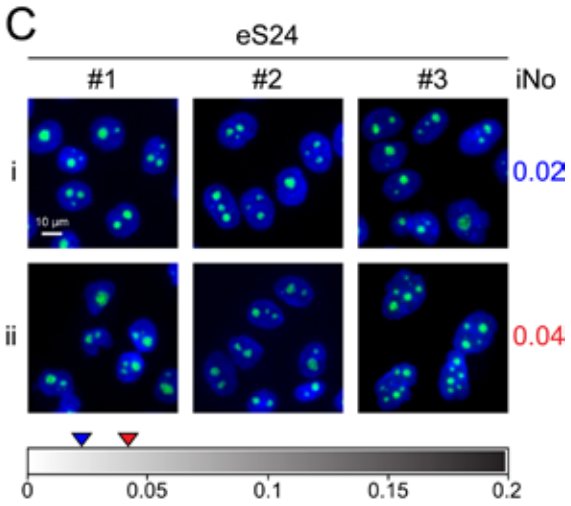
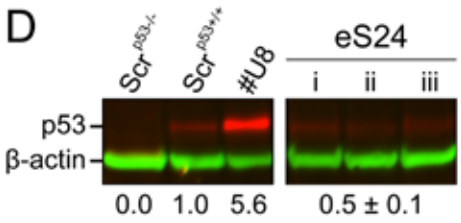
eS24 (RpS24)









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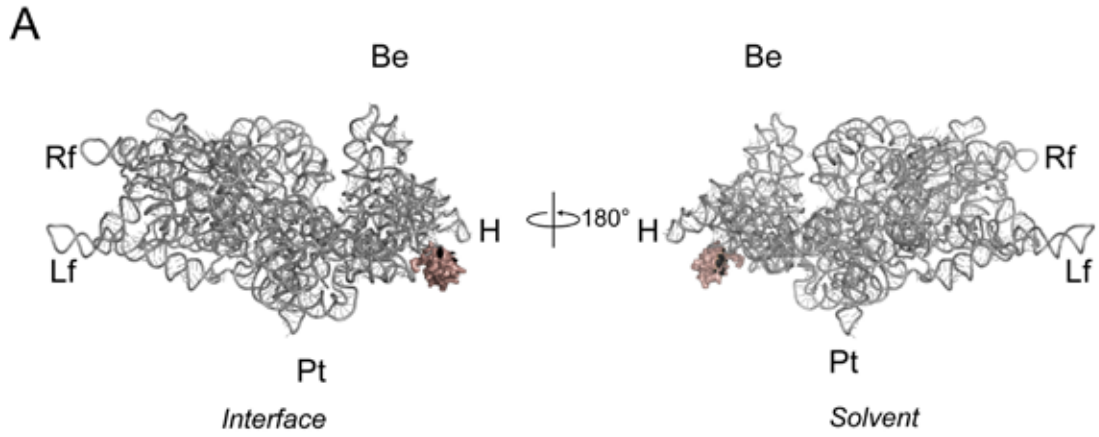
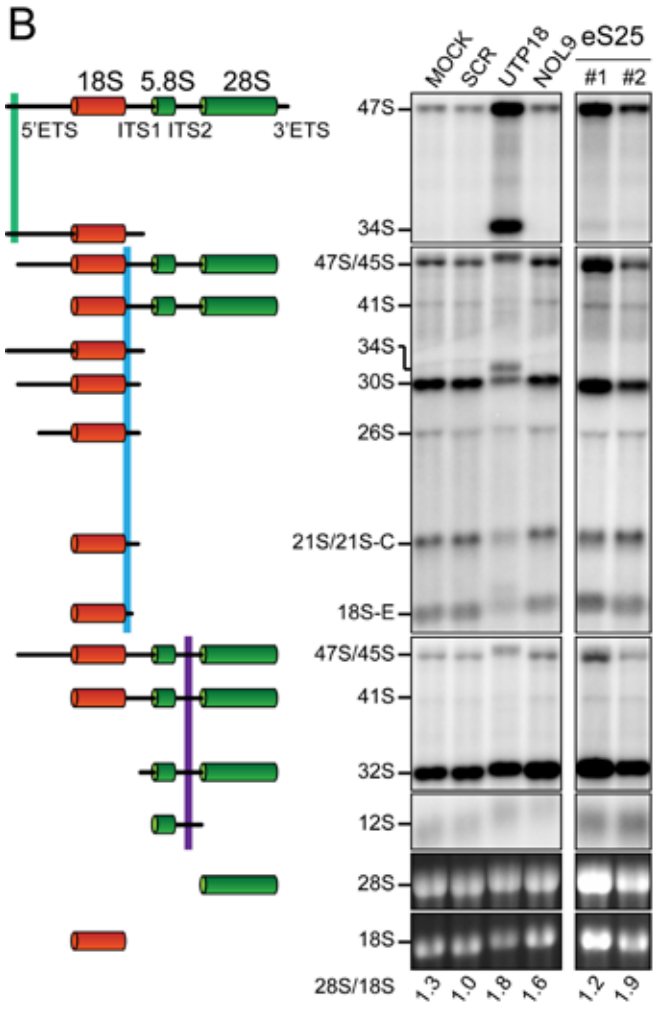
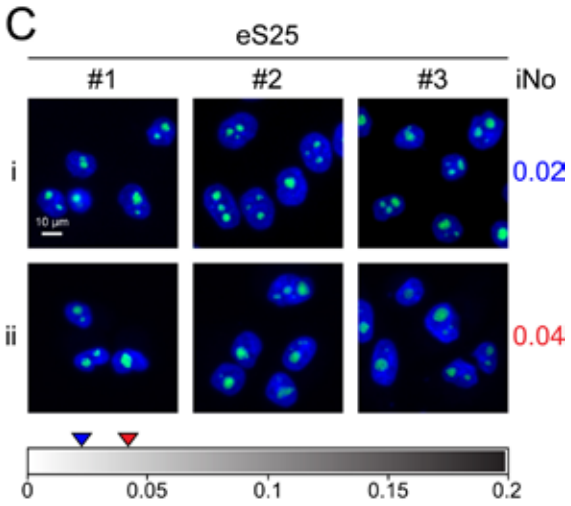
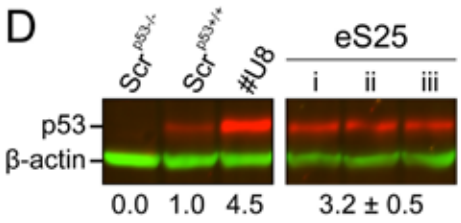
eS25 (RpS25)









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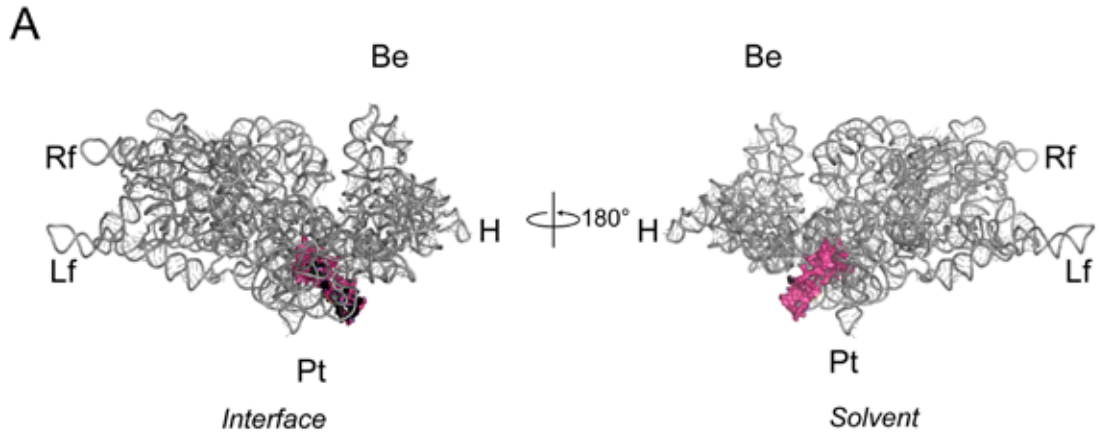
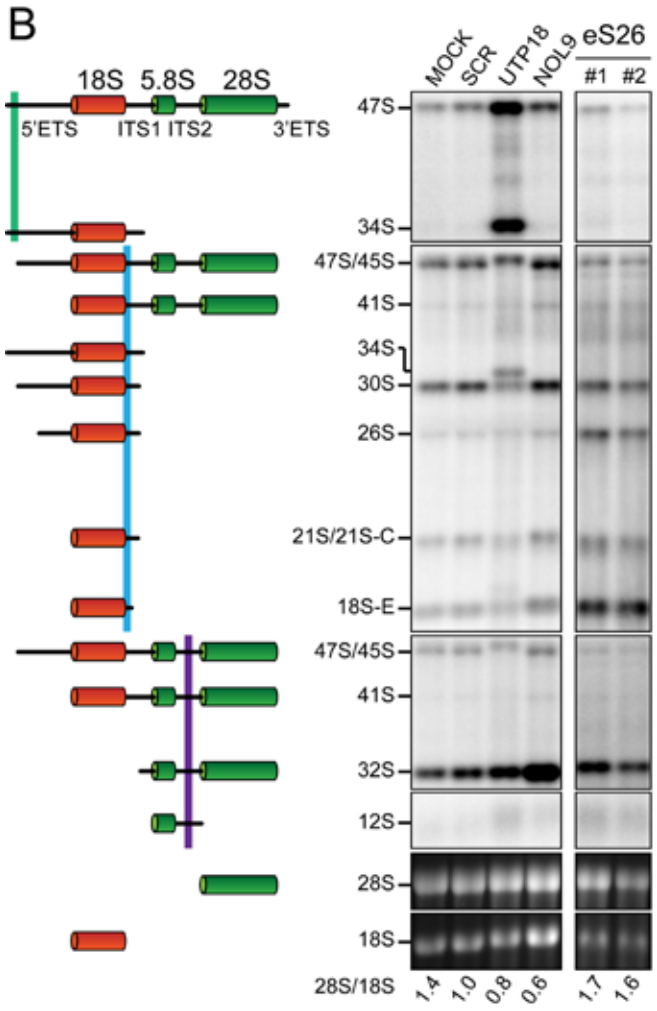
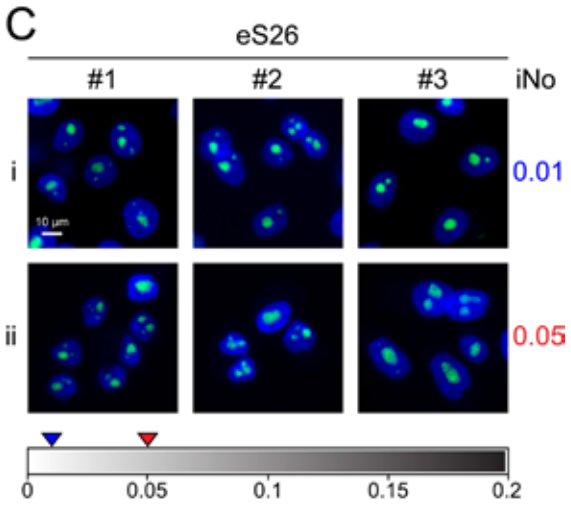
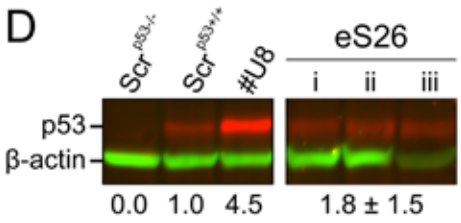
eS26 (RpS26)









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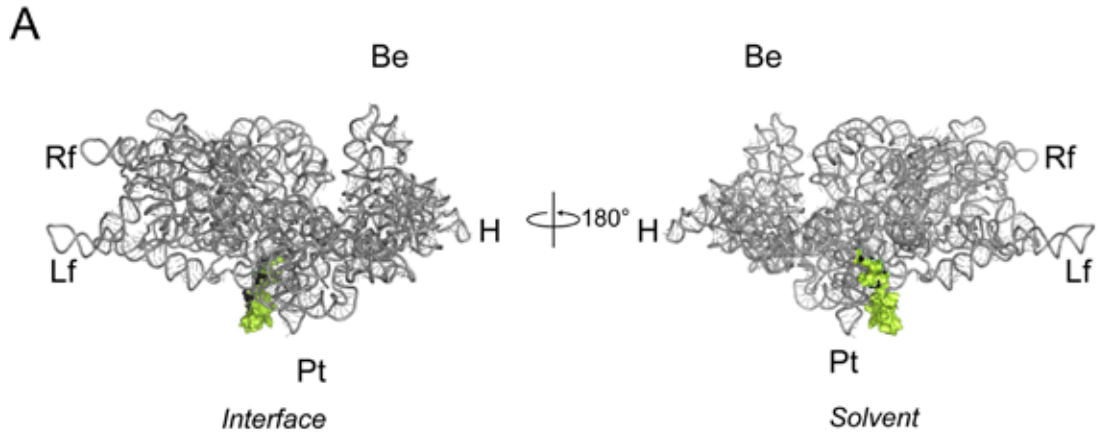
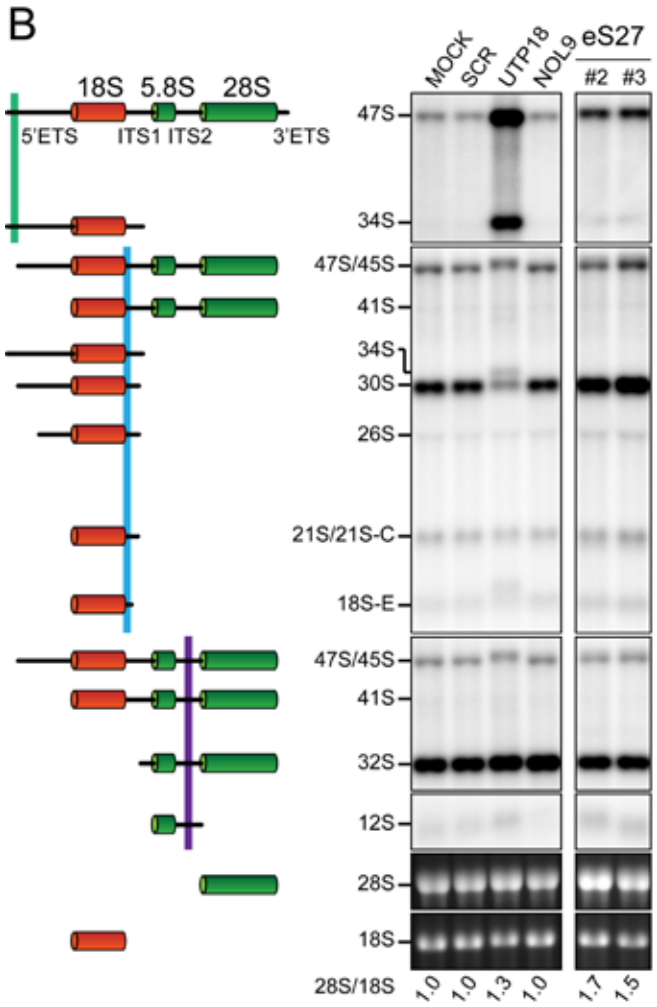
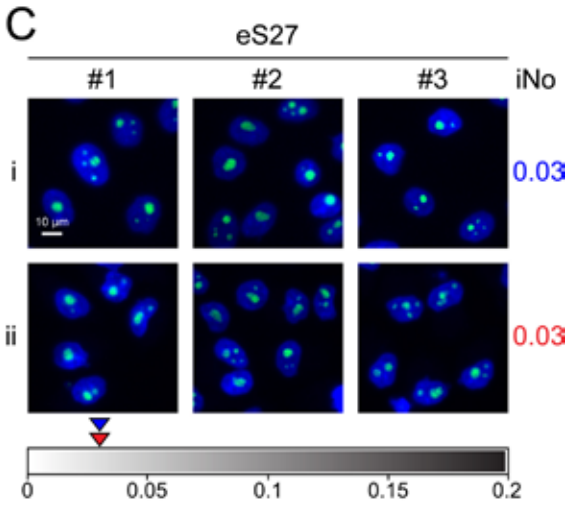
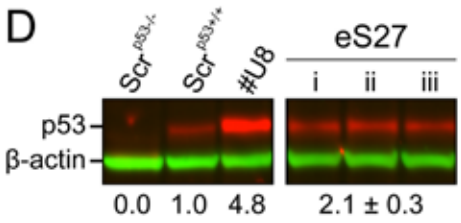
eS27 (RpS27)









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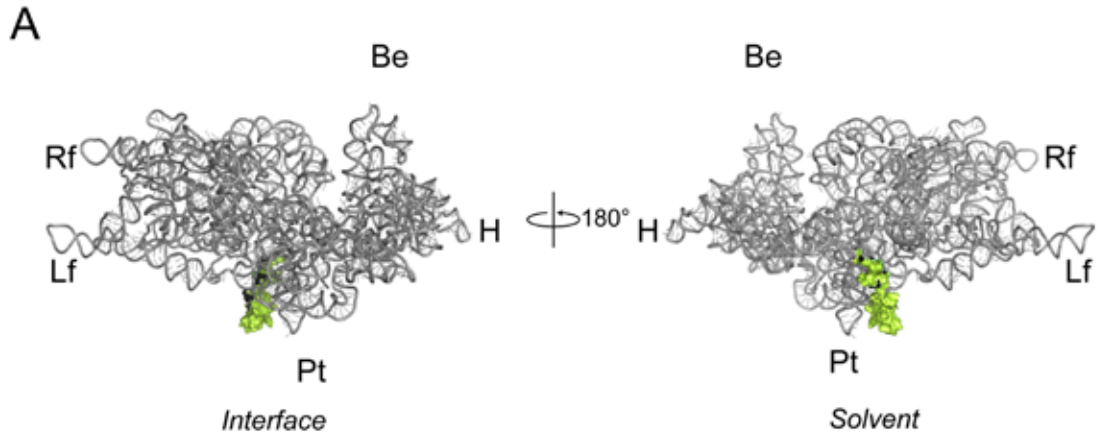
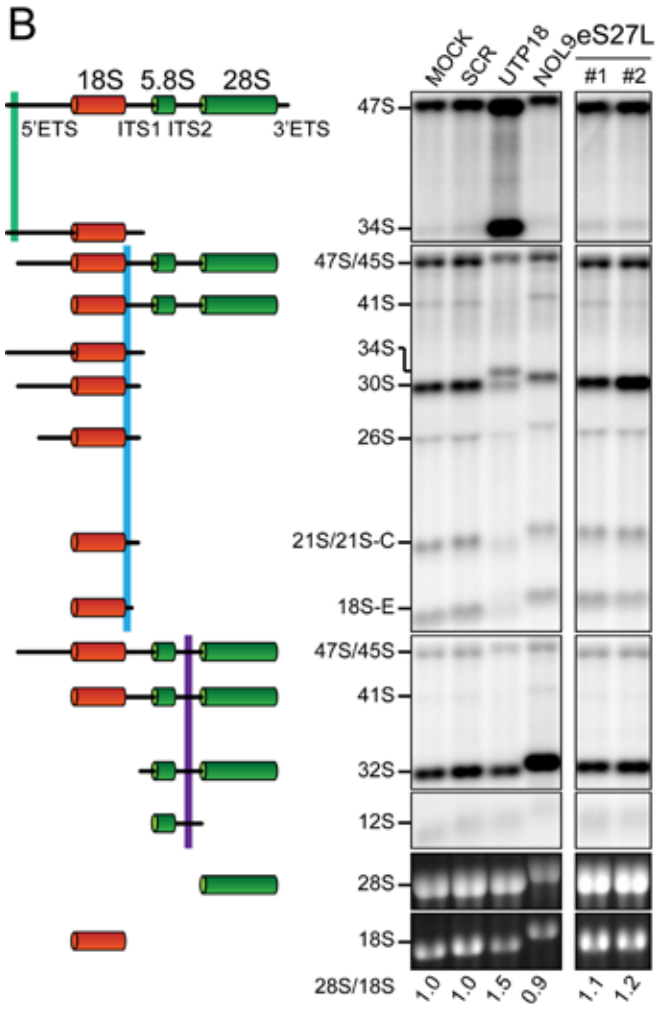
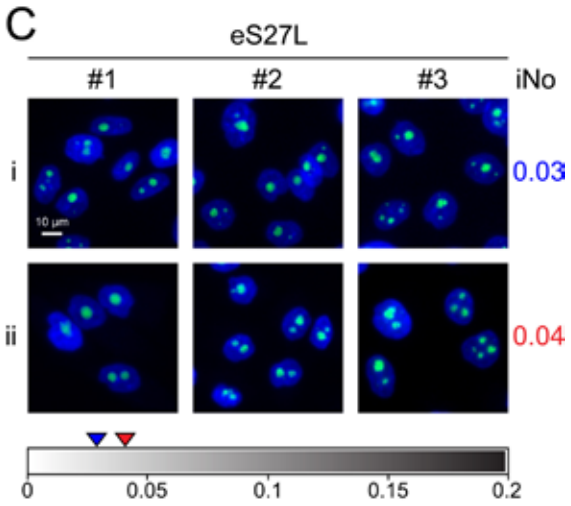
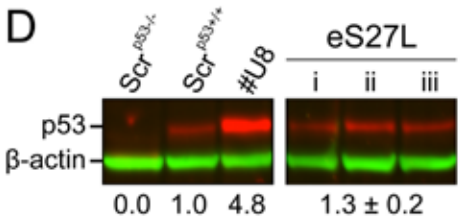
eS27L (RpS27L)









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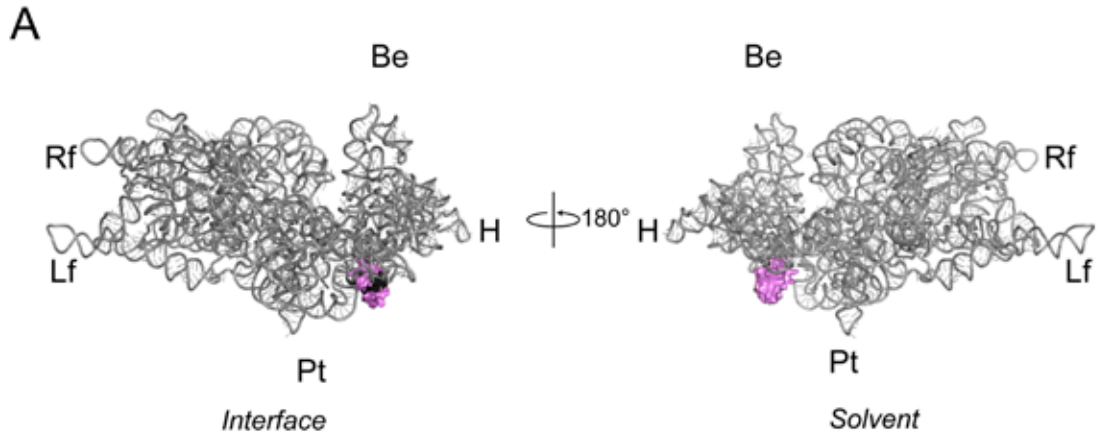
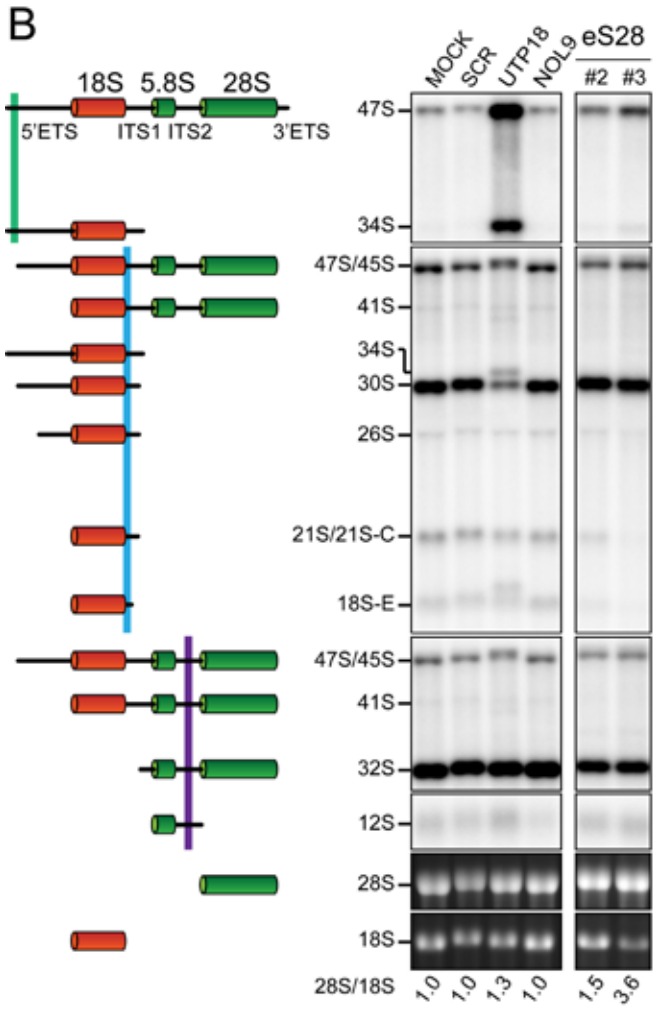
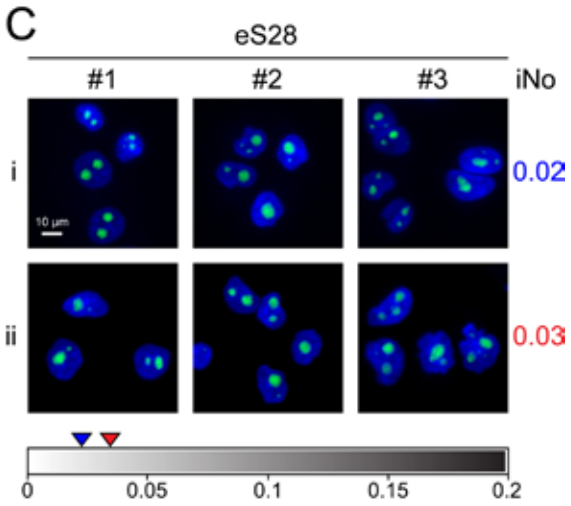
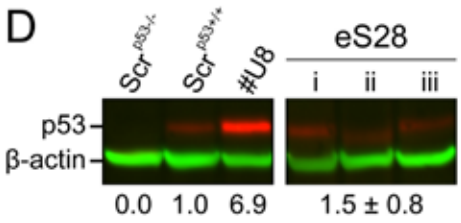
eS28 (RpS28)









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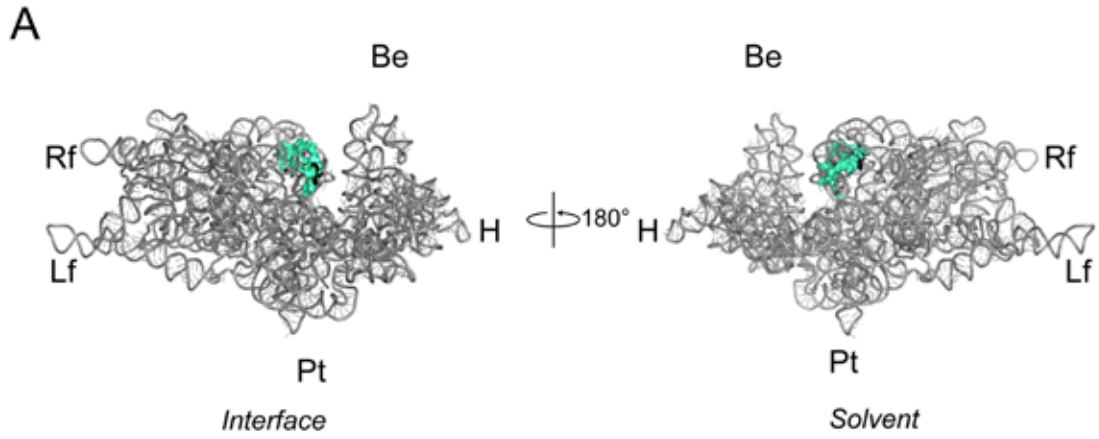
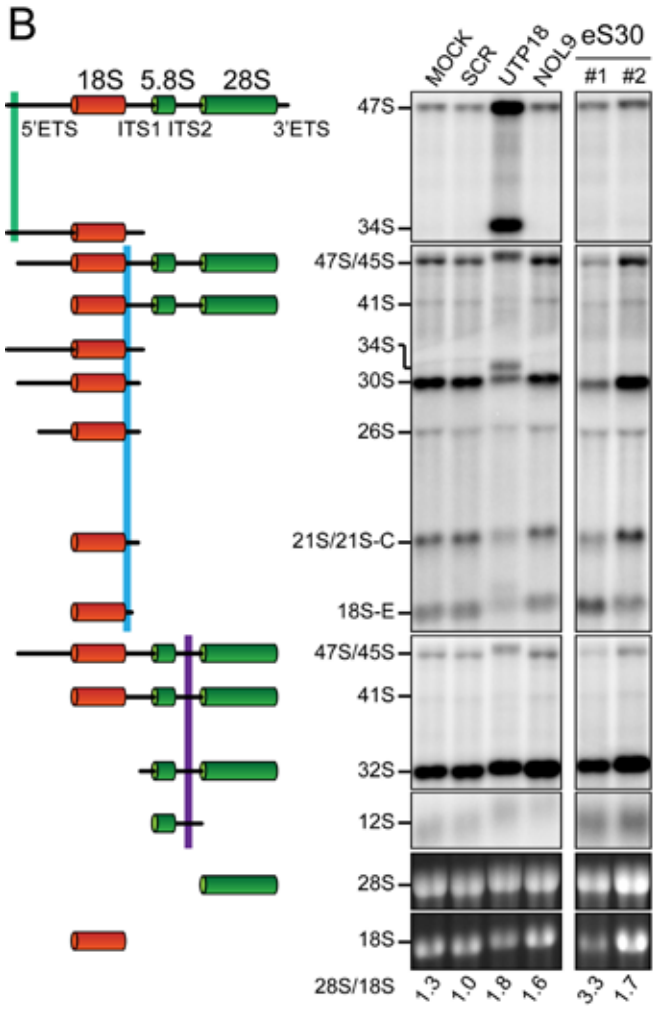
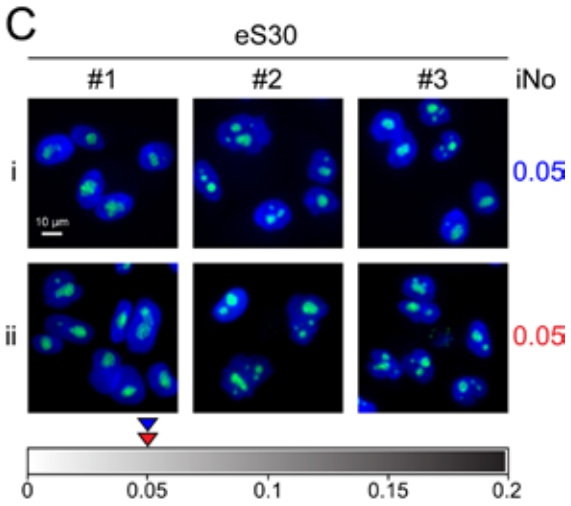
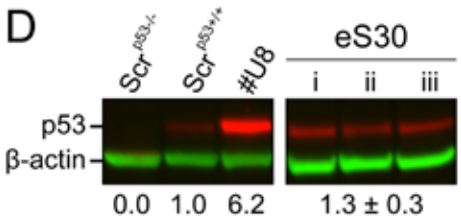
eS30 (RpS30)









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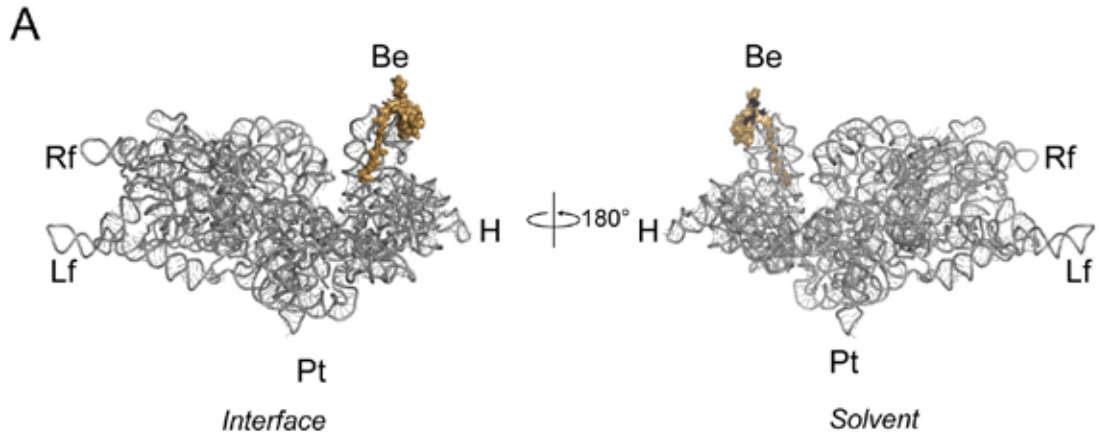
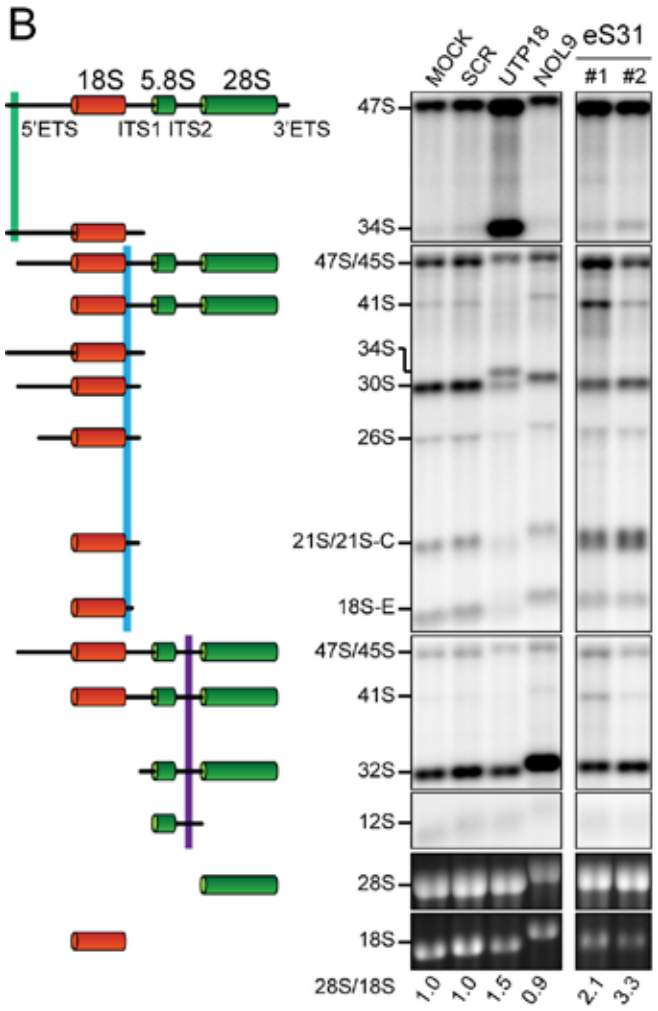
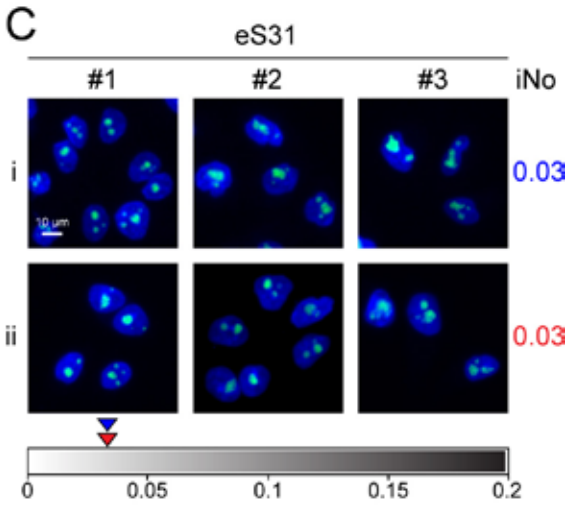
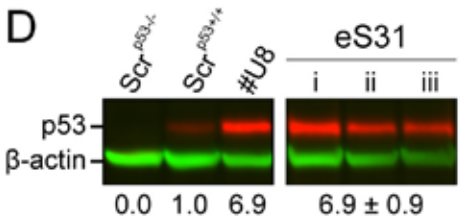
eS31 (RpS27a)









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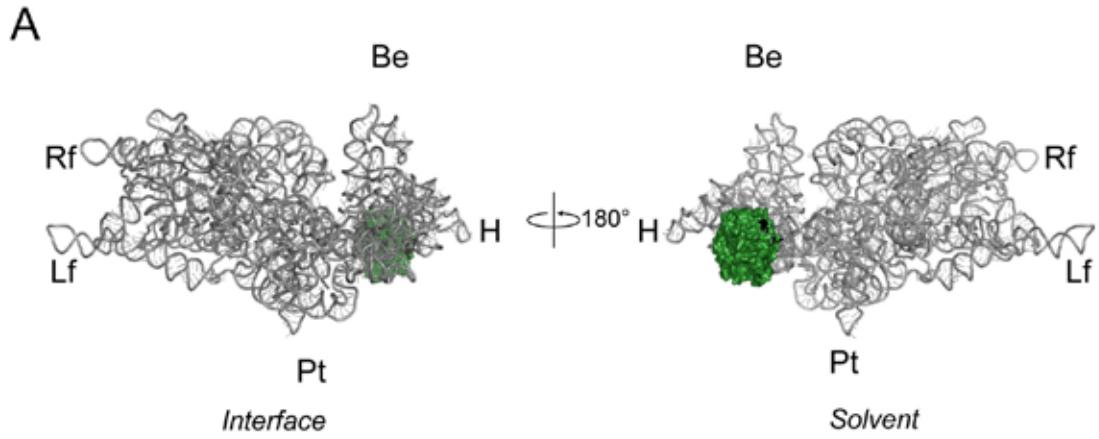
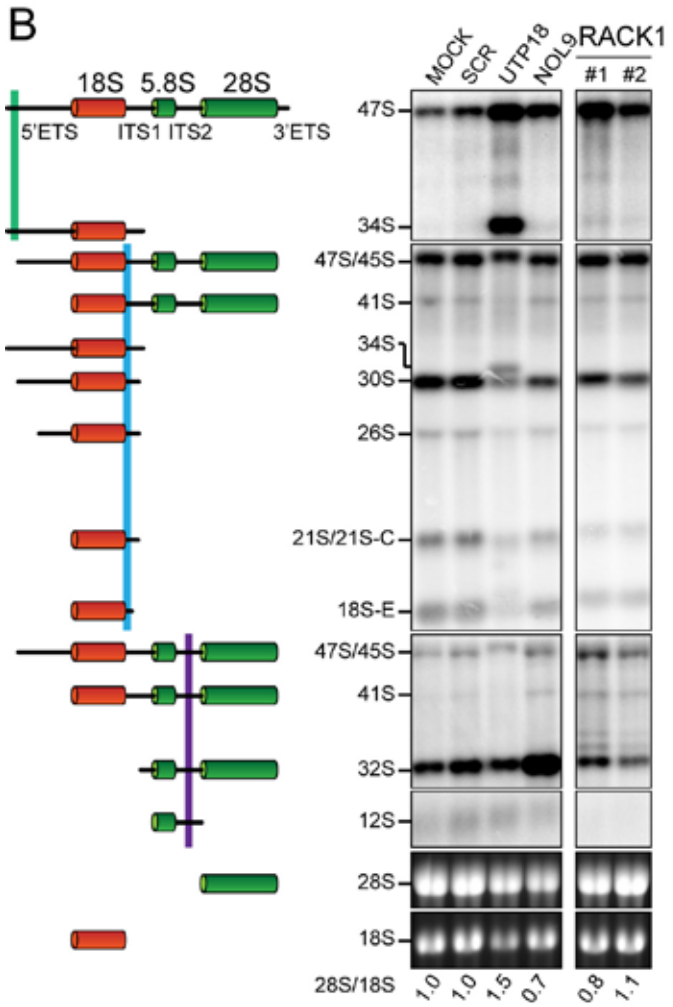
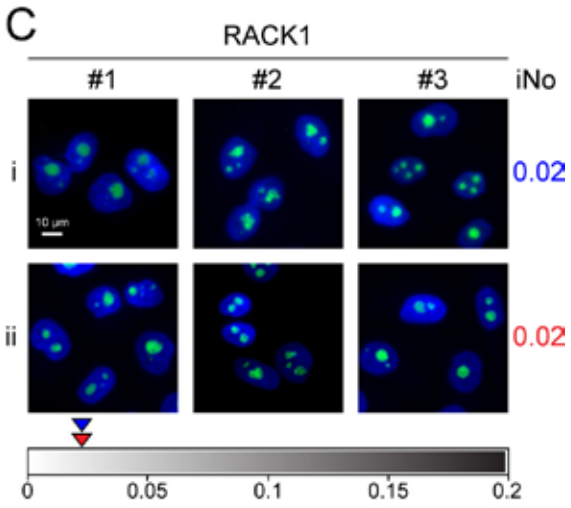
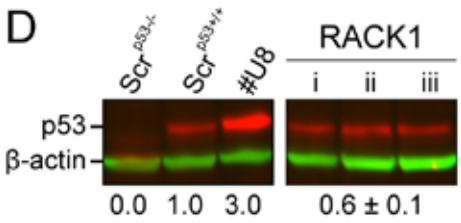
RACK1 (RACK1)









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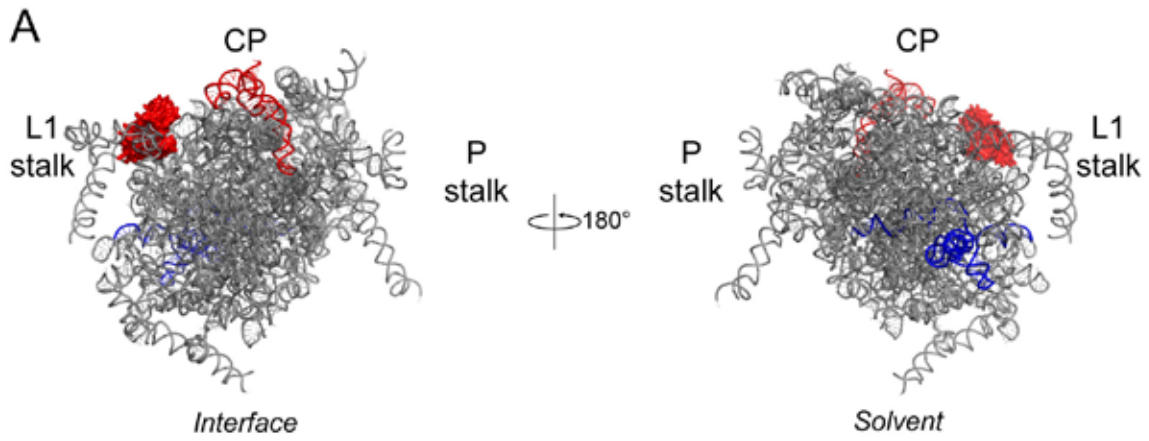
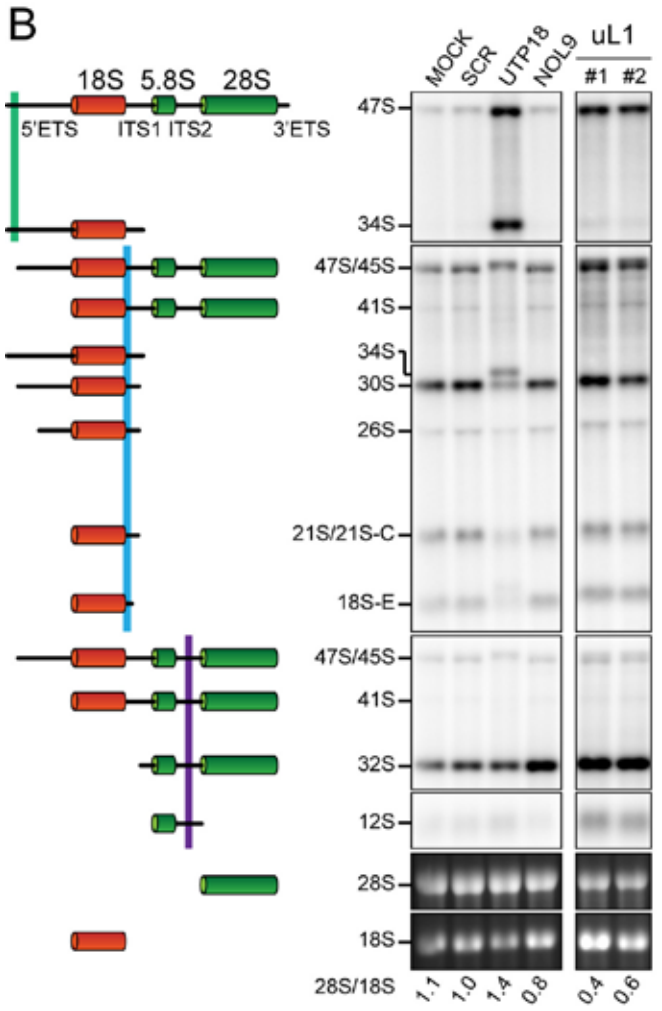
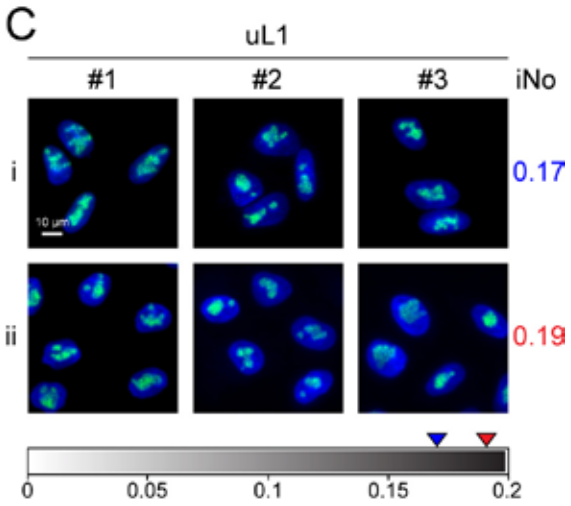
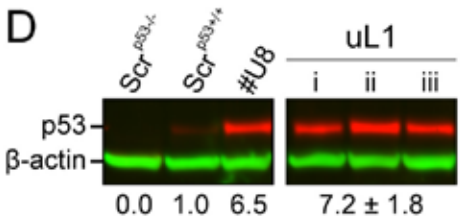
uL1 (RpL10a)









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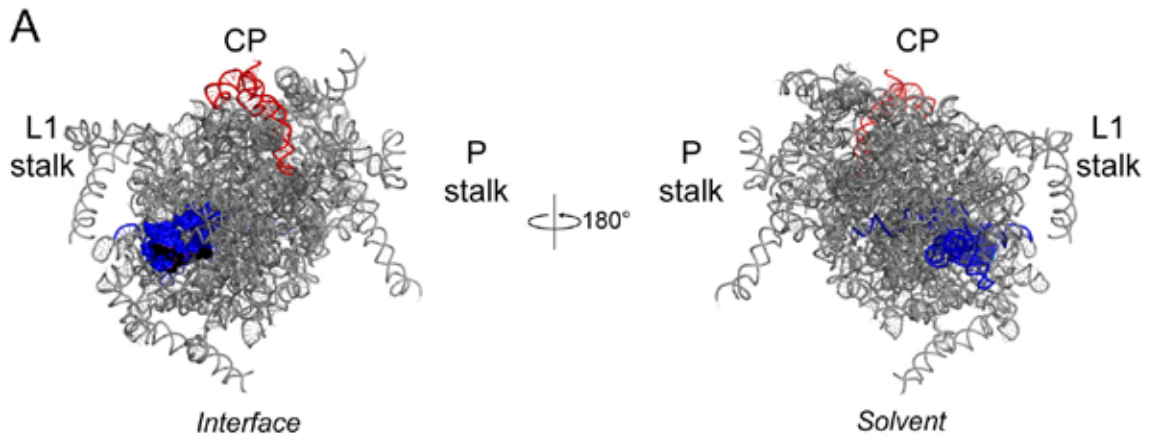
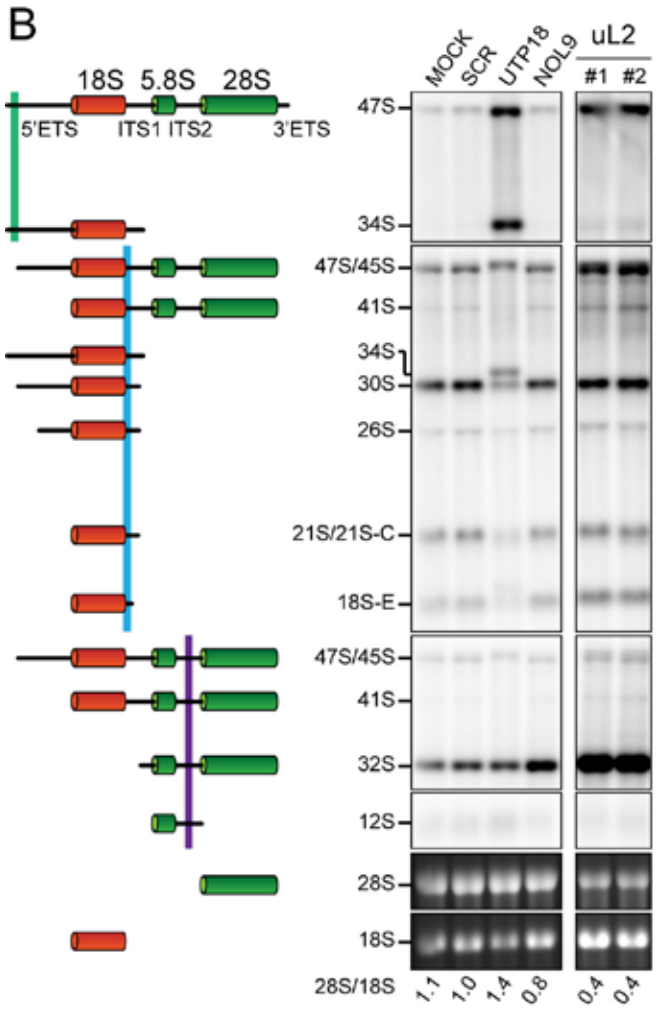
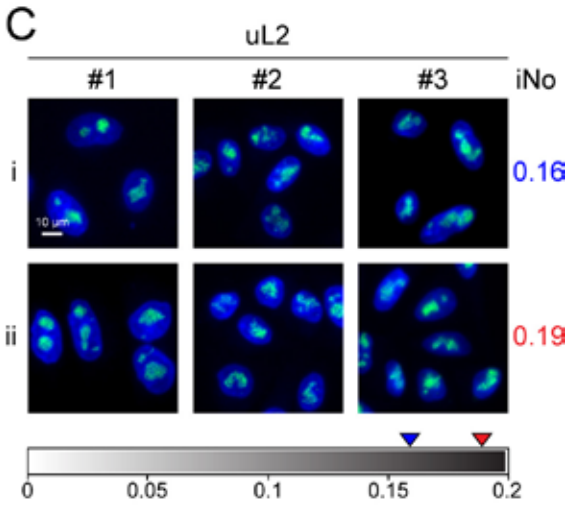
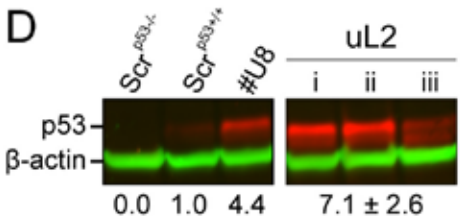
uL2 (RpL8)









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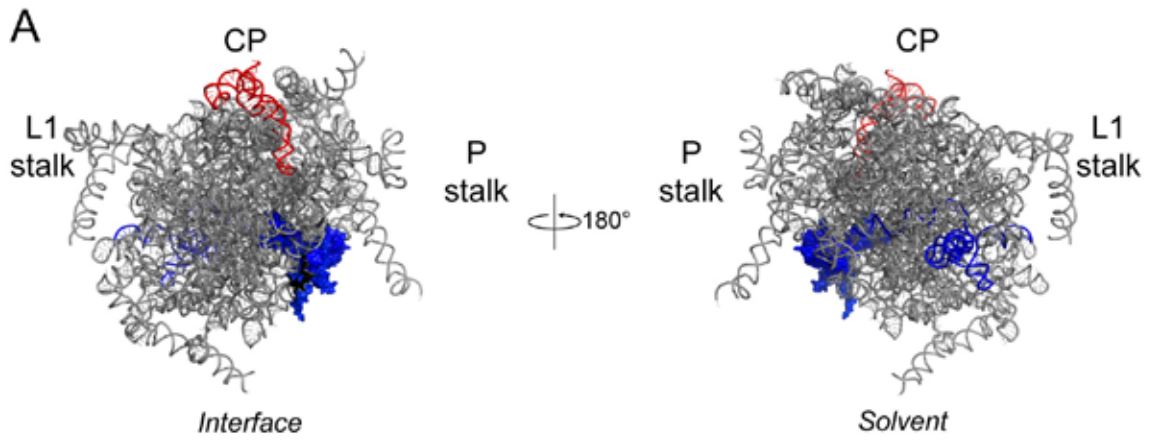
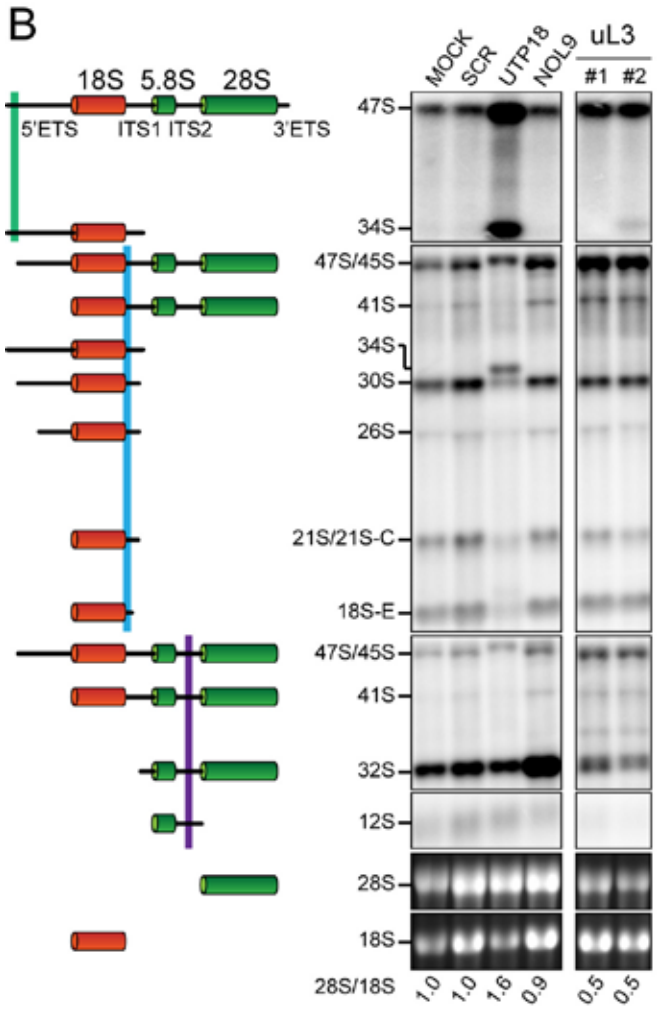
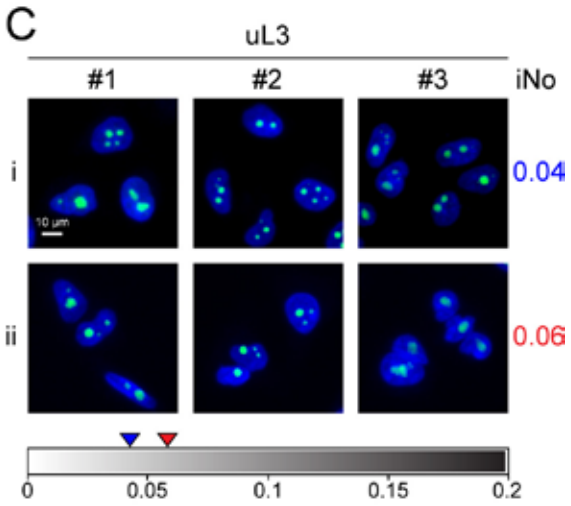
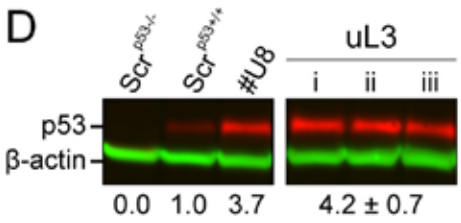
uL3 (RpL3)









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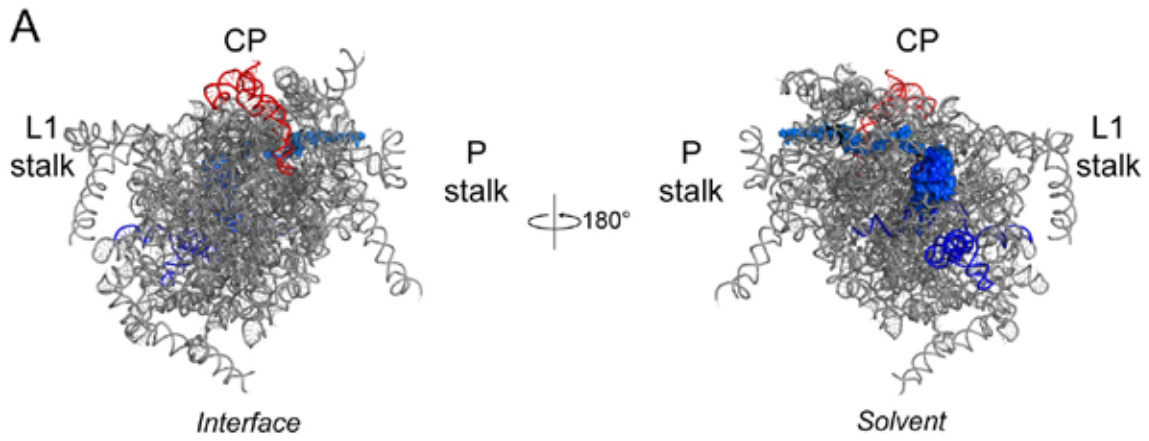
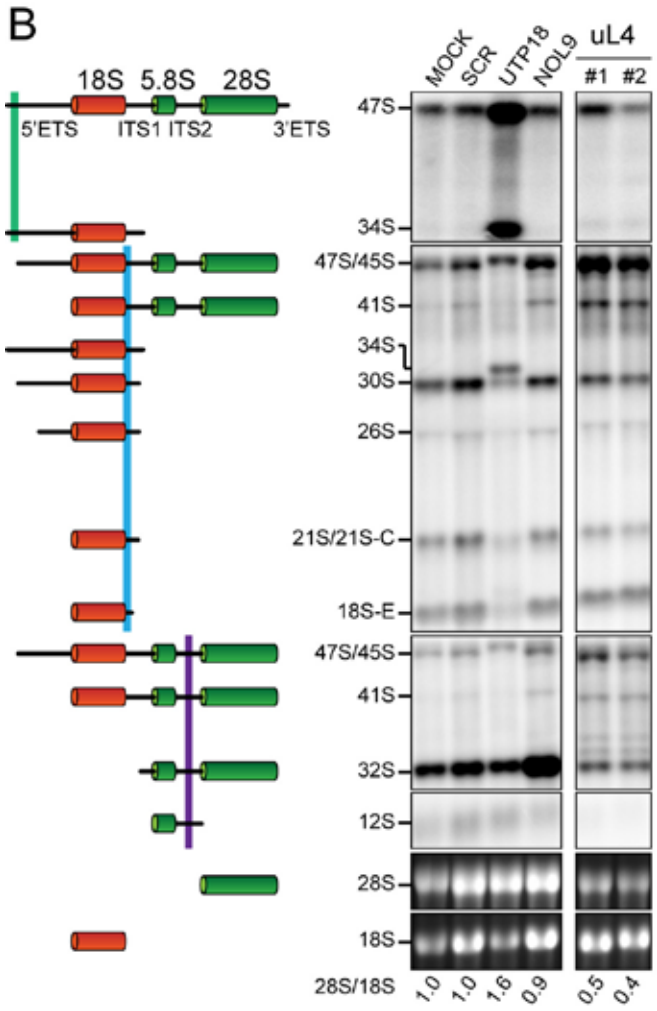
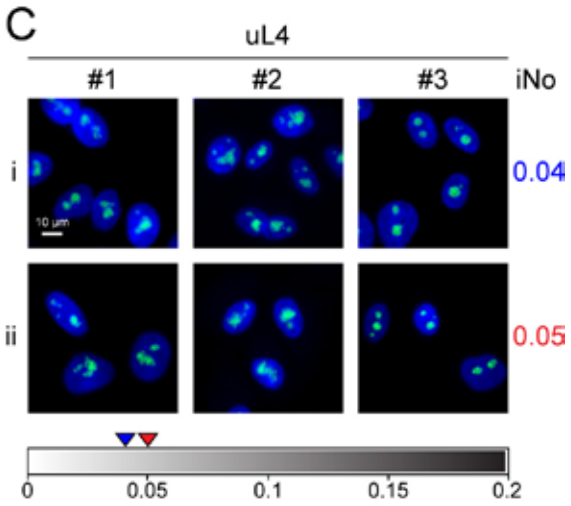
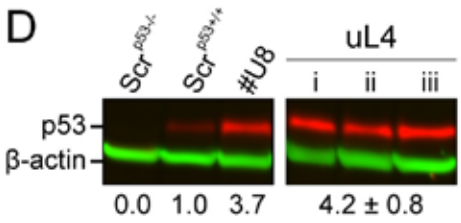
uL4 (RpL4)









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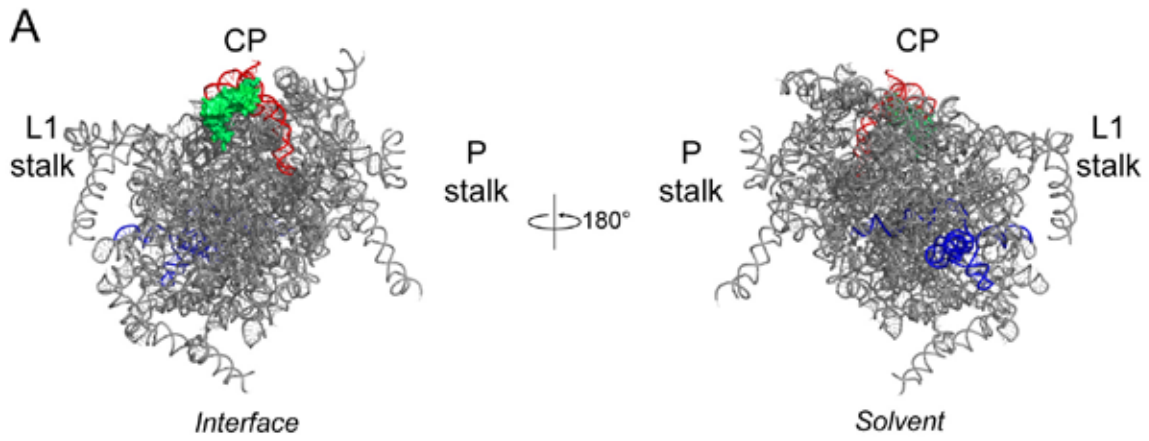
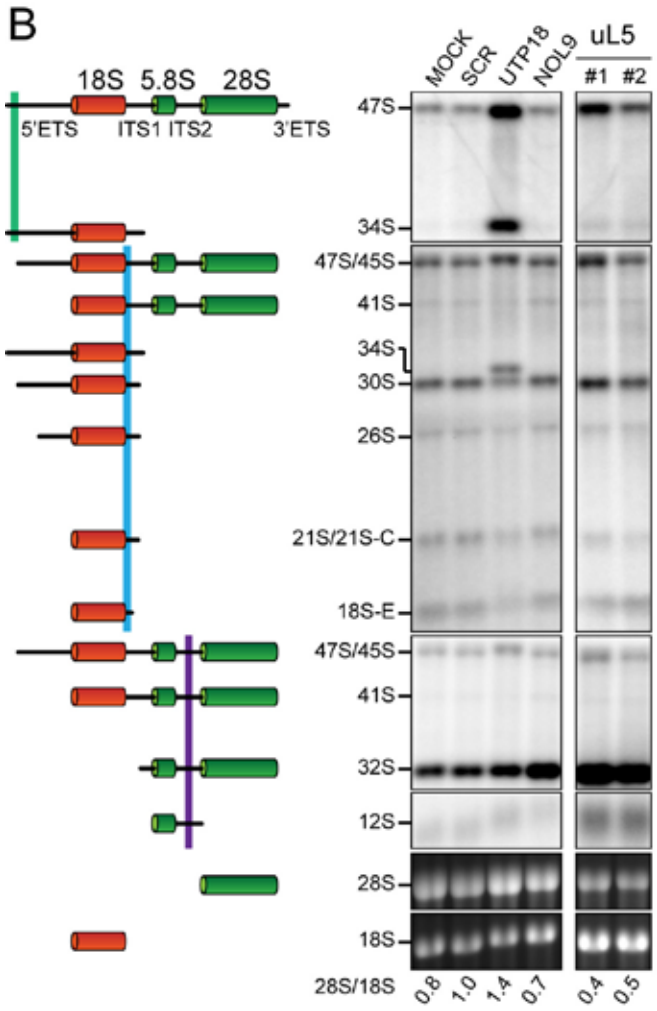
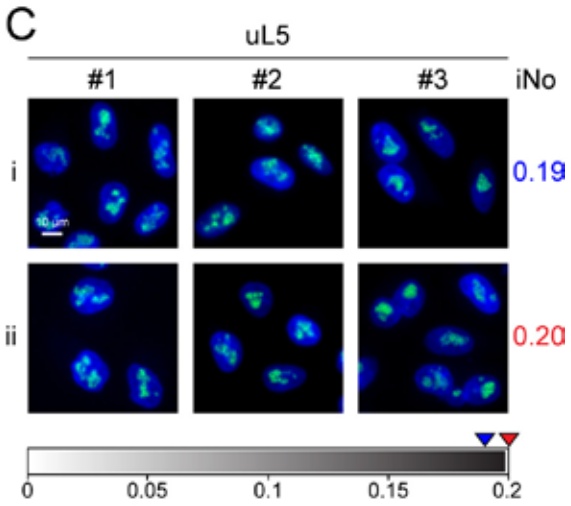
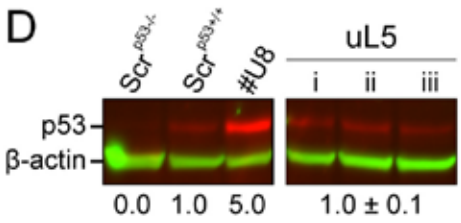
uL5 (RpL11)









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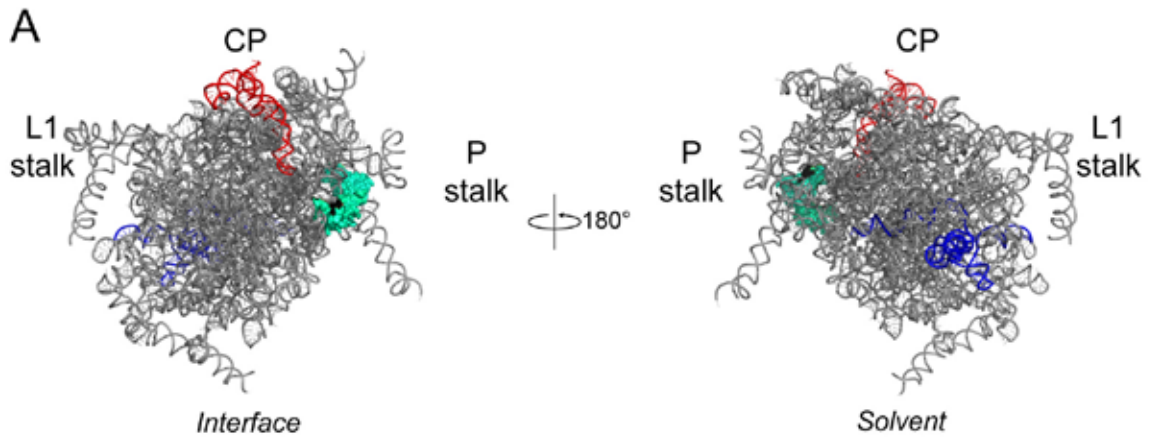
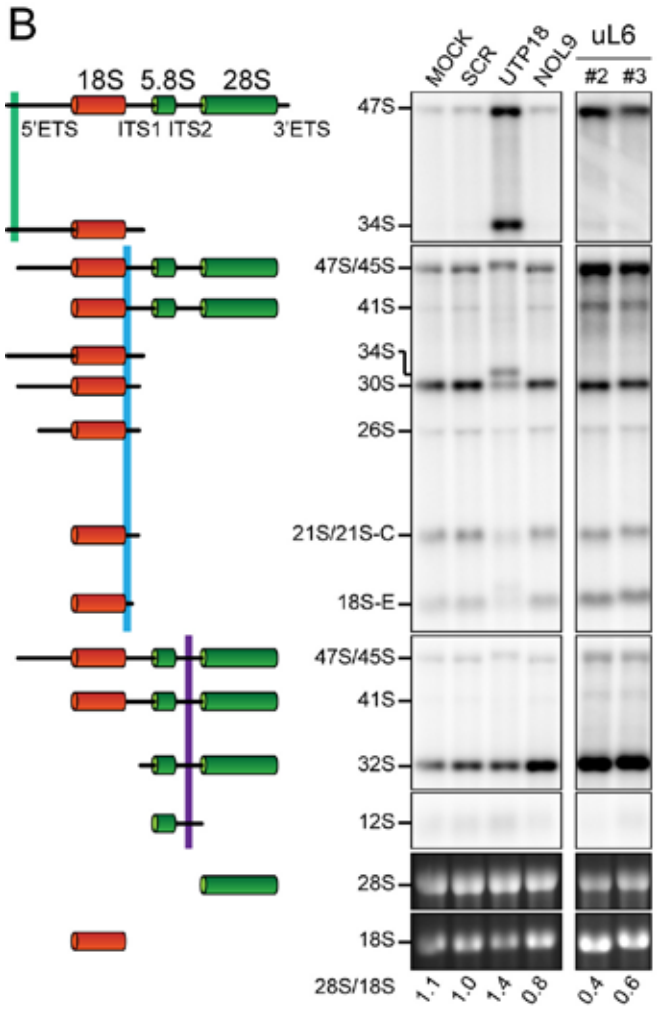
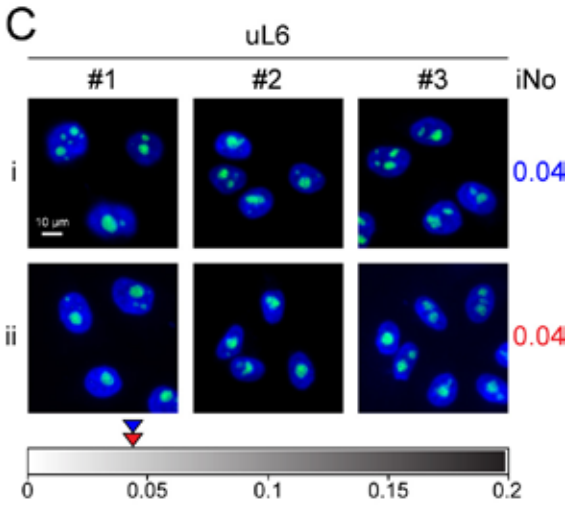
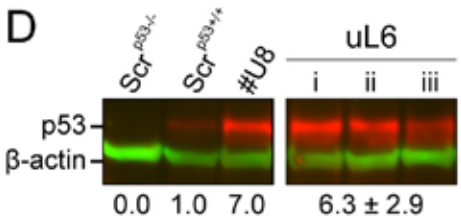
uL6 (RpL9)









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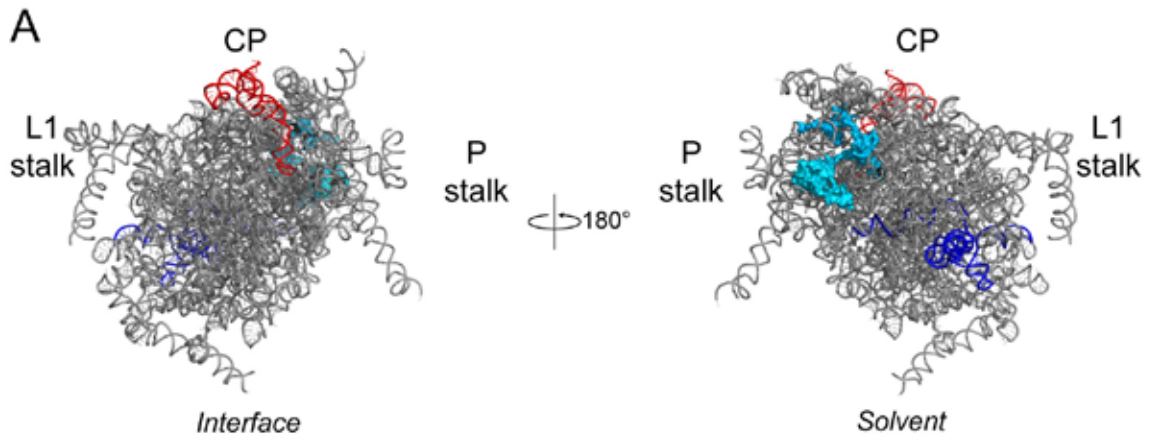
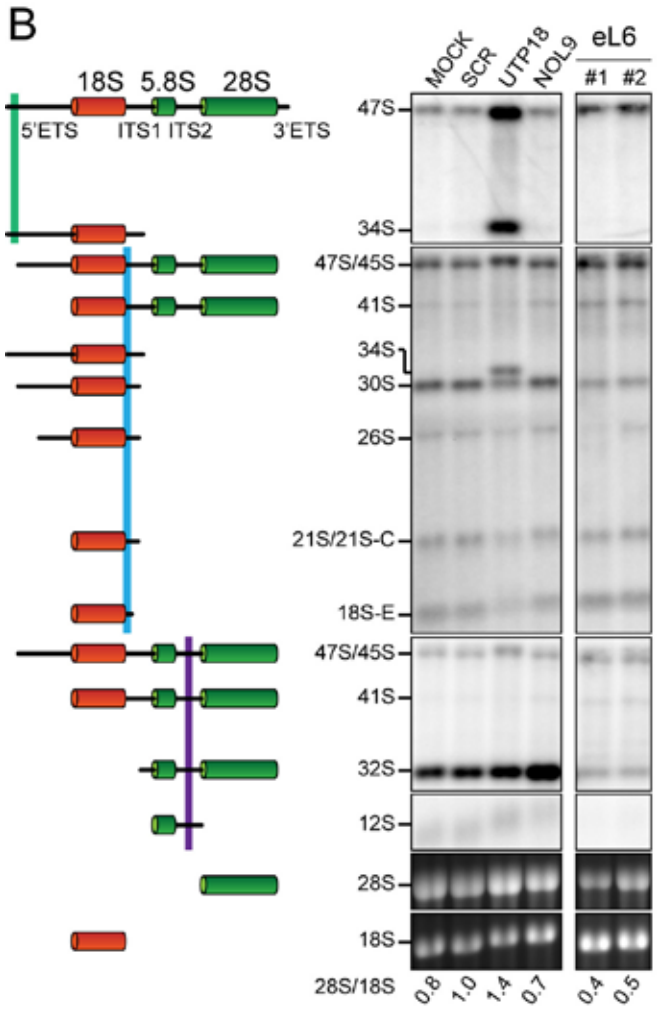
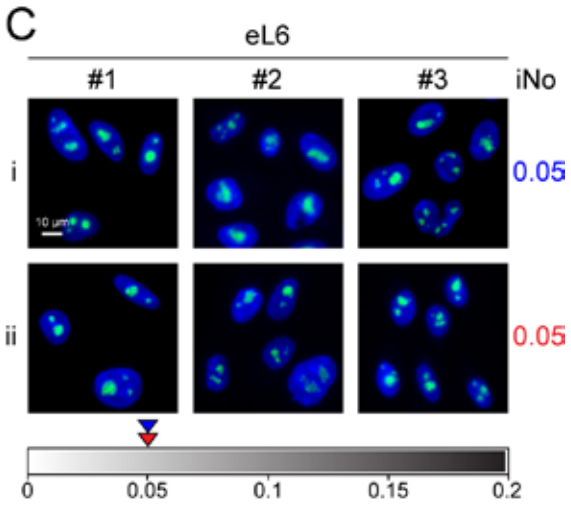
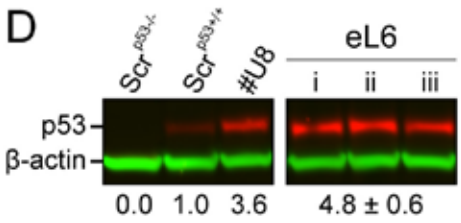
eL6 (RpL6)









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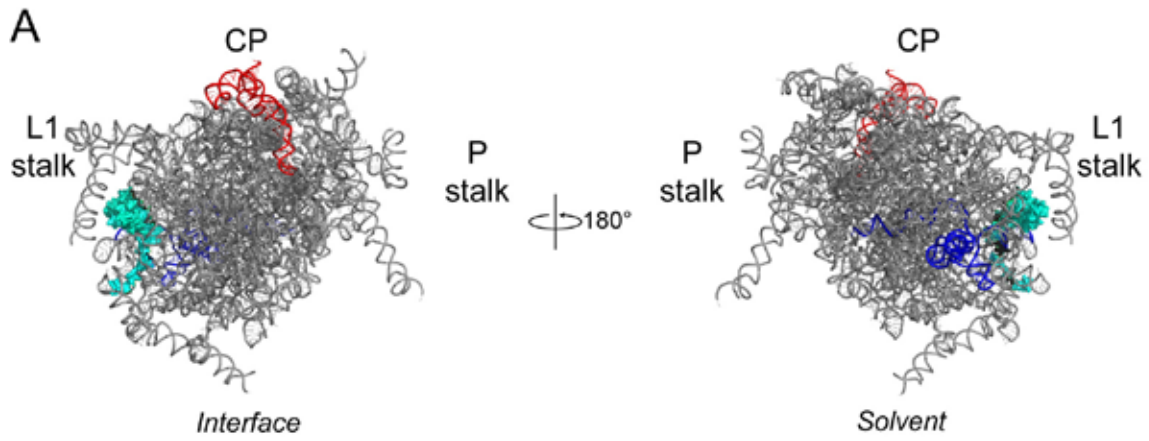
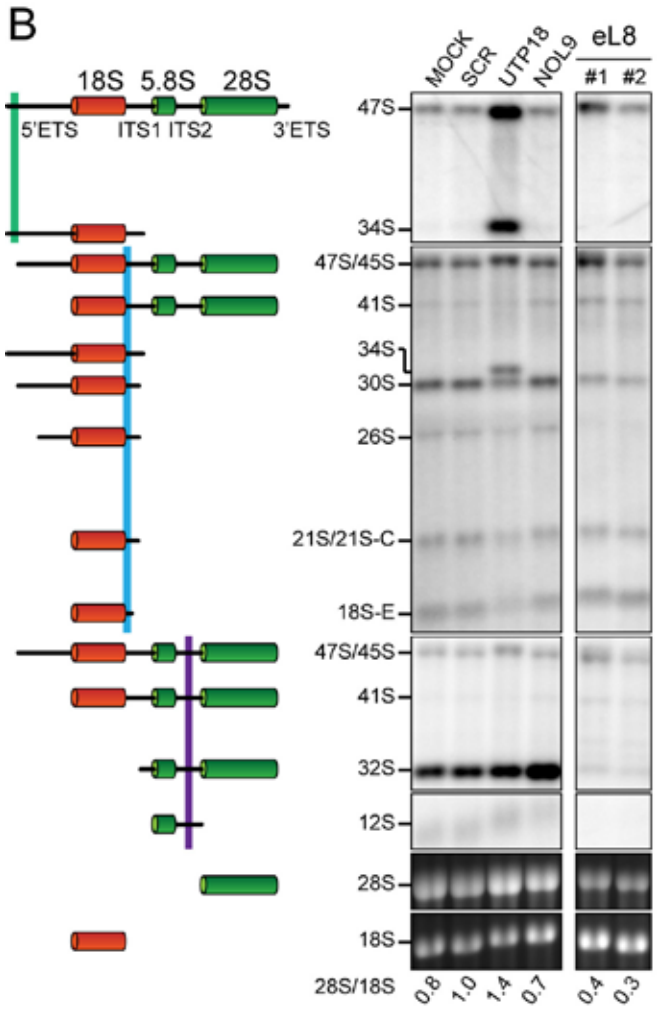
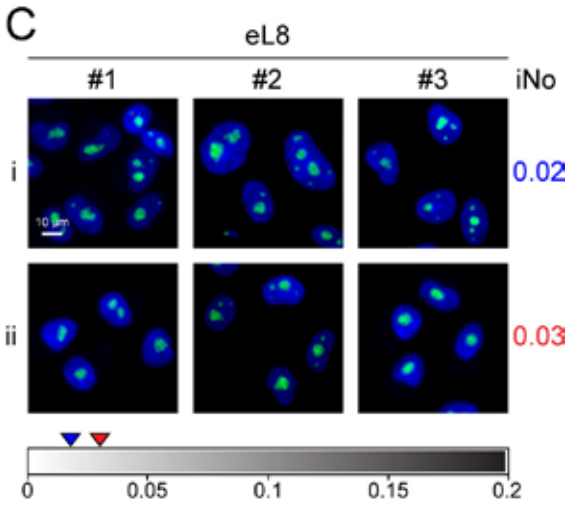
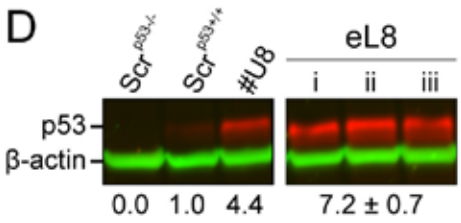
eL8 (RpL7a)









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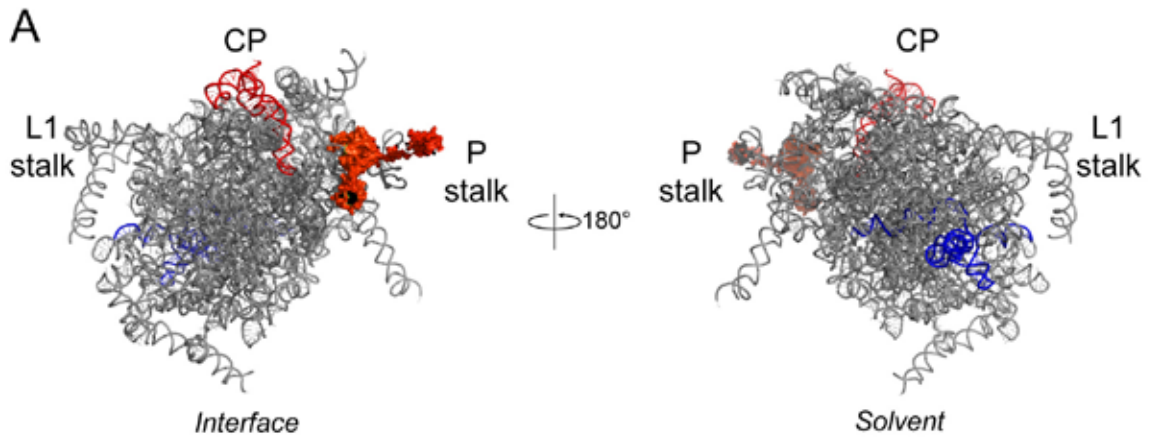
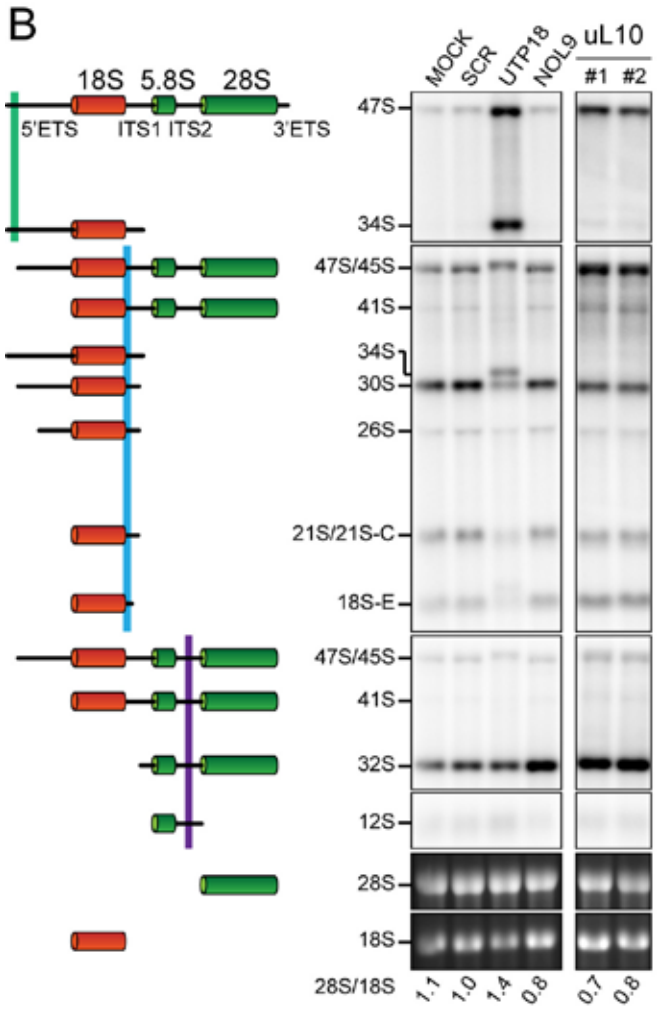
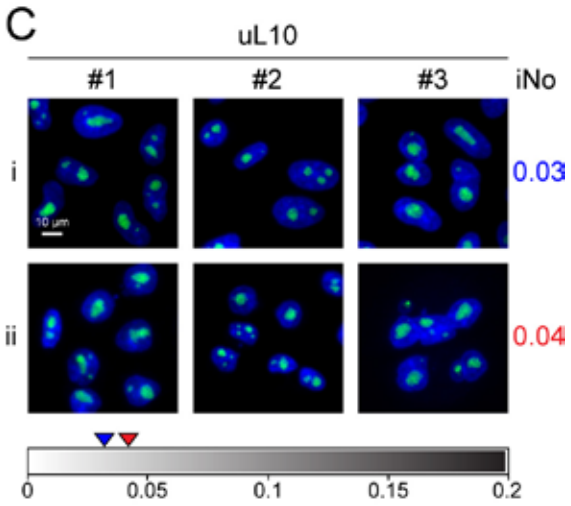
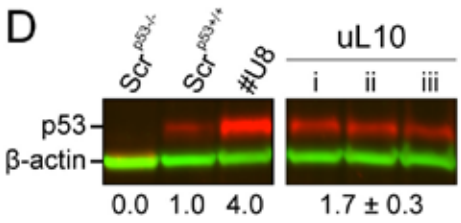
uL10 (P0)









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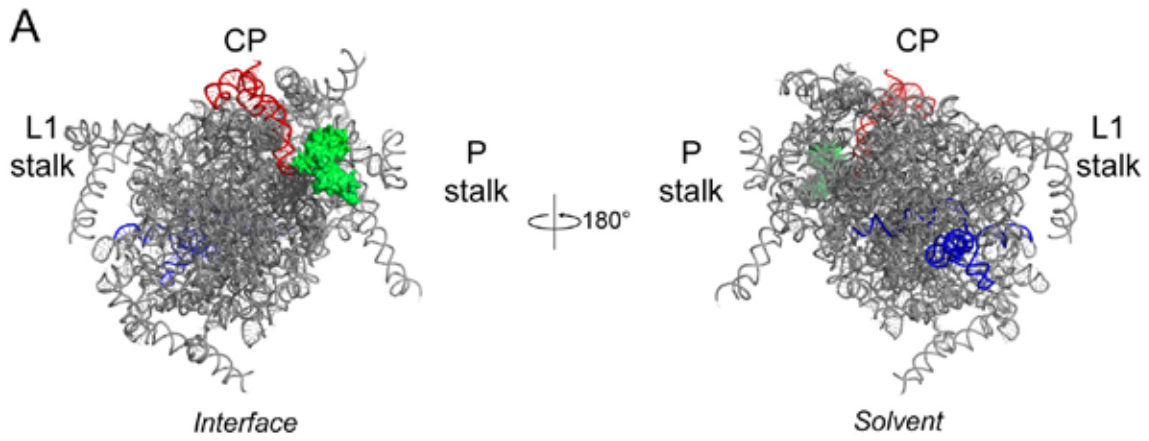
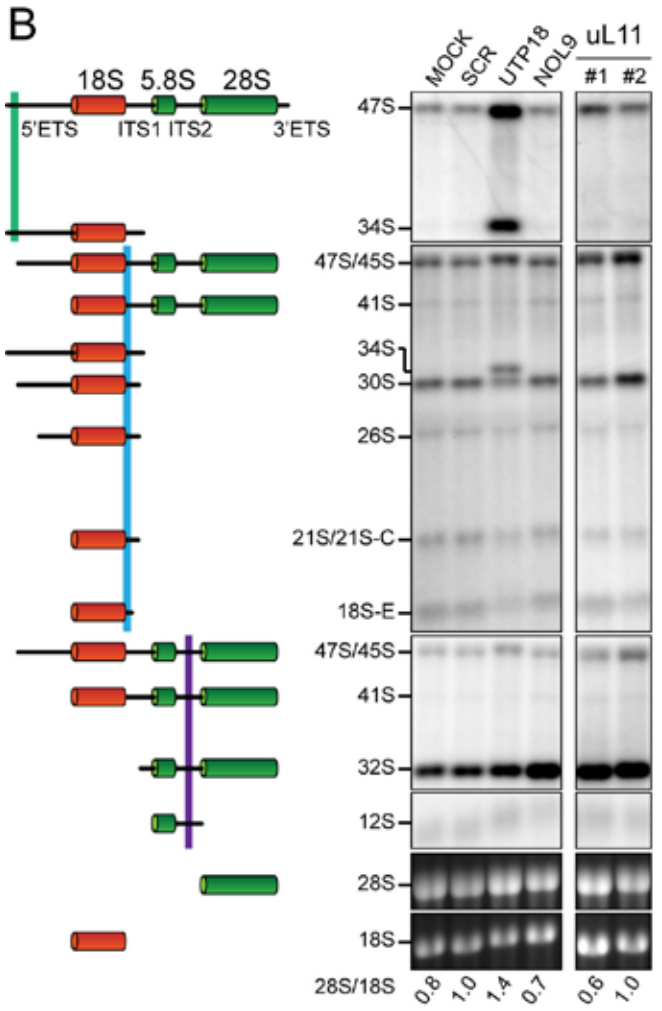
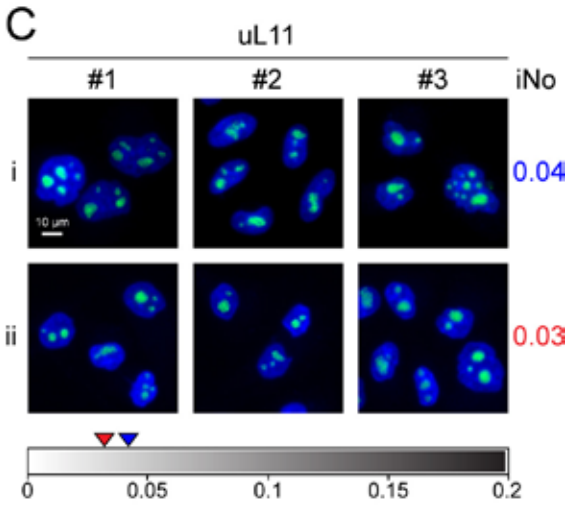
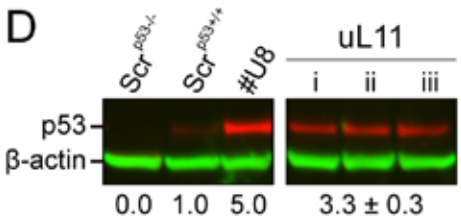
uL11 (RpL12)









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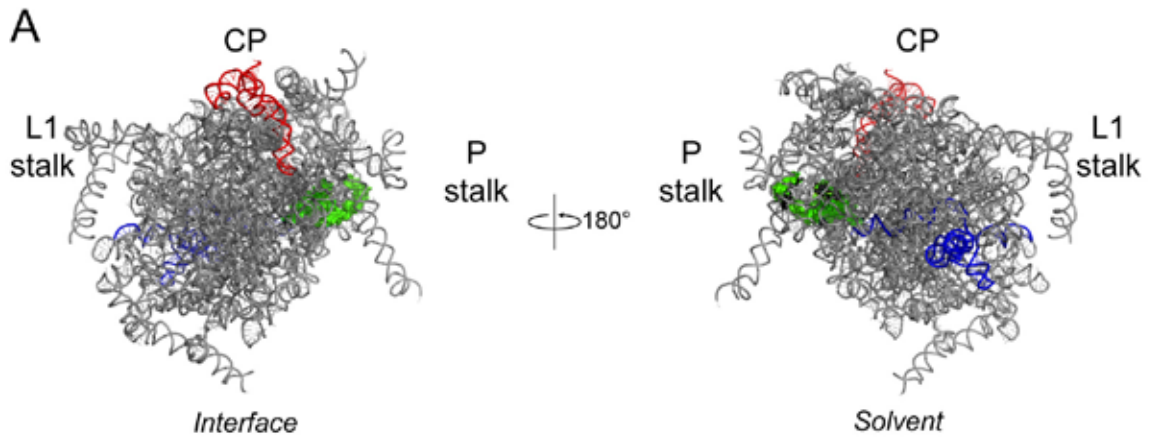
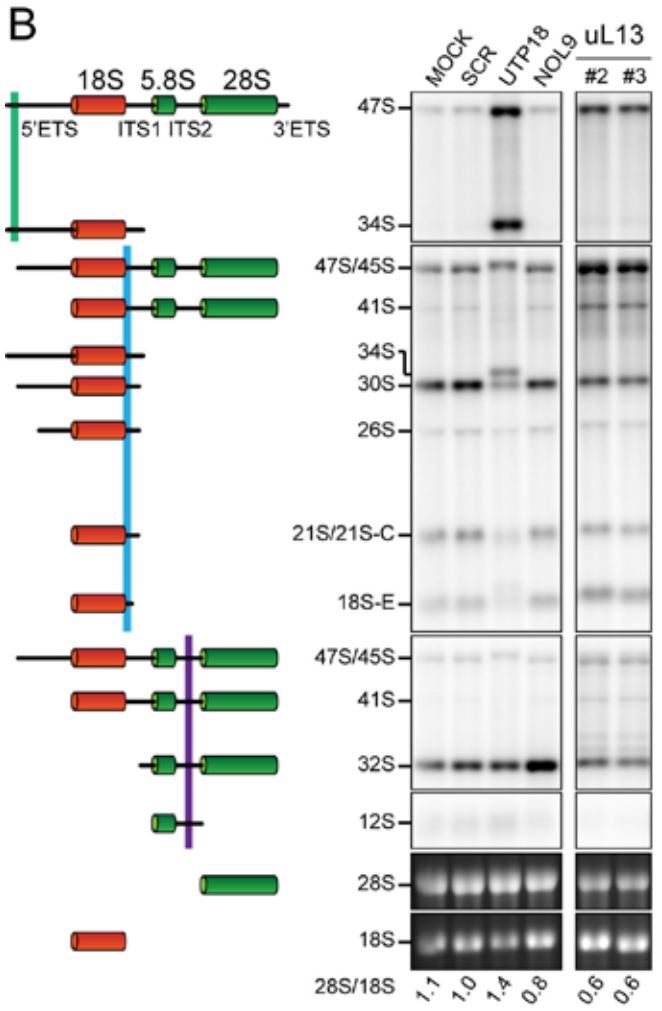
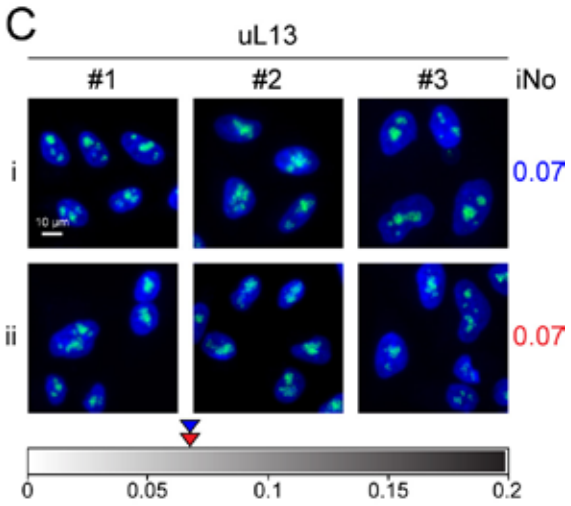
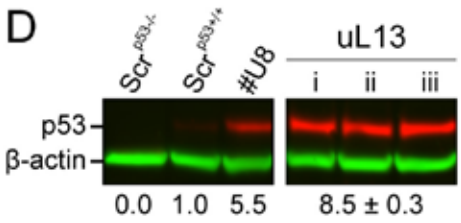
uL13 (RpL13a)









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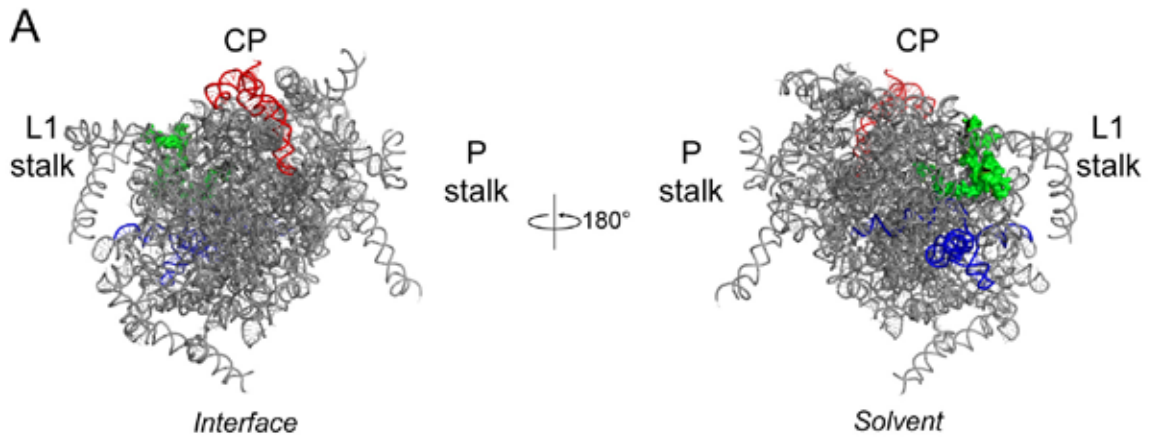
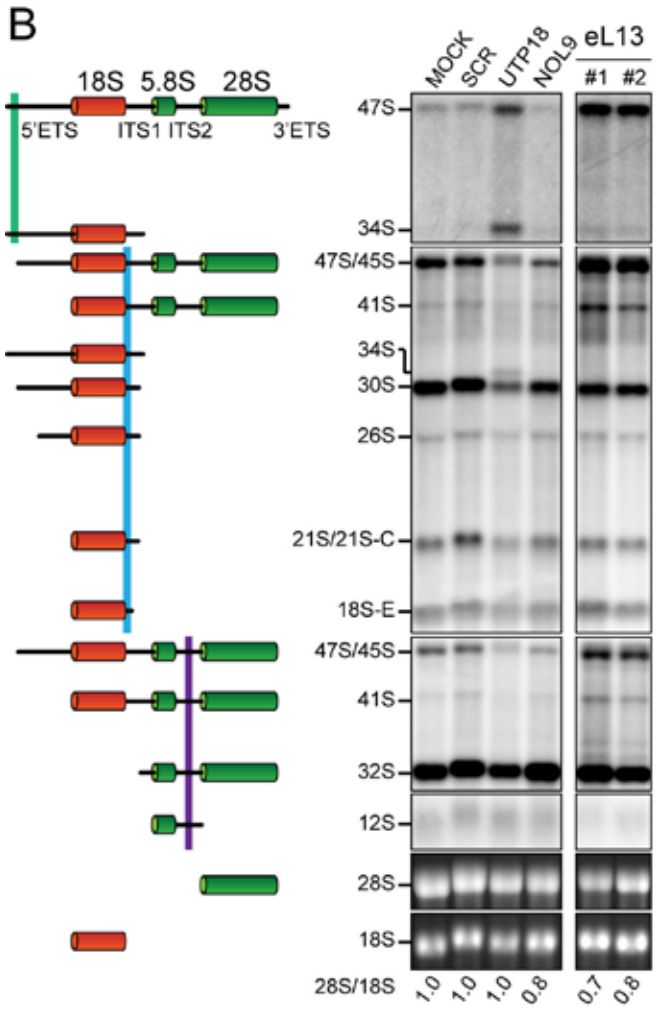
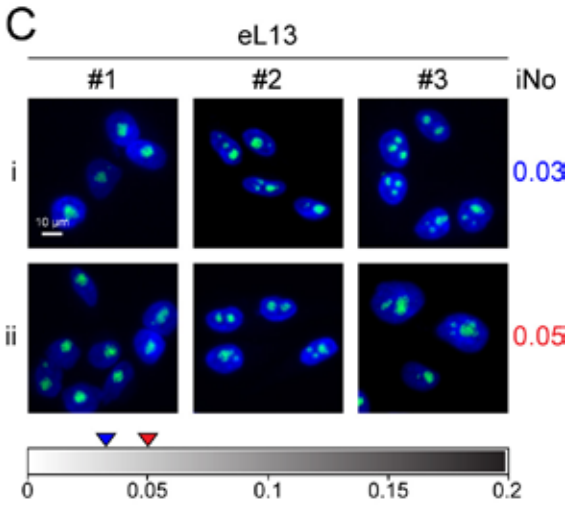
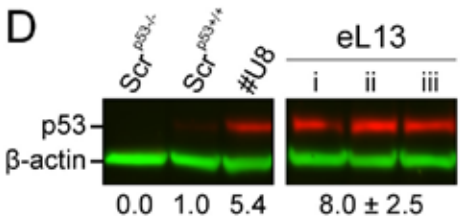
eL13 (RpL13)









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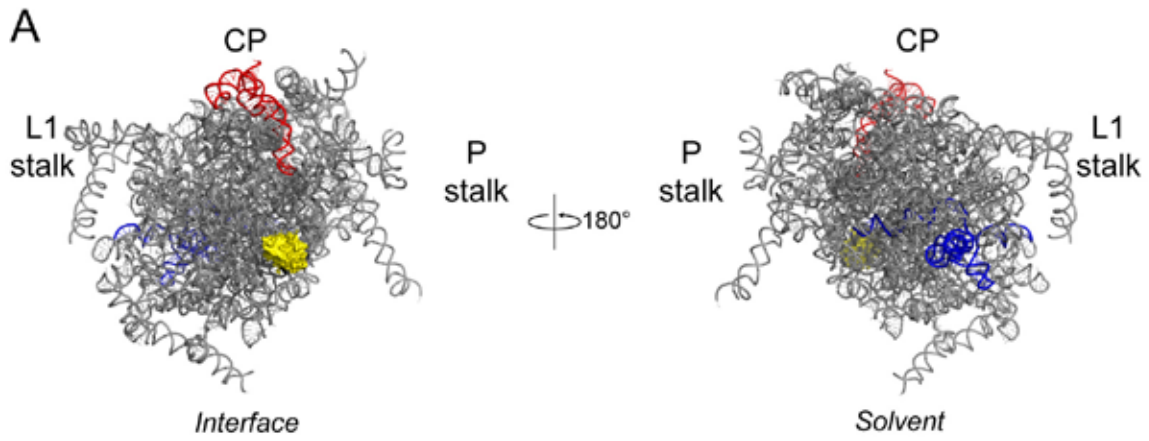
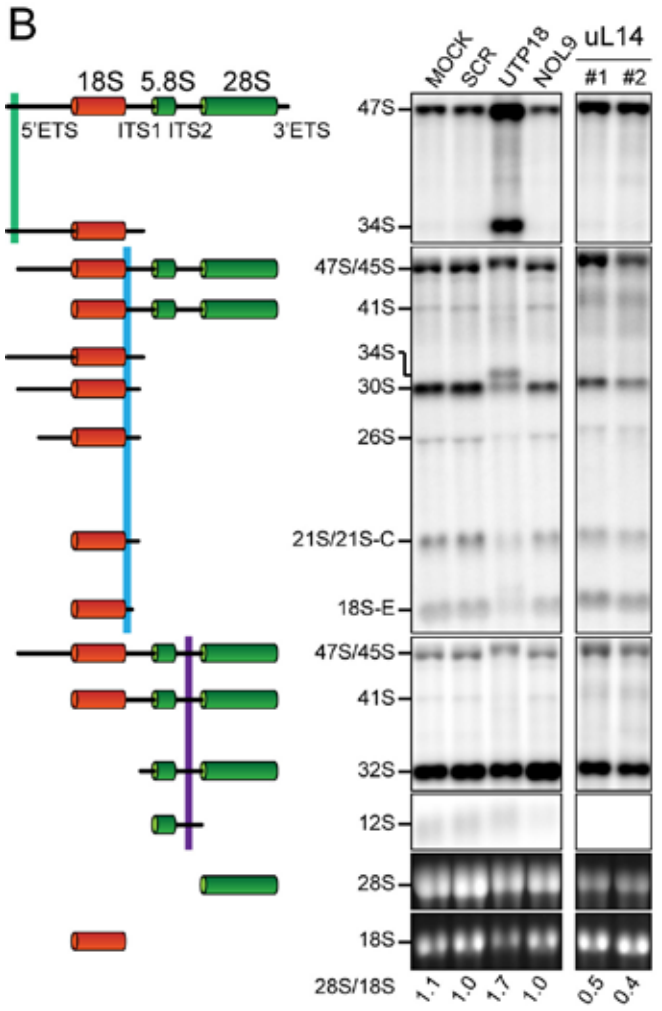
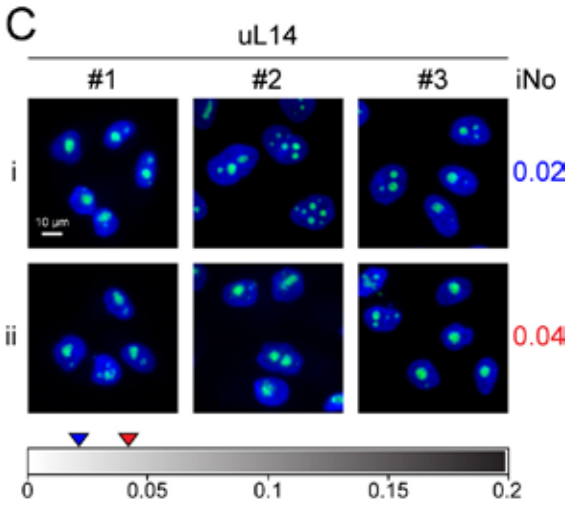
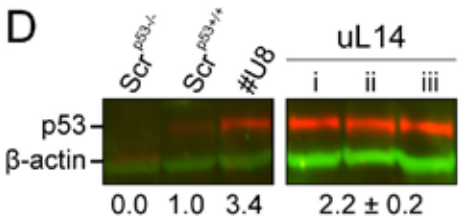
uL14 (RpL23)









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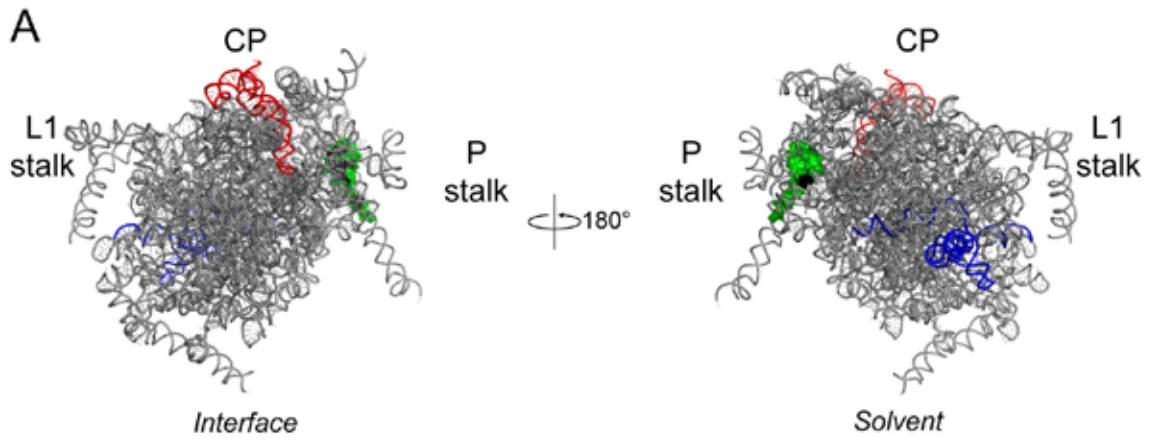
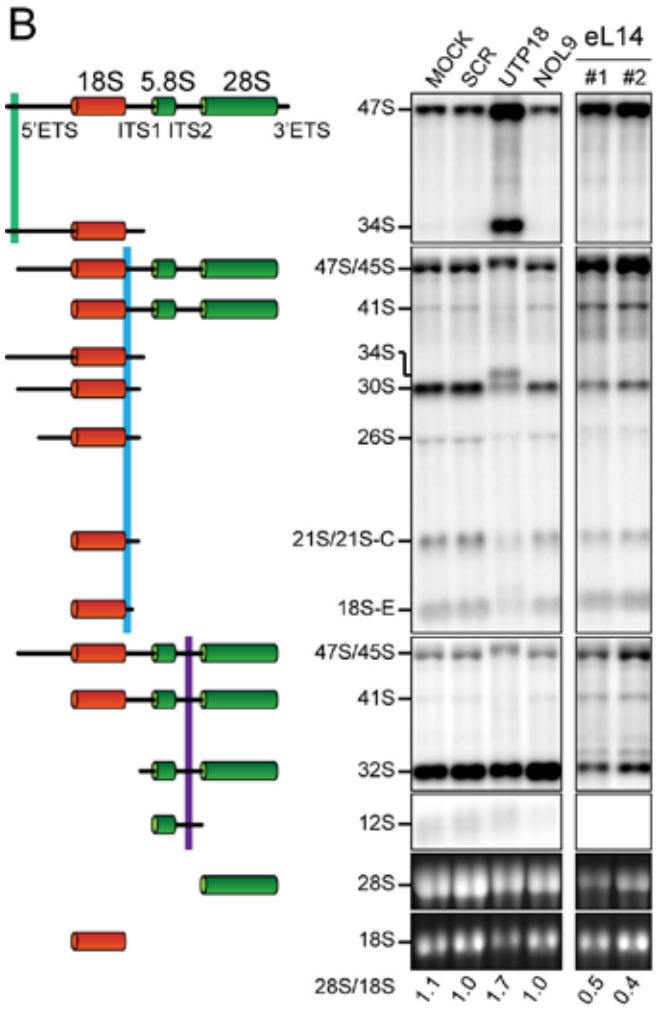
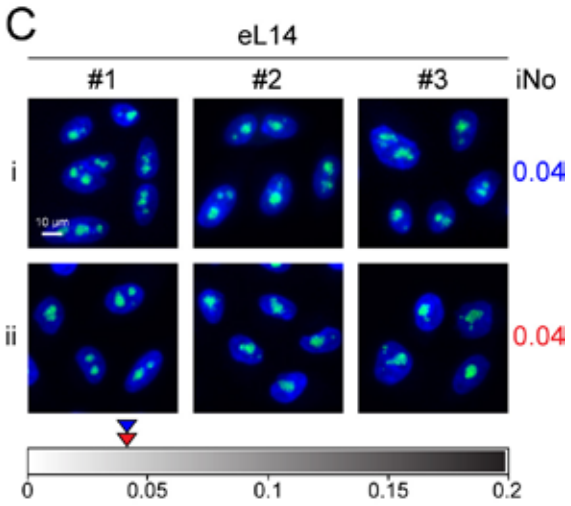
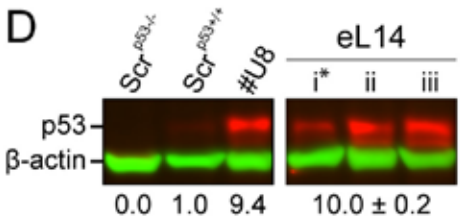
eL14 (RpL14)









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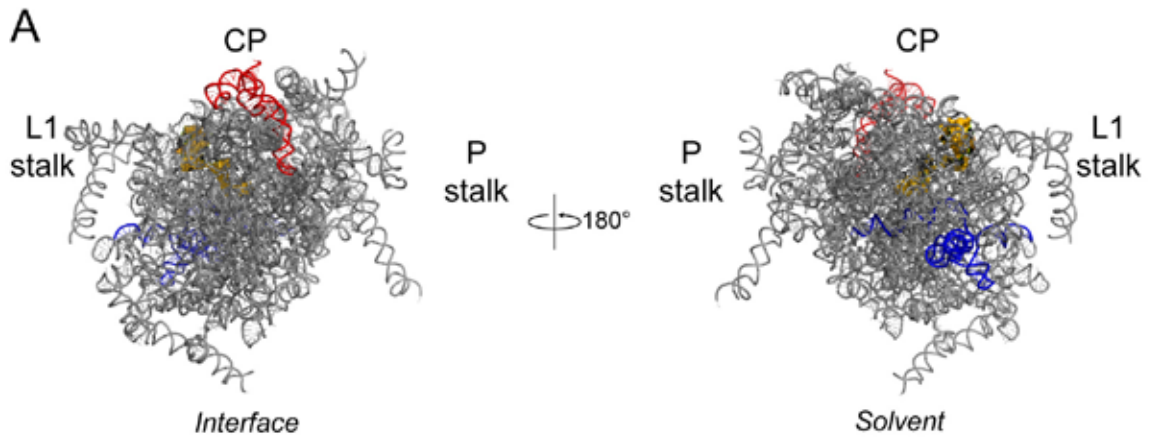
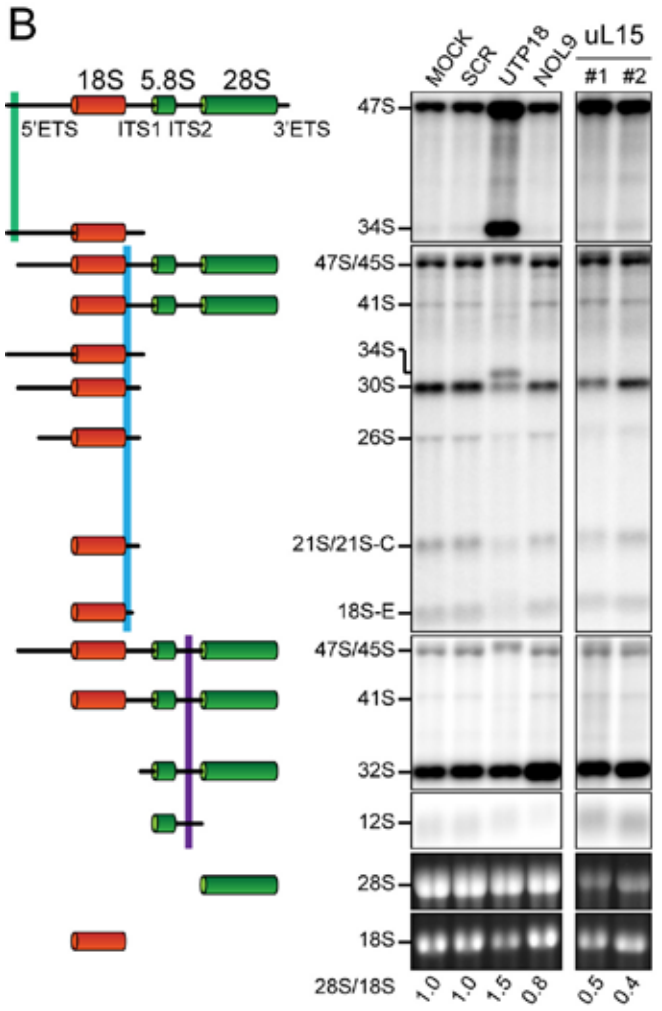
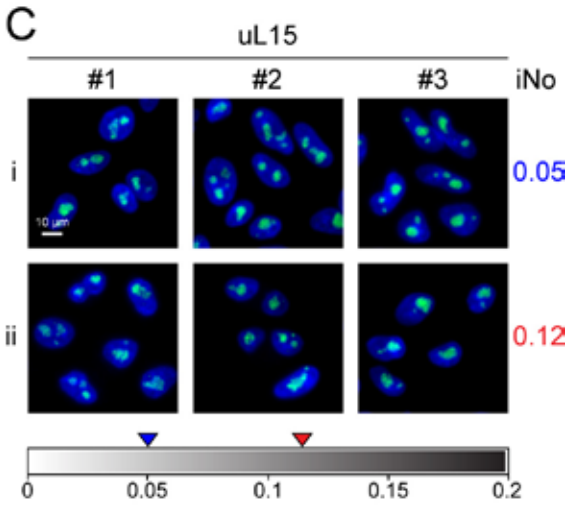
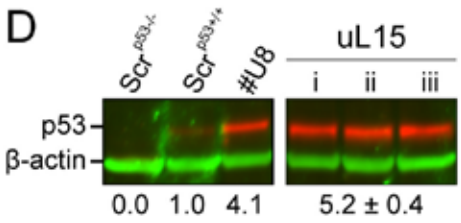
uL15 (RpL27a)









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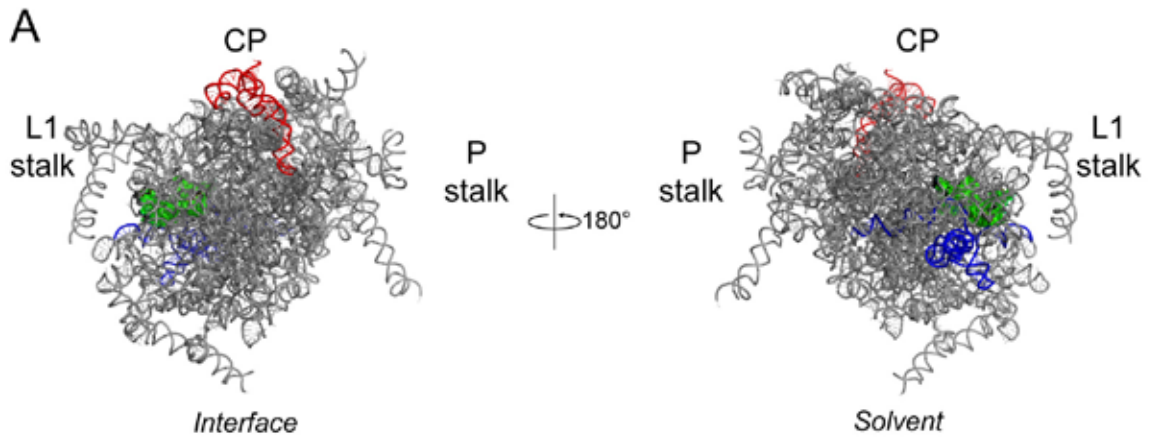
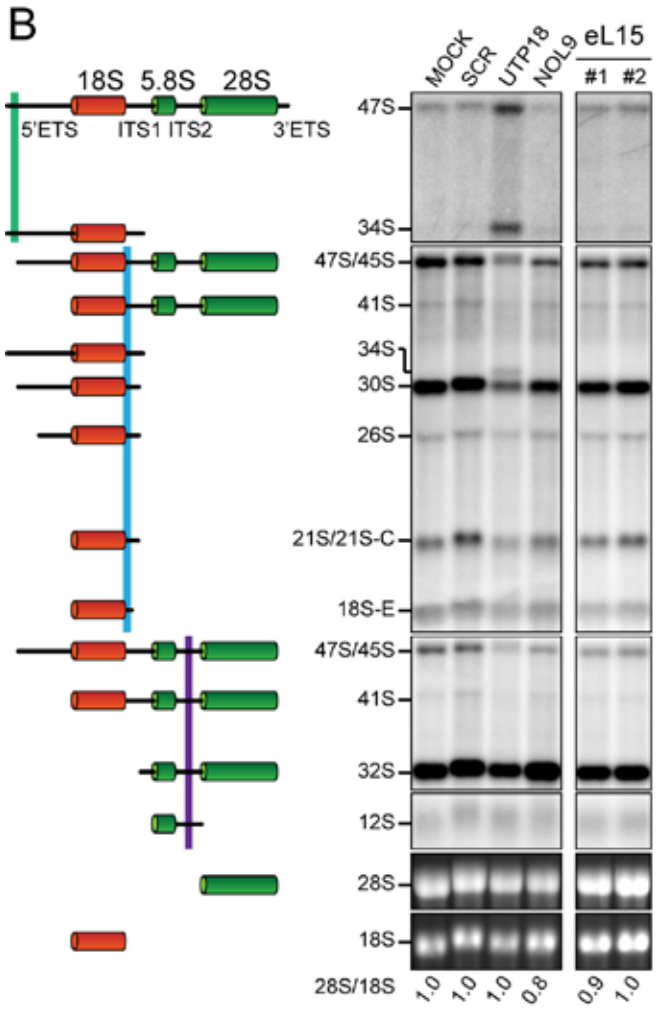
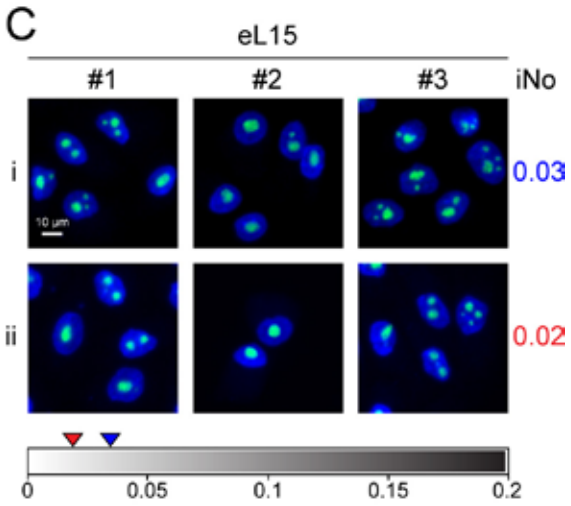
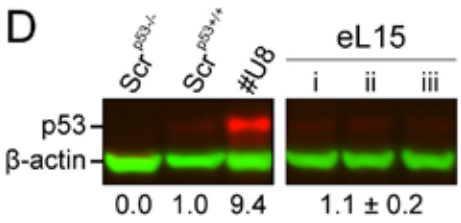
eL15 (RpL15)









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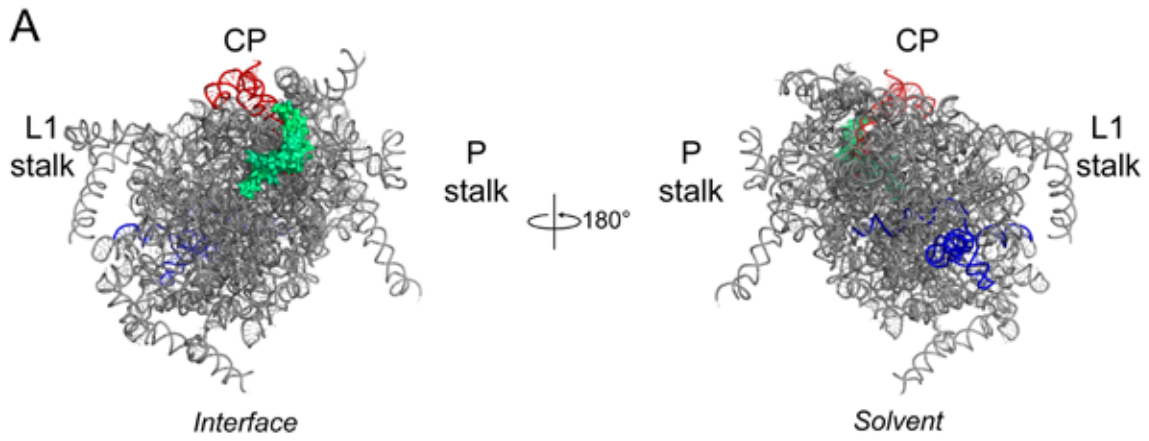
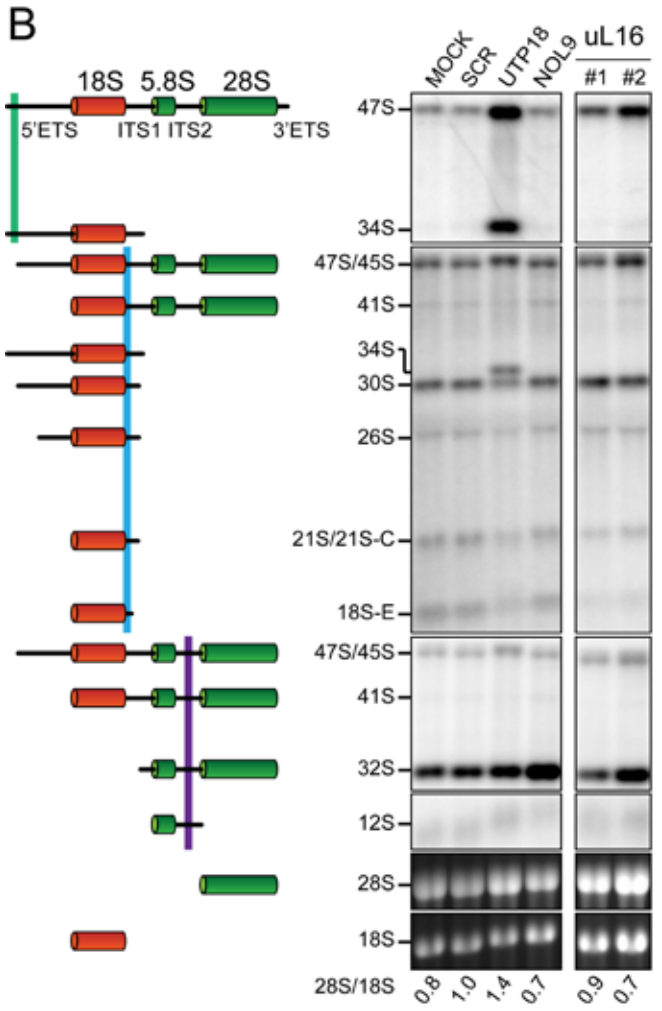
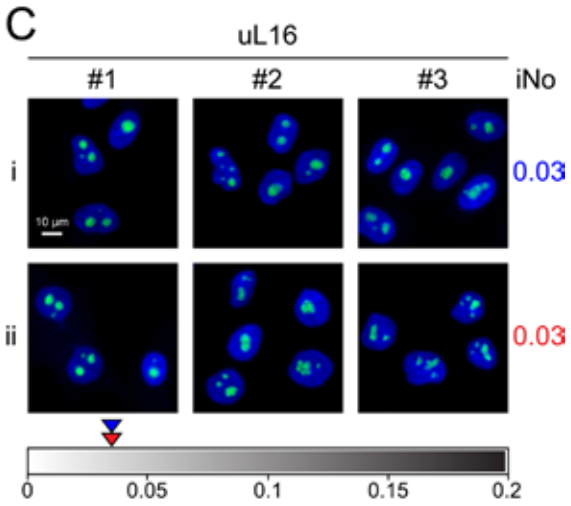
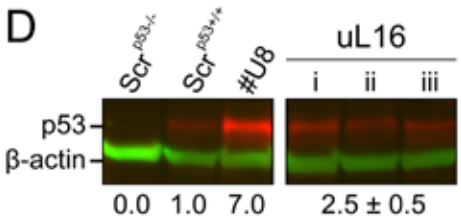
uL16 (RpL10)









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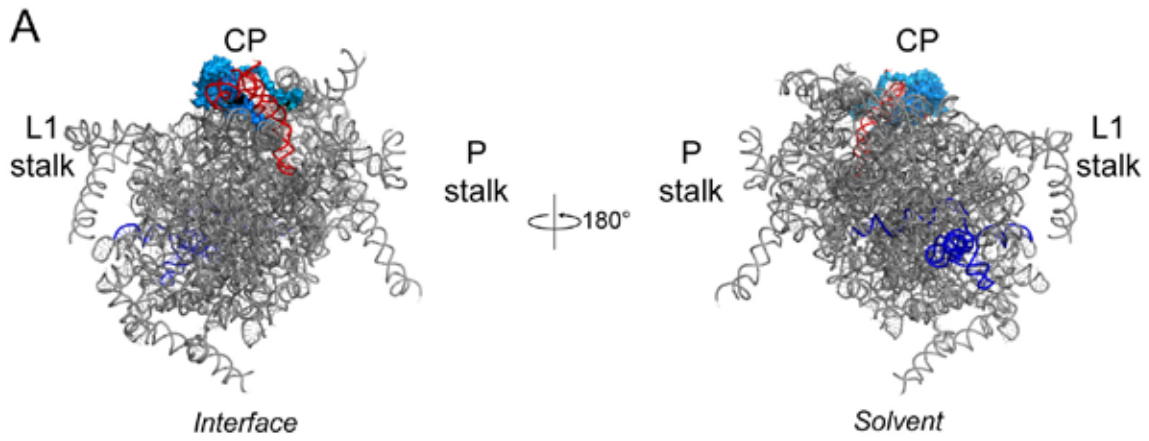
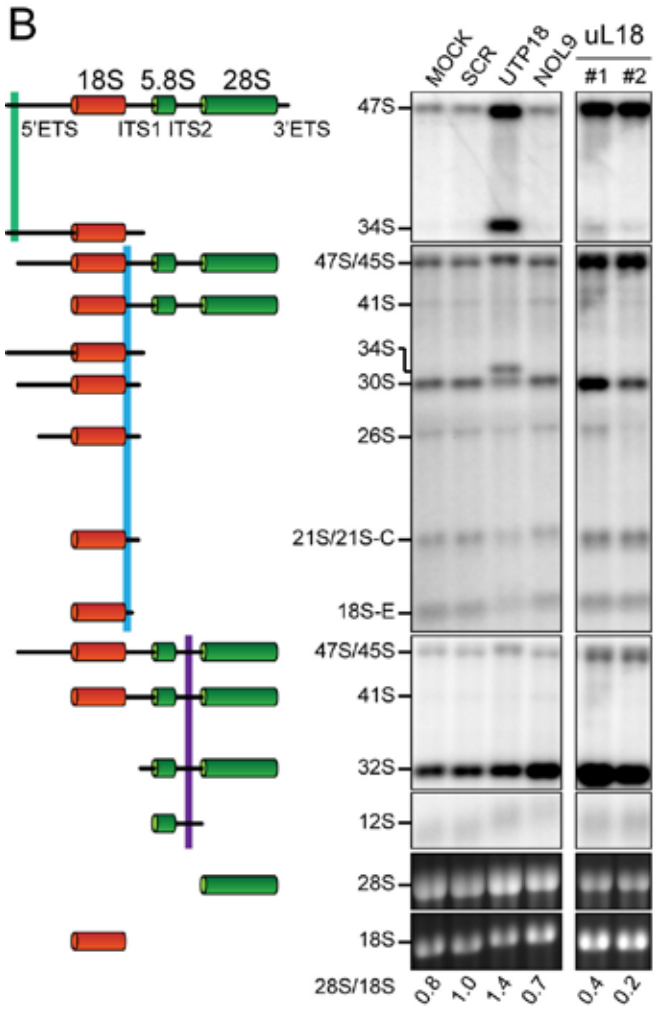
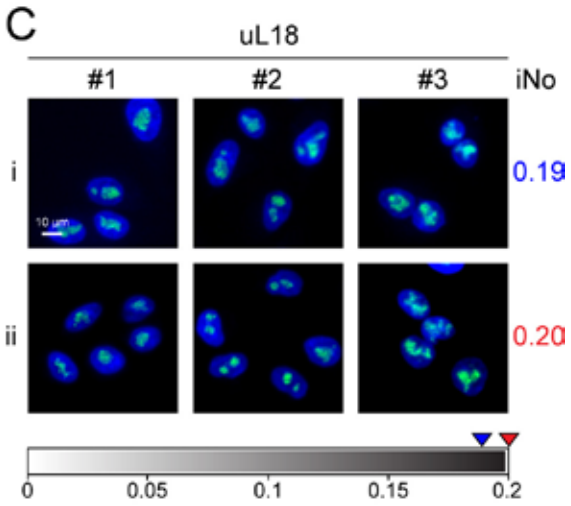
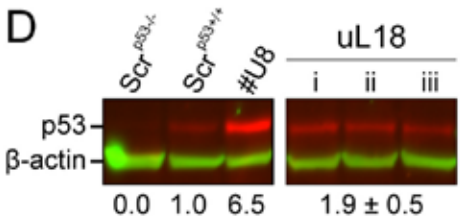
uL18 (RpL5)









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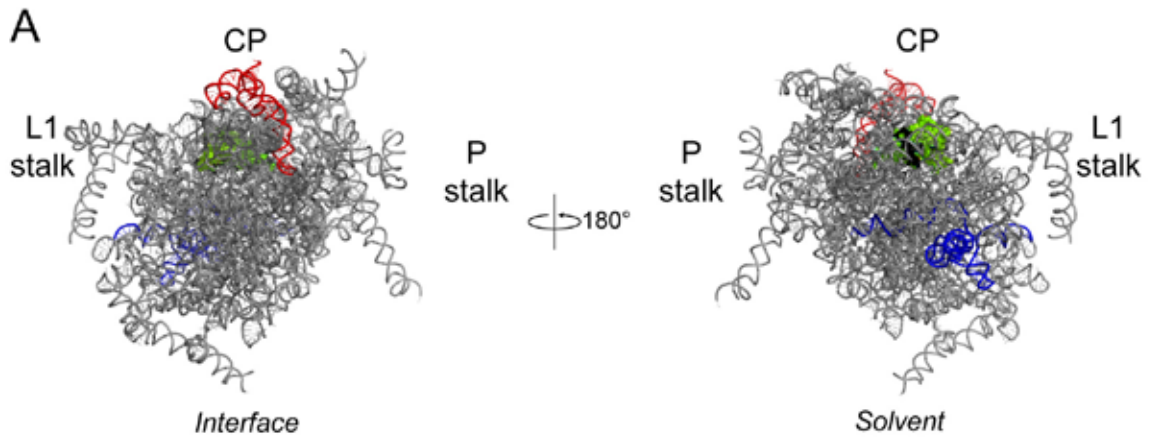
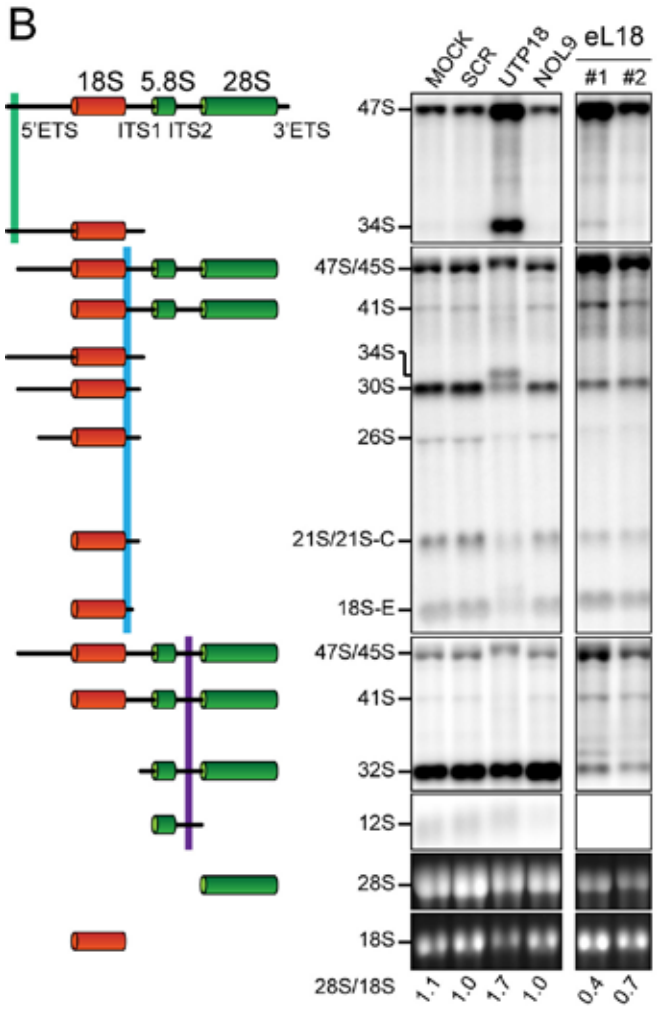
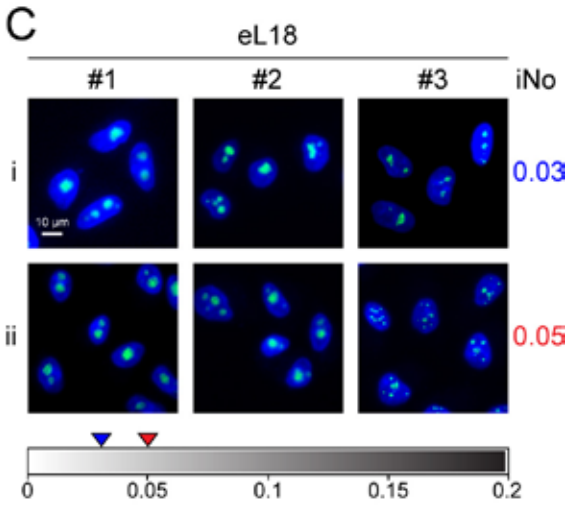
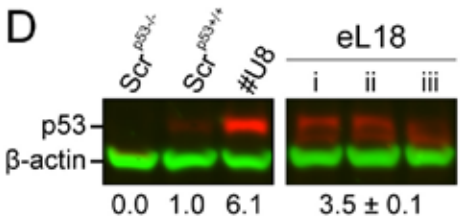
eL18 (RpL18)









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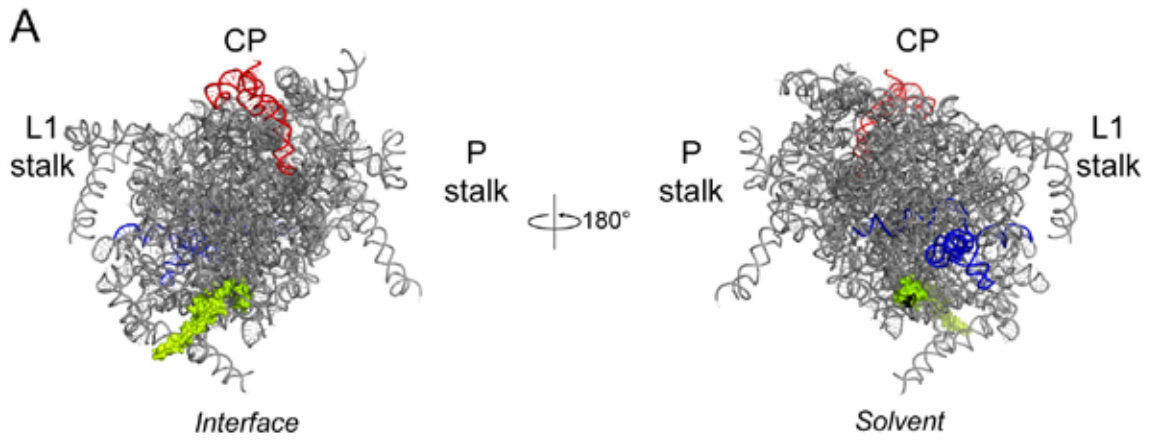
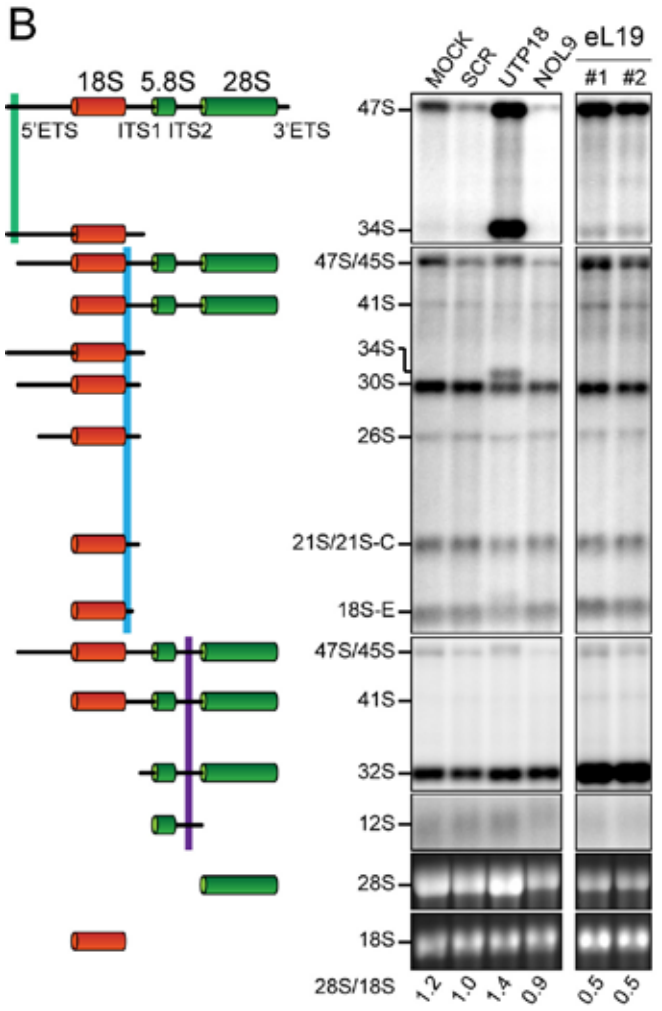
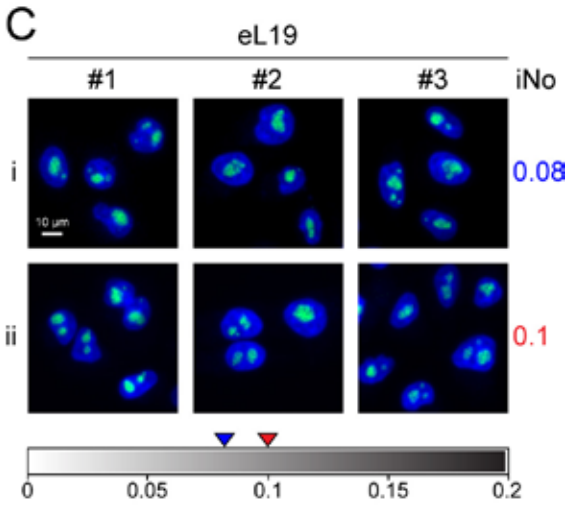
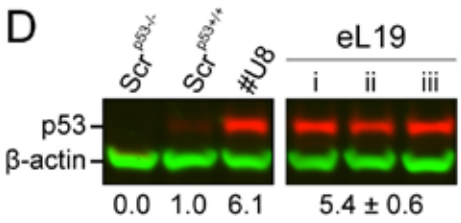
eL19 (RpL19)









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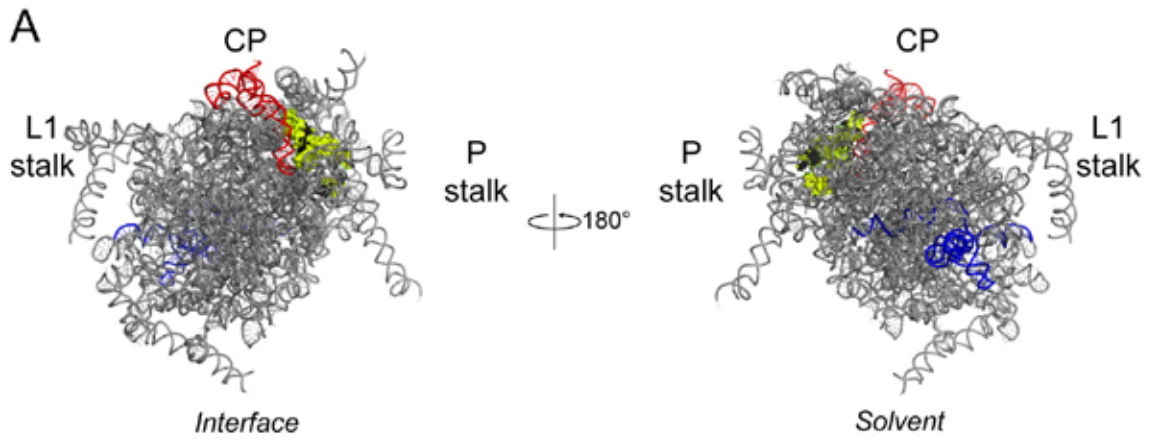
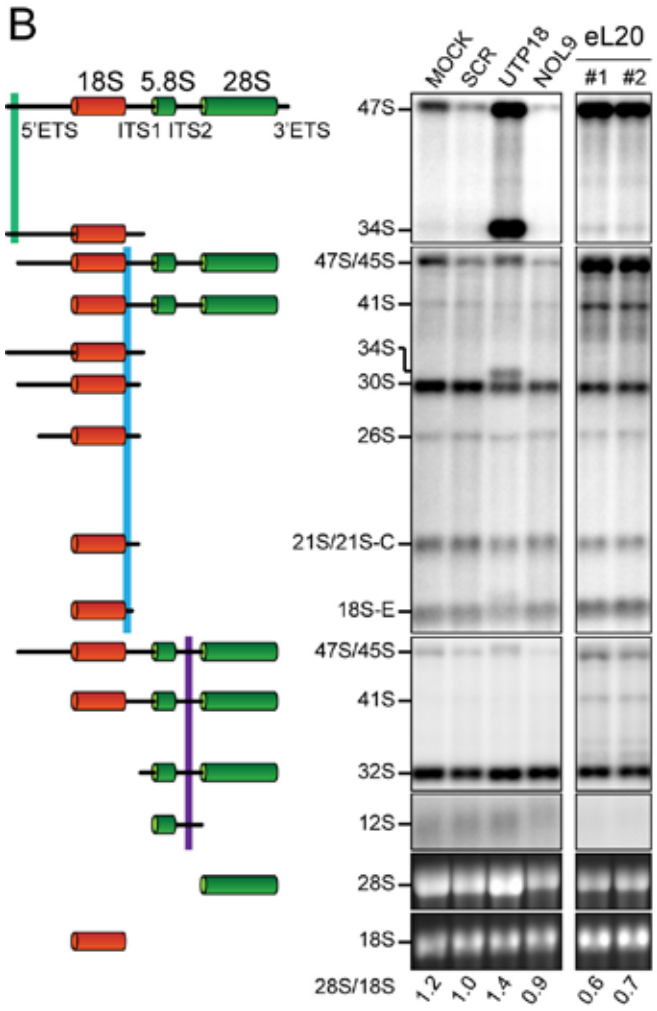
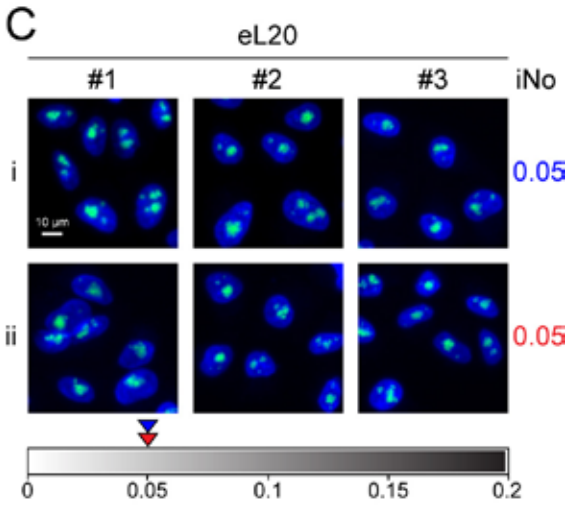
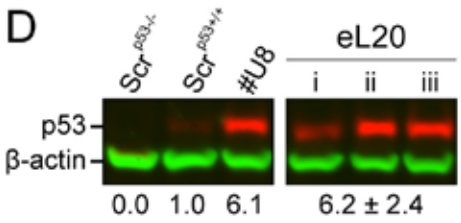
eL20 (RpL18a)









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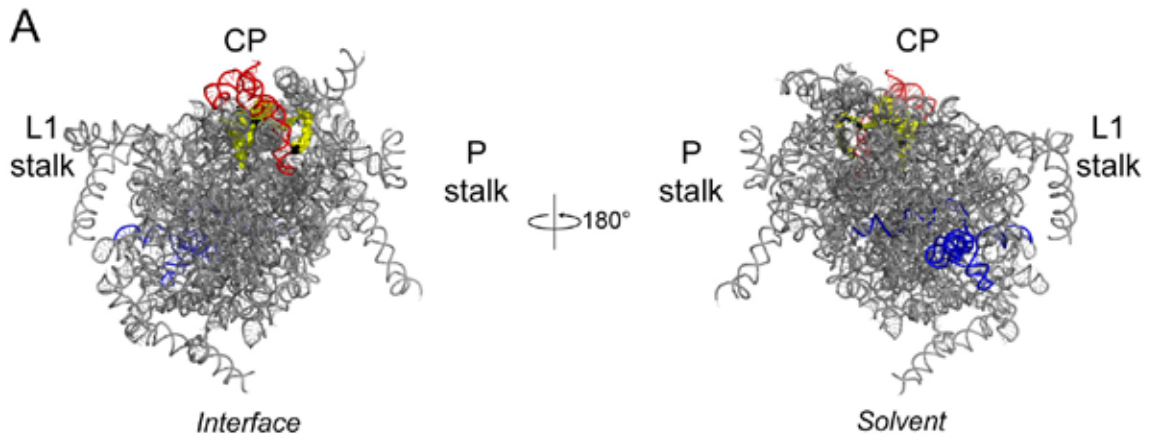
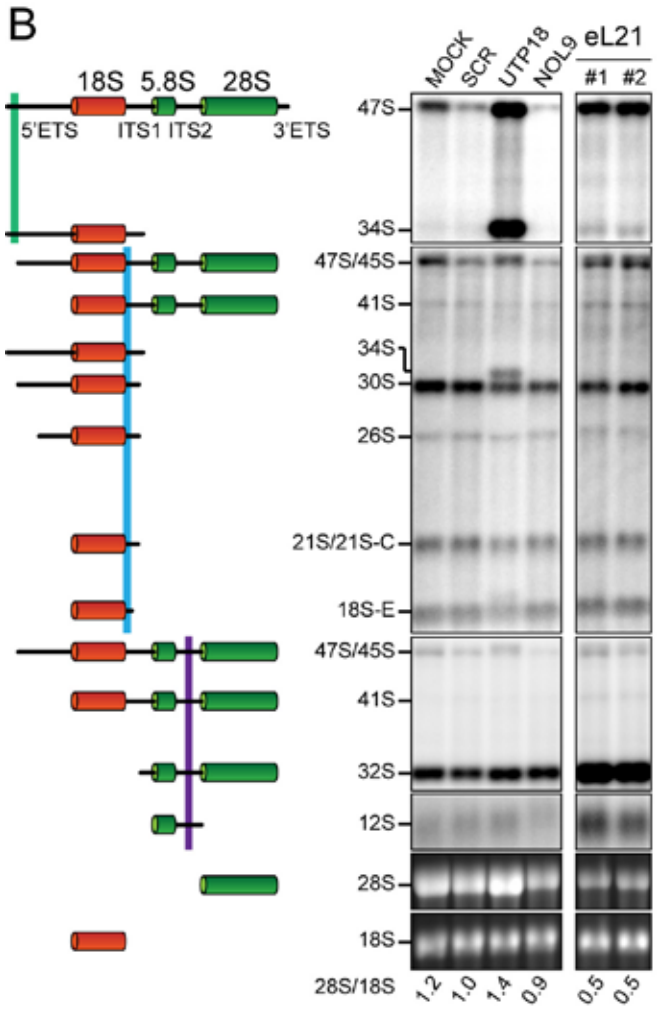
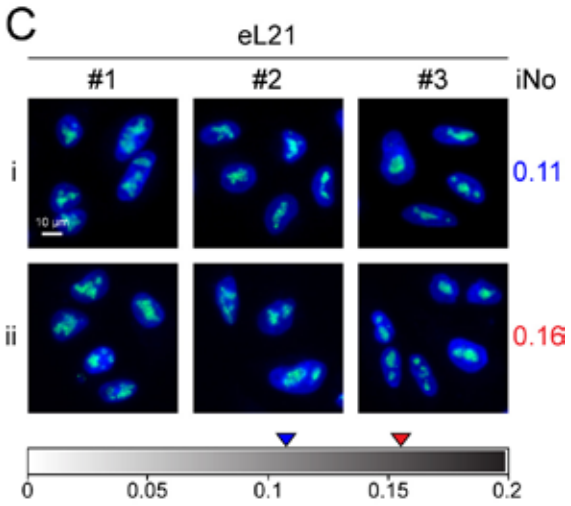
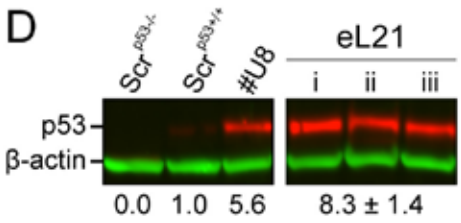
eL21 (RpL21)









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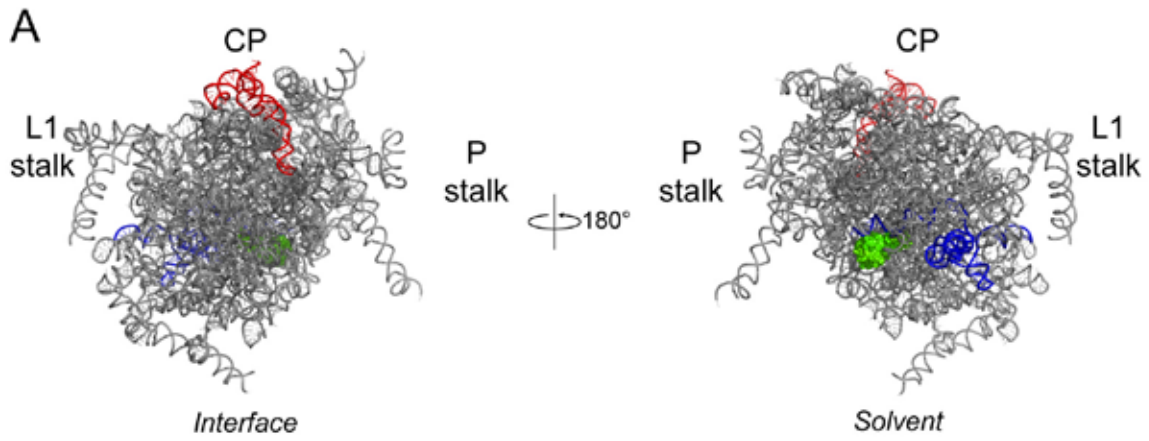
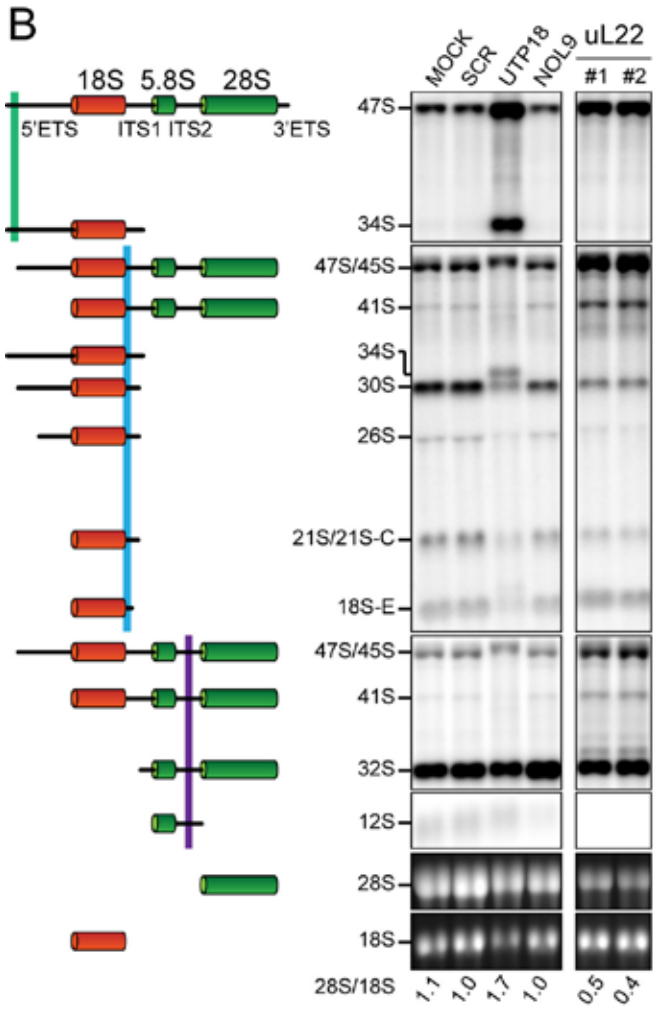
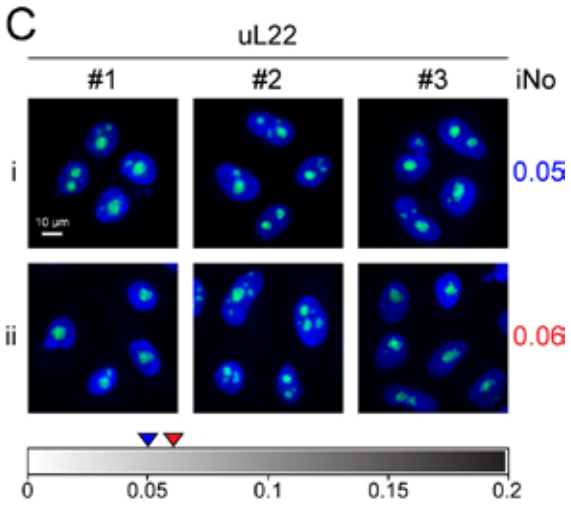
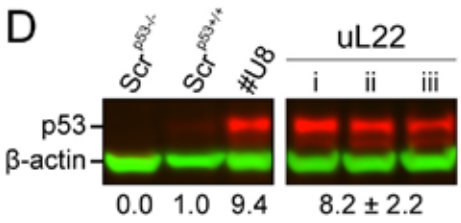
uL22 (RpL17)









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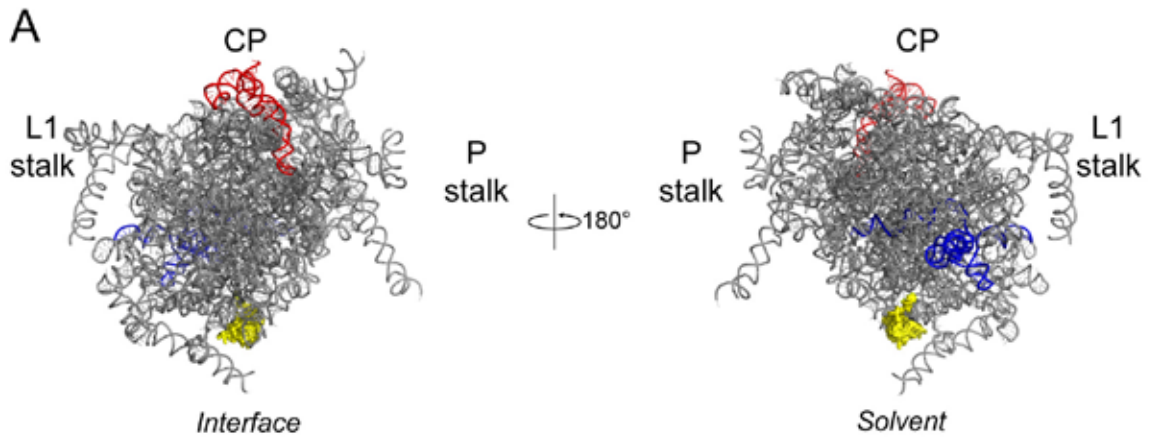
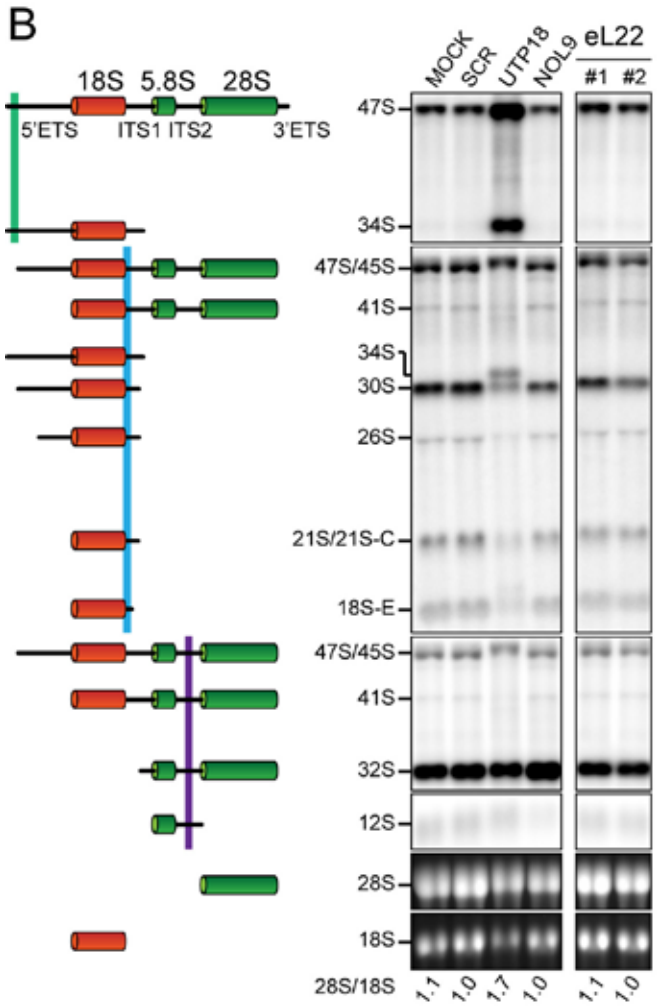
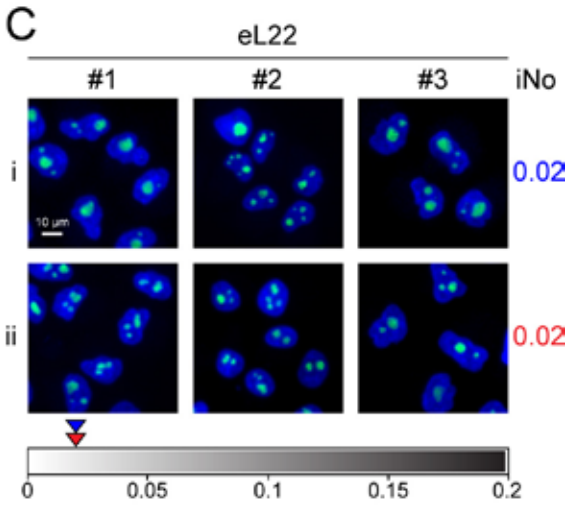
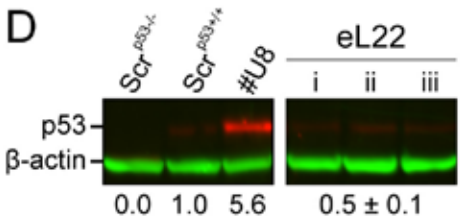
eL22 (RpL22)









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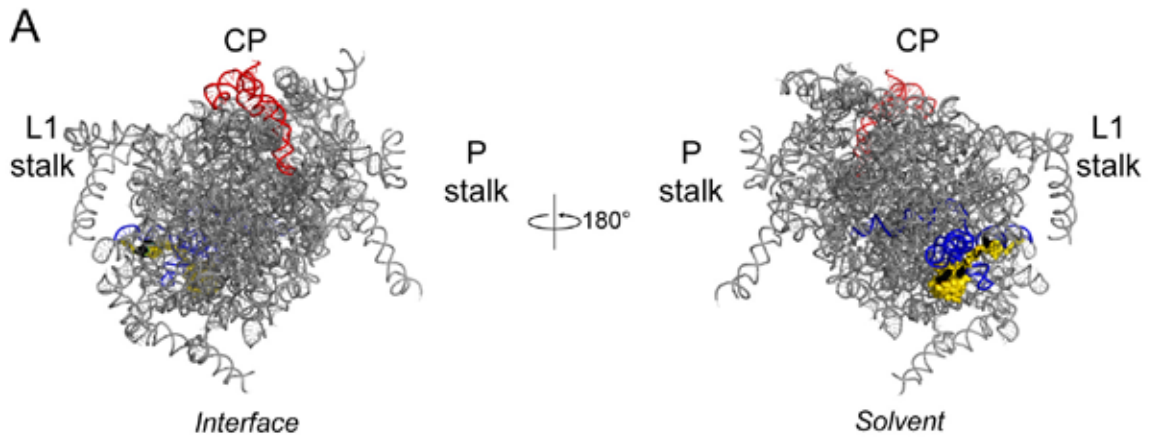
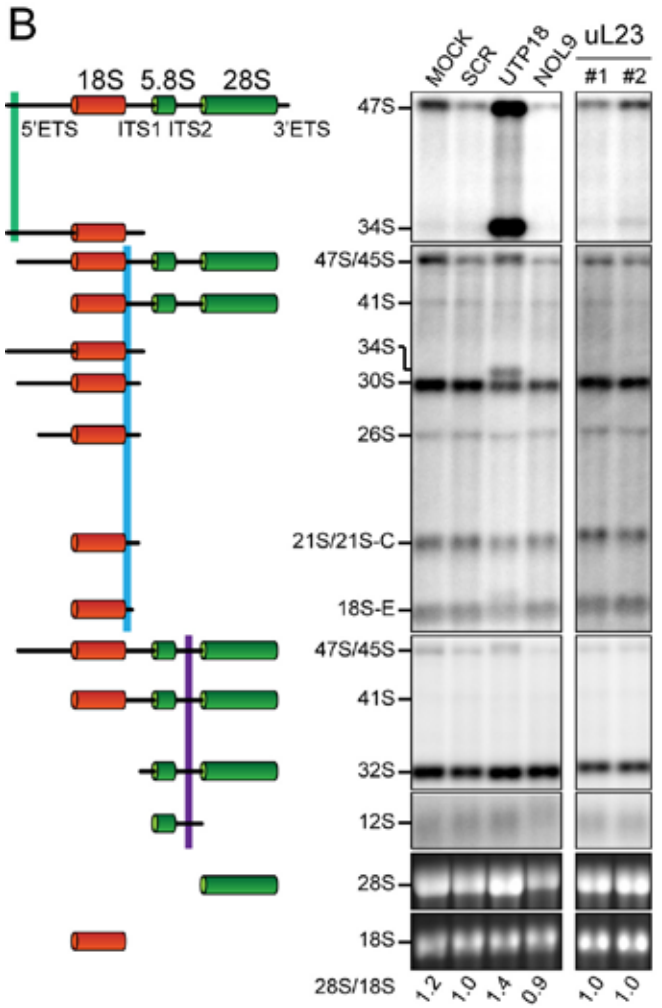
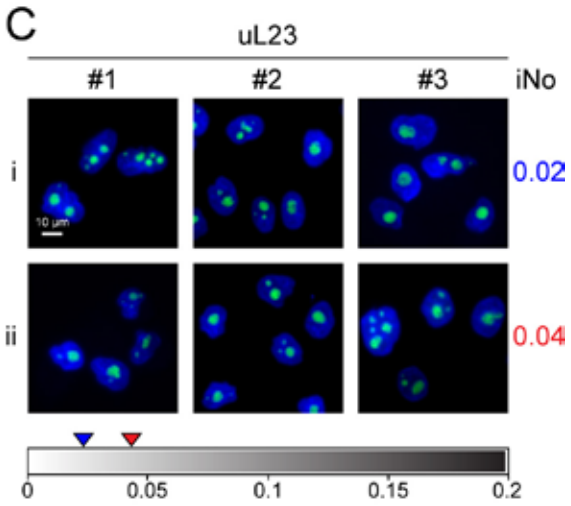
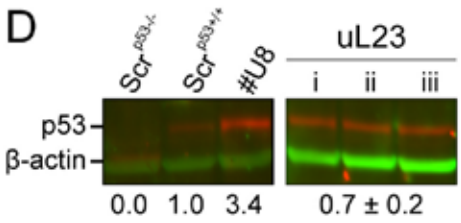
uL23 (RpL23a)









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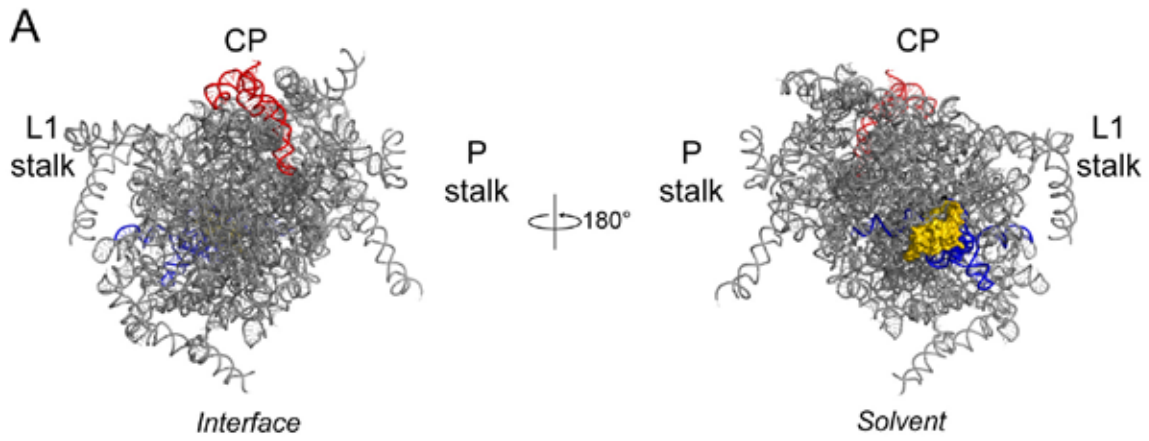
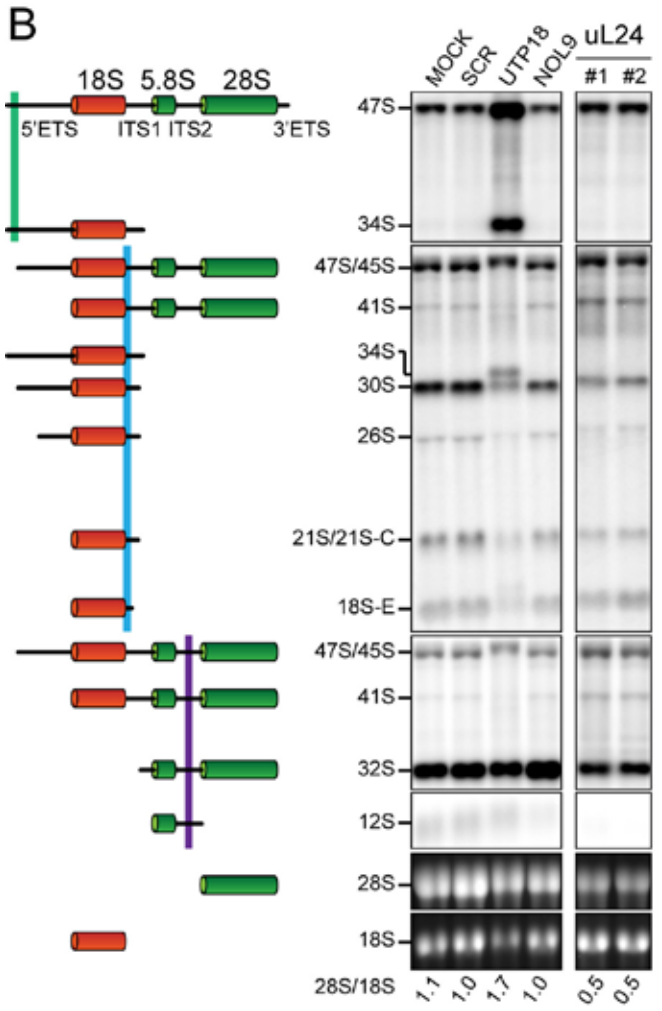
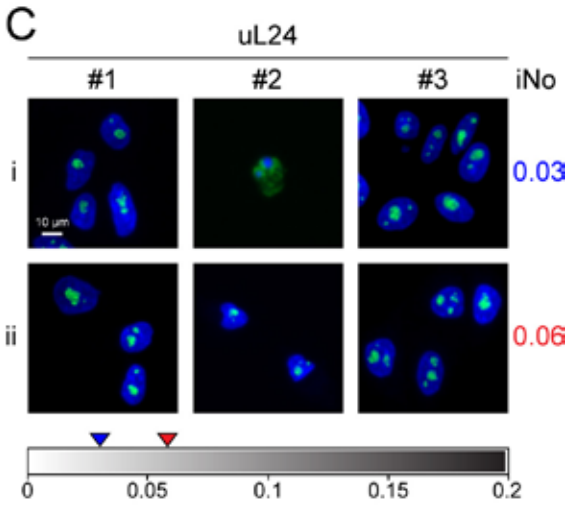
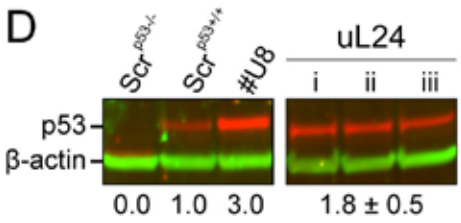
uL24 (RpL26)









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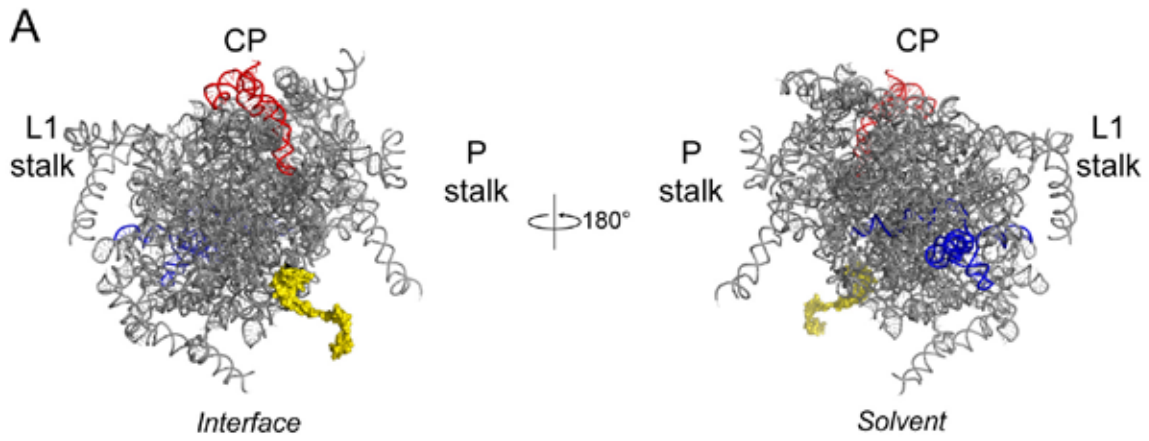
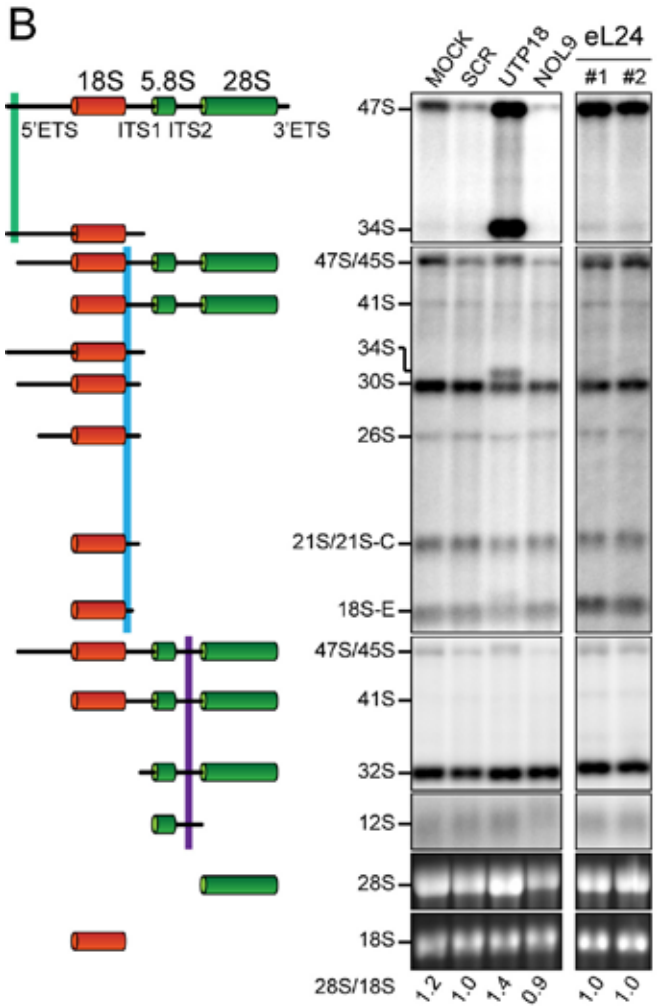
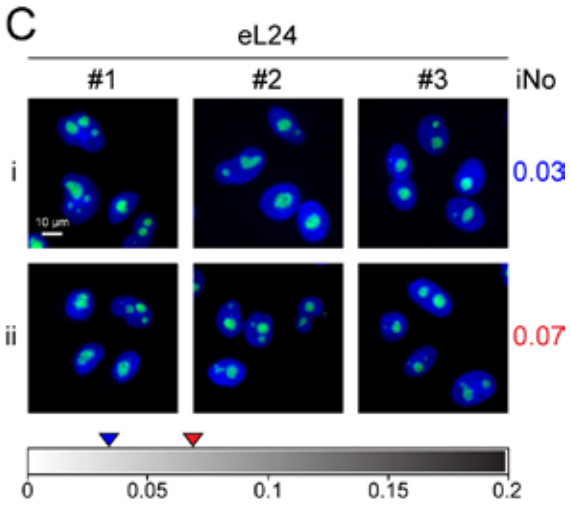
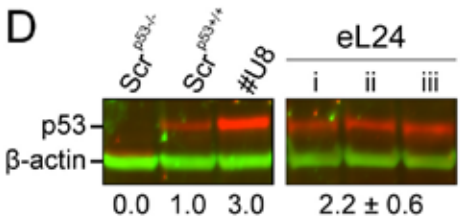
eL24 (RpL24)









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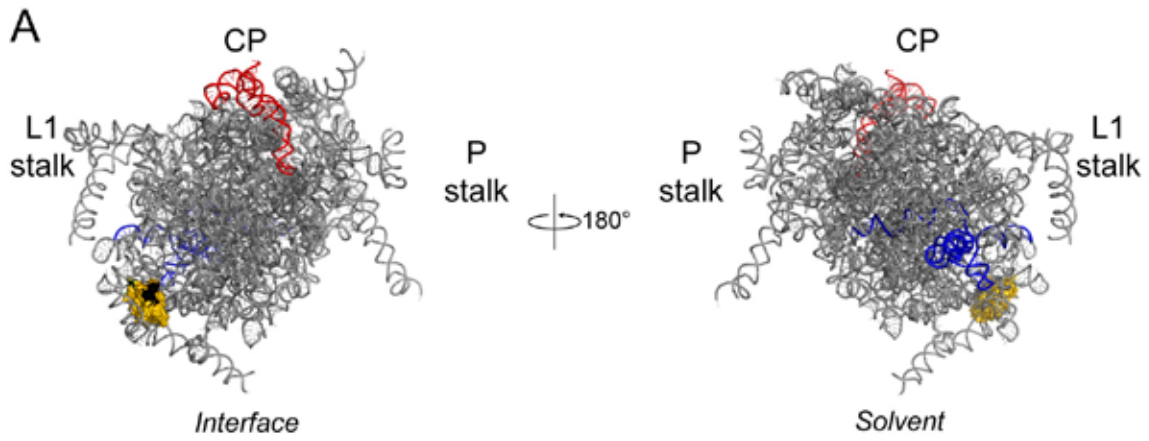
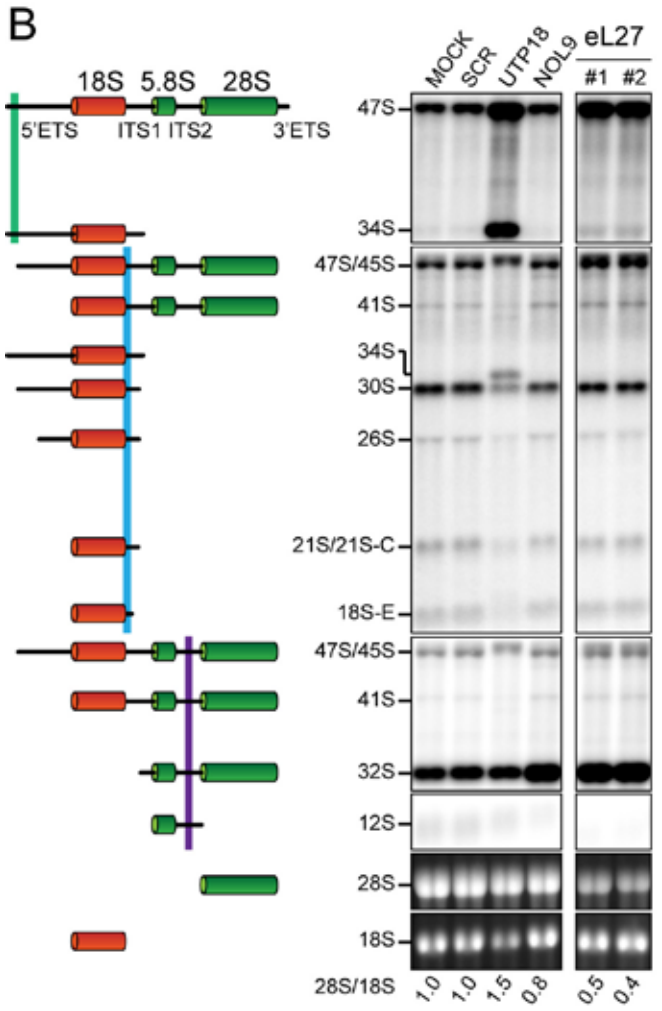
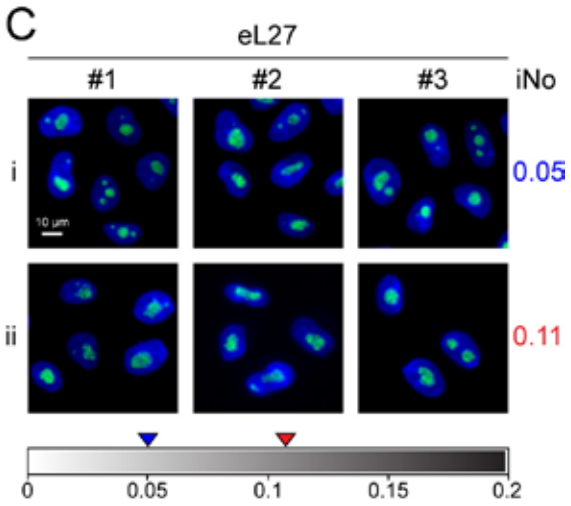
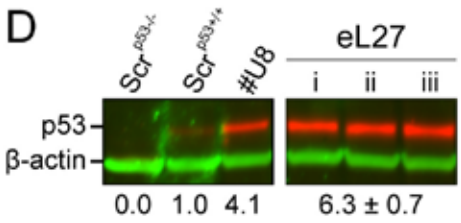
eL27 (RpL27)









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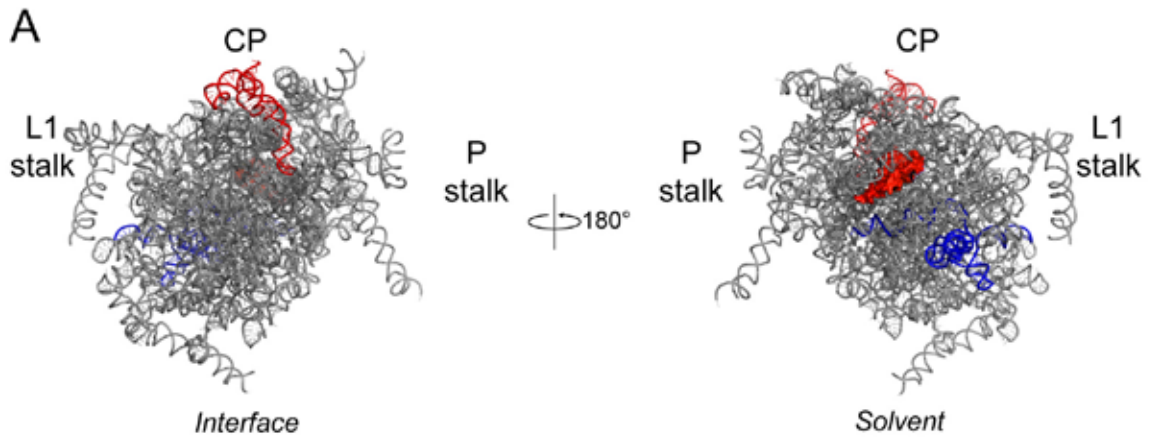
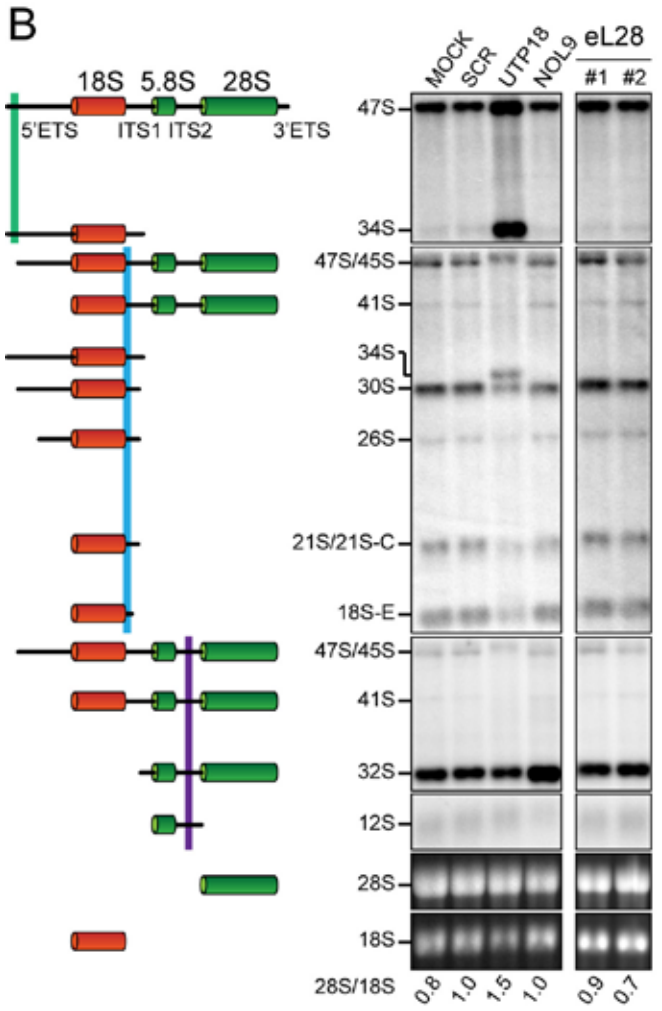
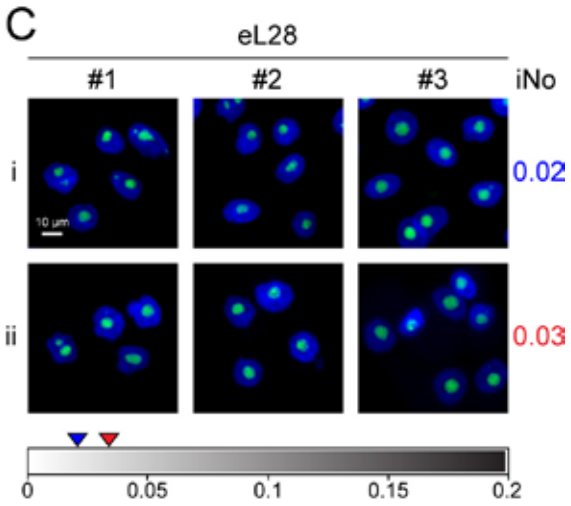
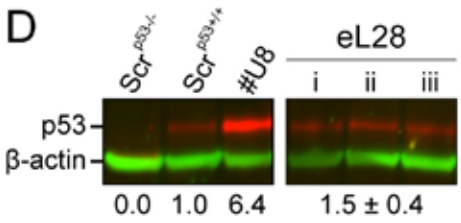
eL28 (RpL28)









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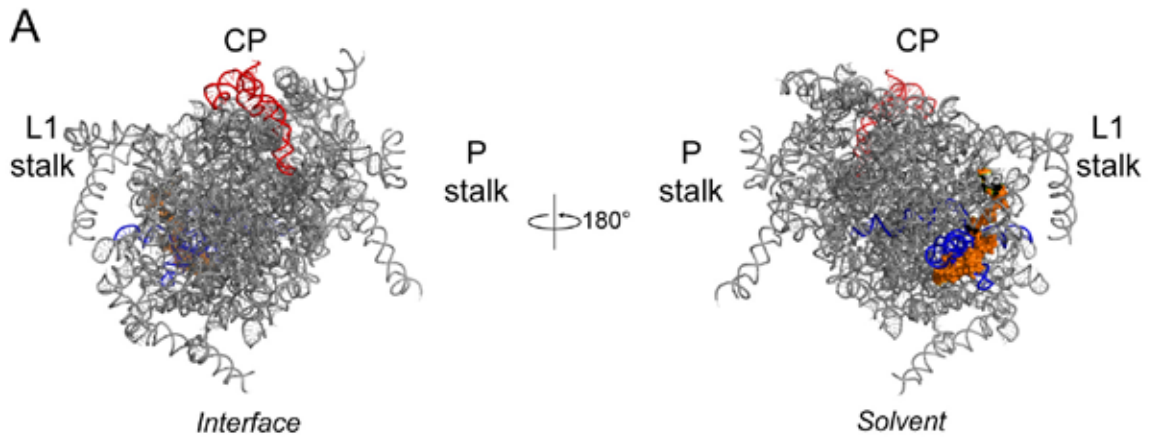
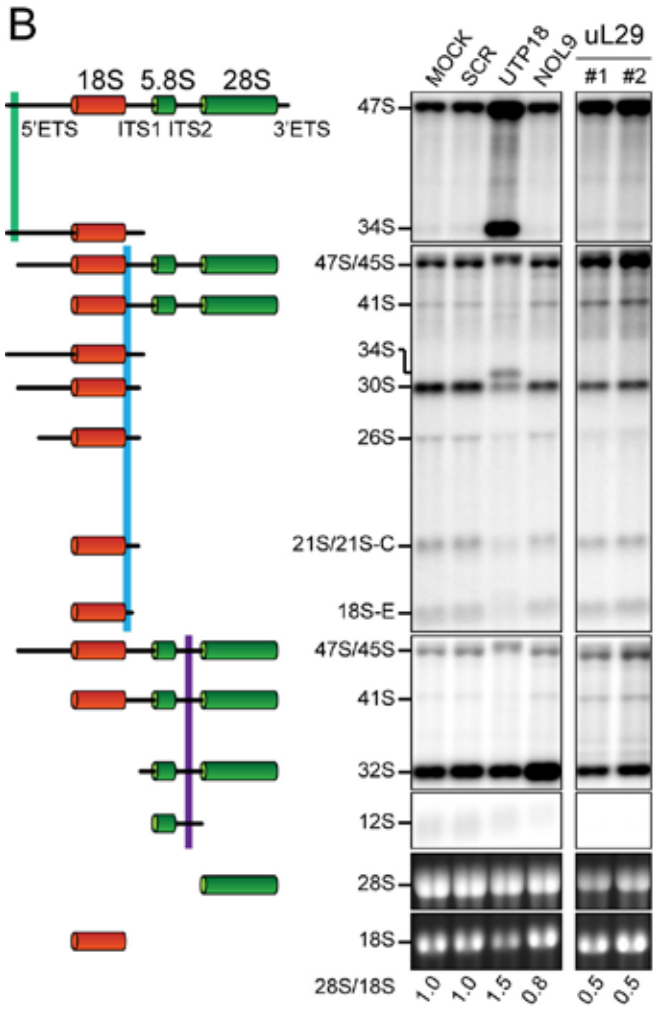
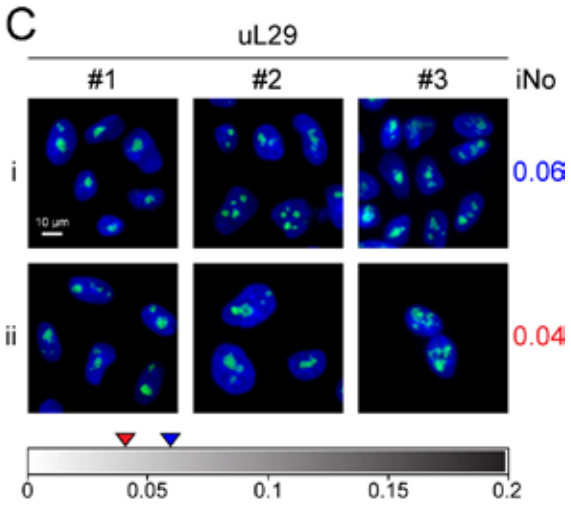
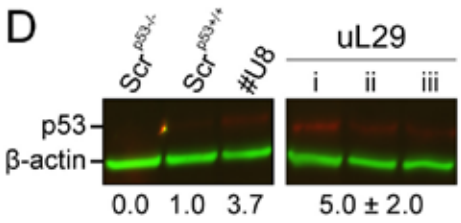
uL29 (RpL35)









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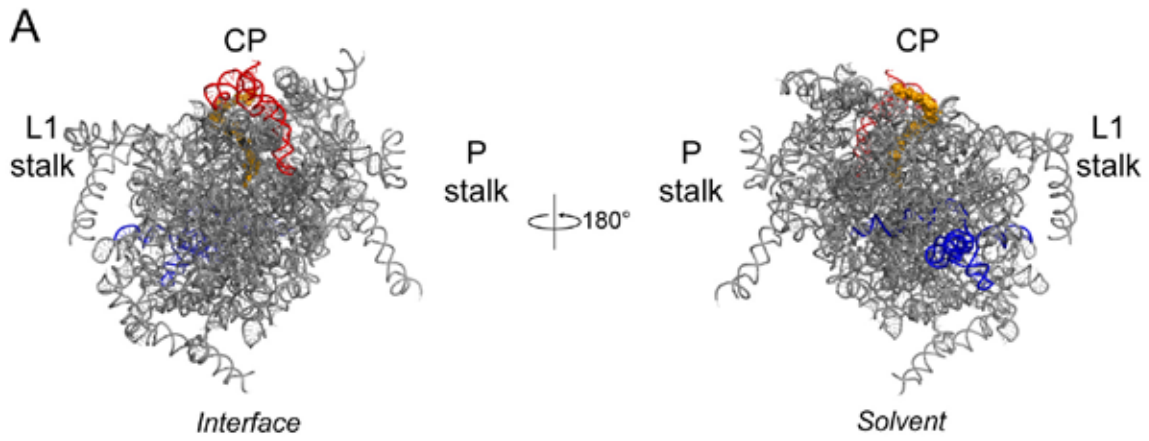
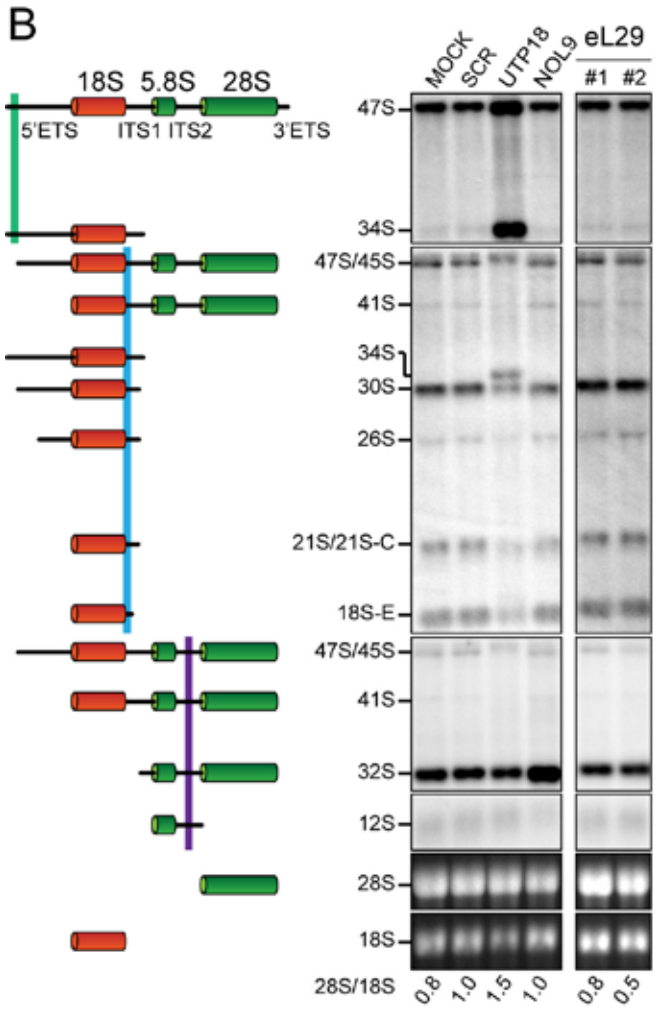
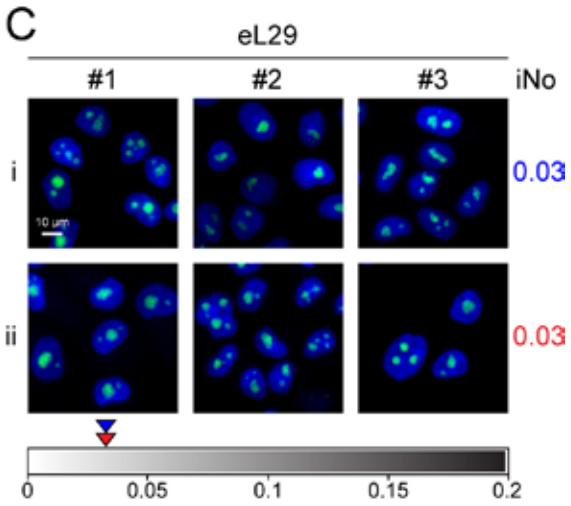
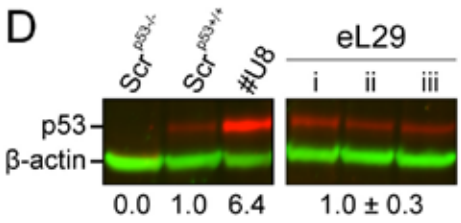
eL29 (RpL29)









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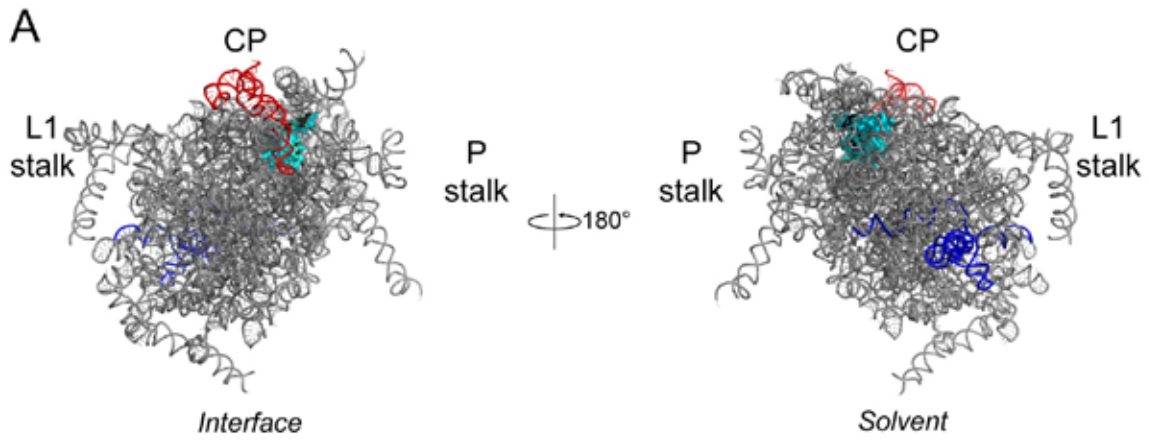
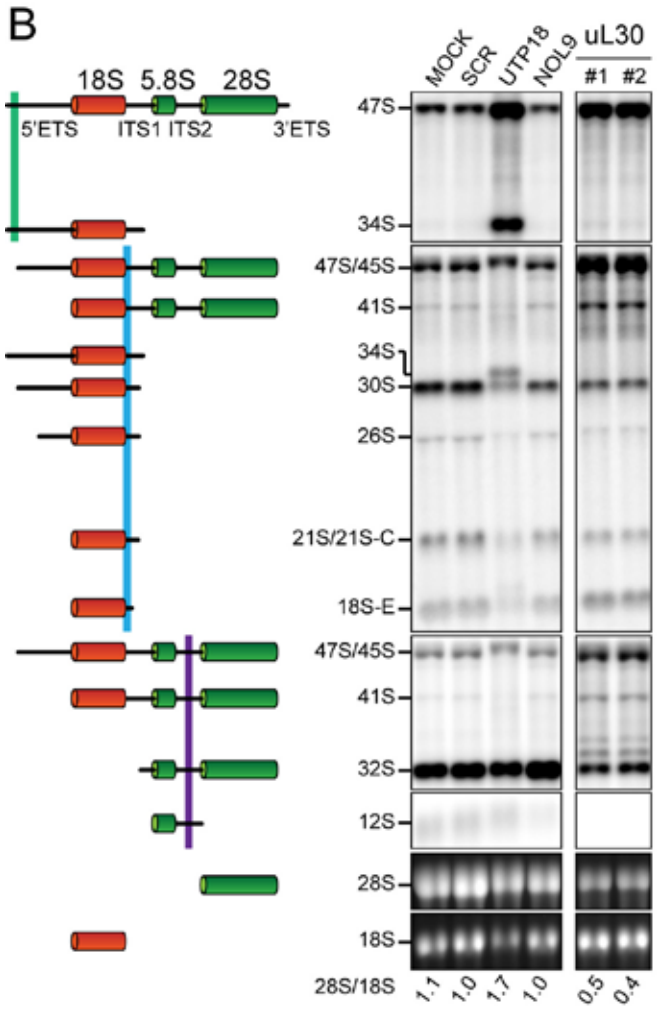
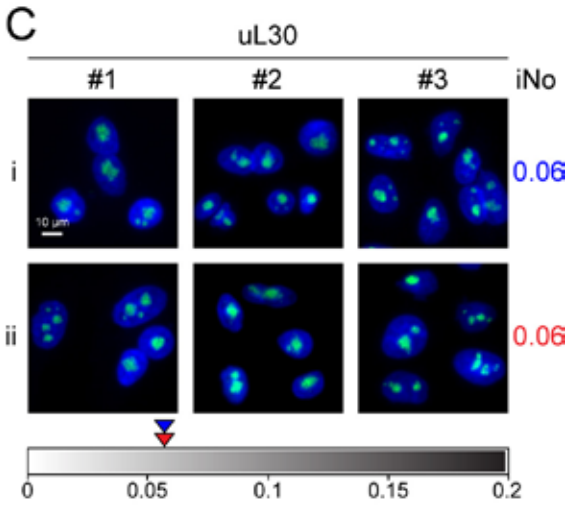
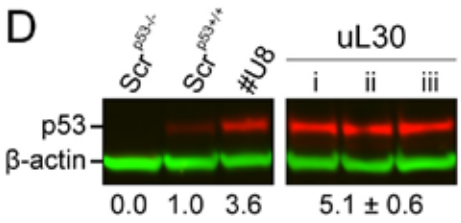
uL30 (RpL7)









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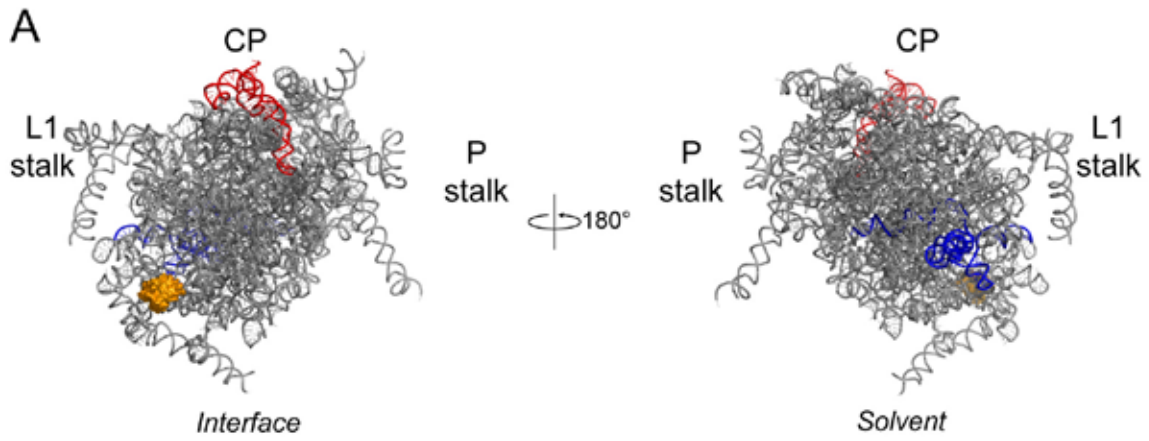
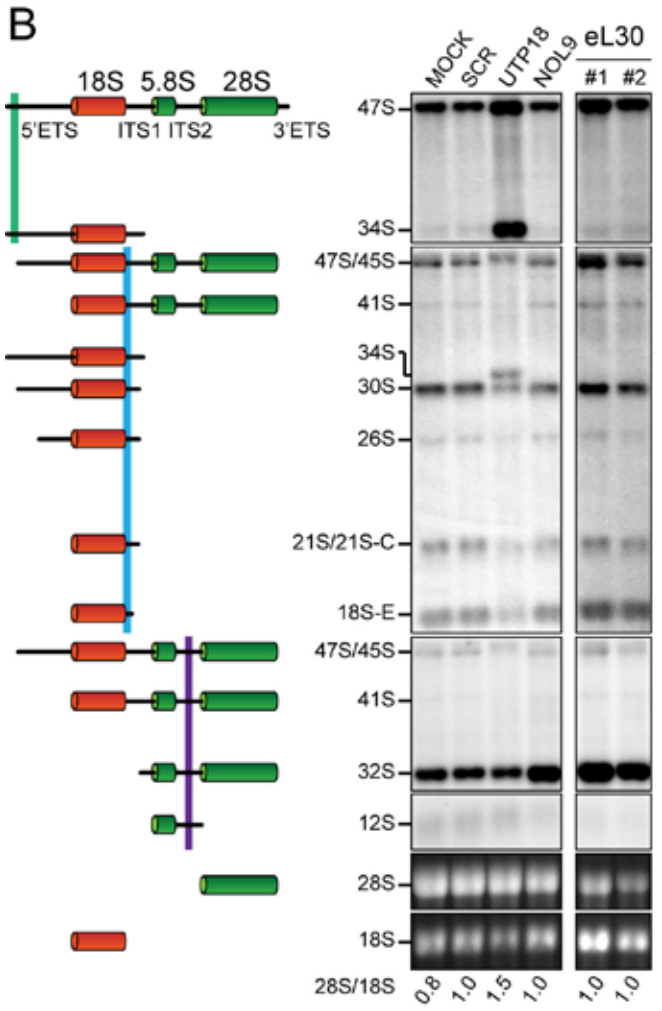
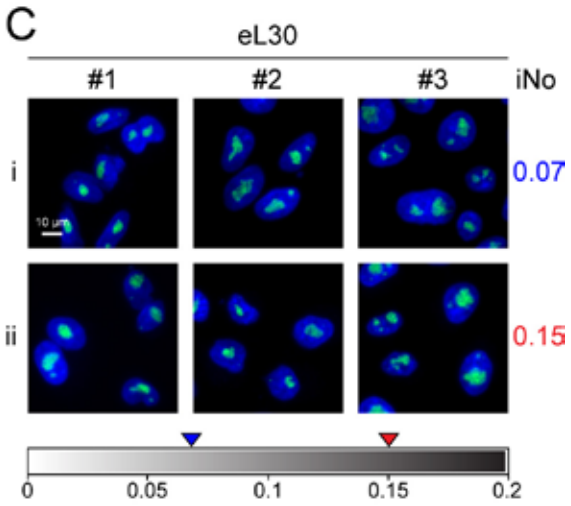
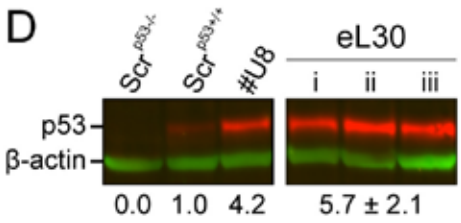
eL30 (RpL30)









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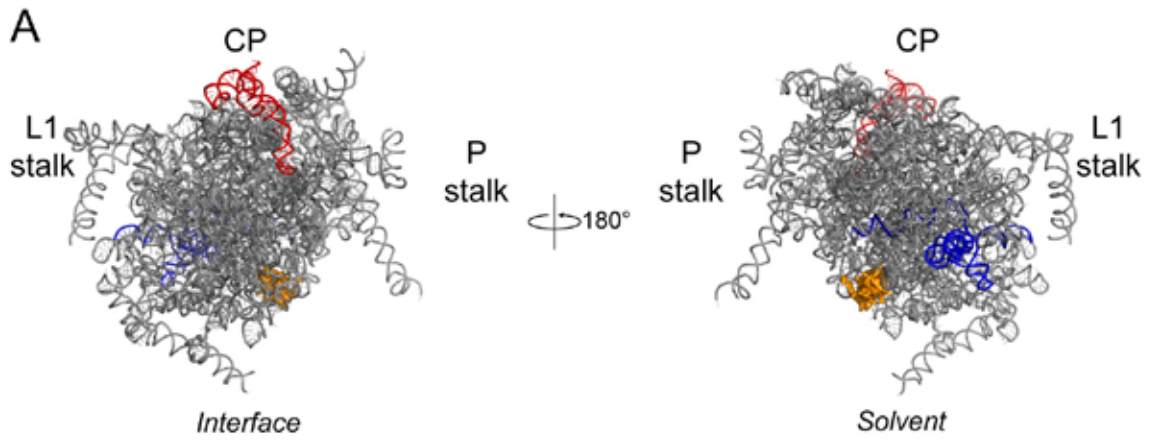
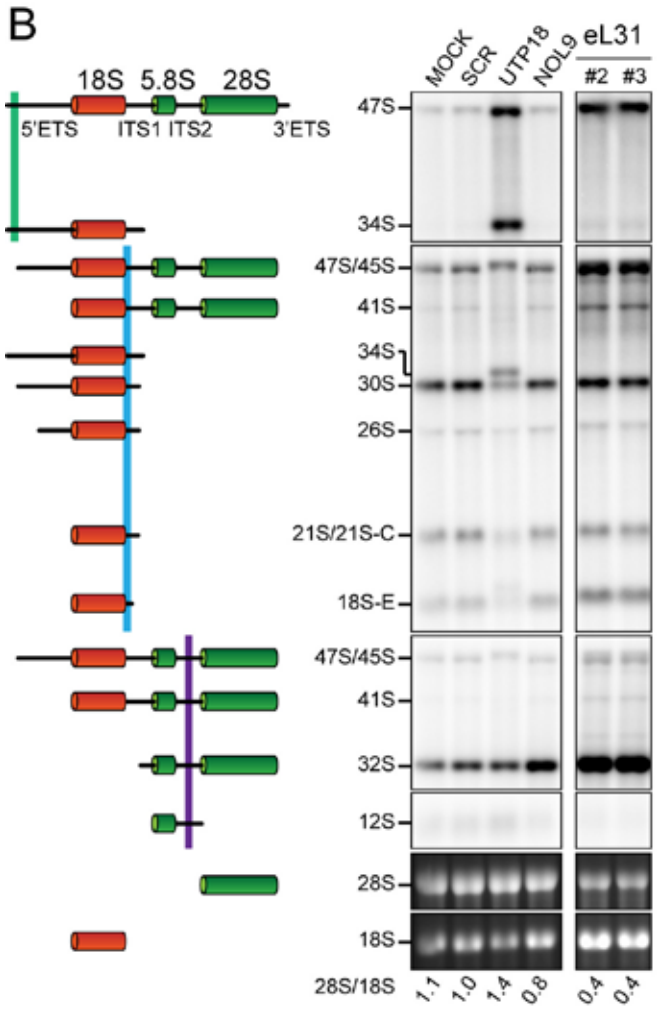
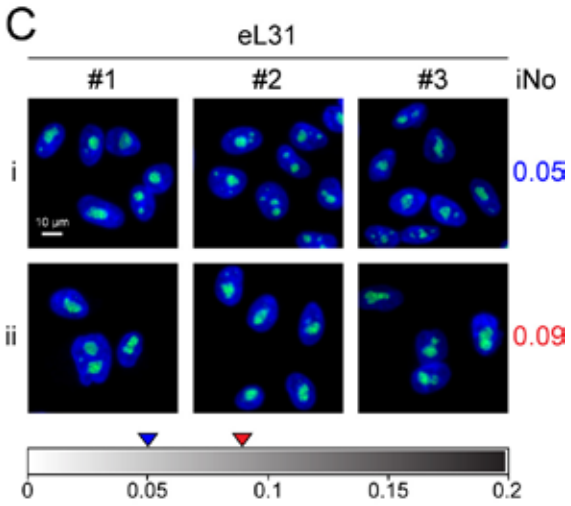
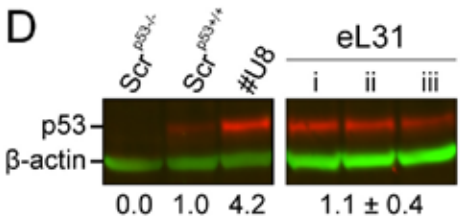
eL31 (RpL31)









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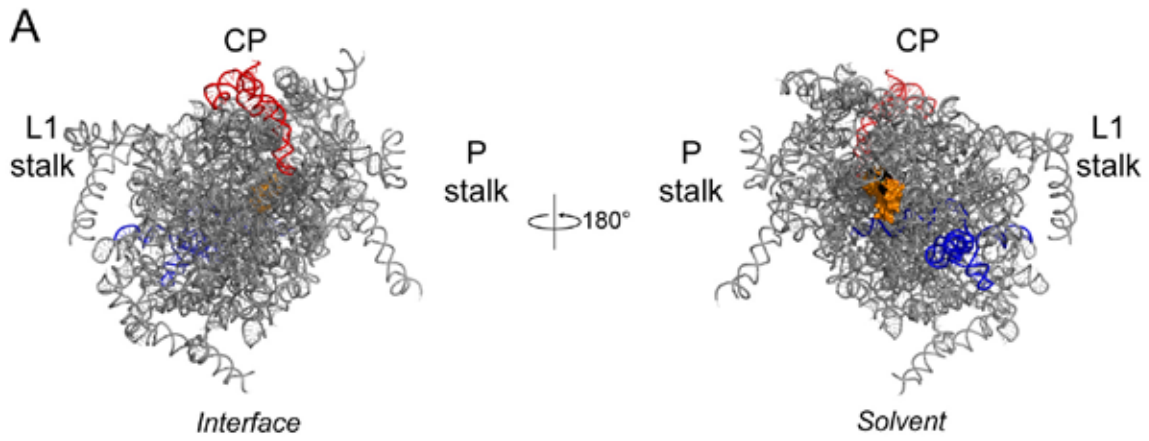
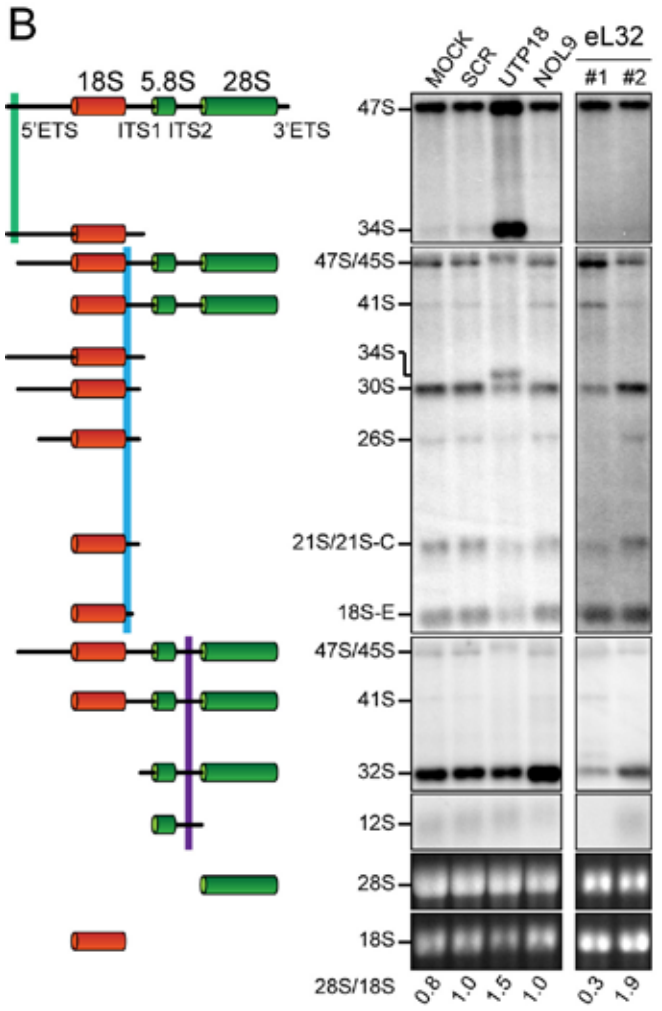
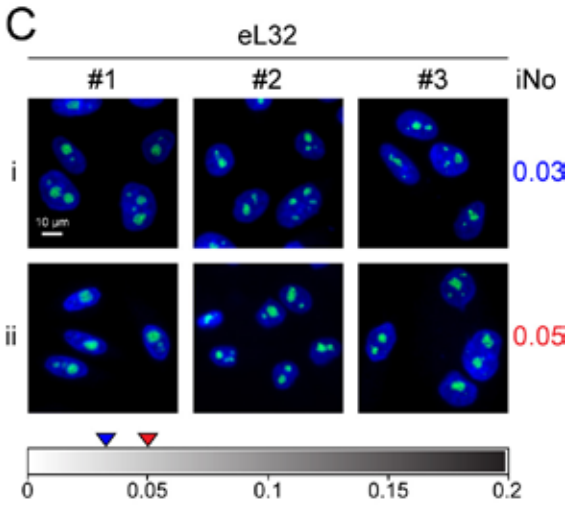
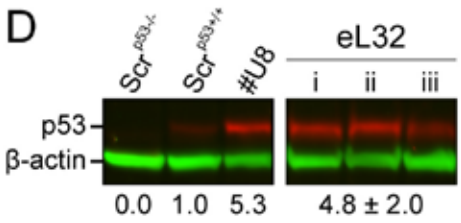
eL32 (RpL32)









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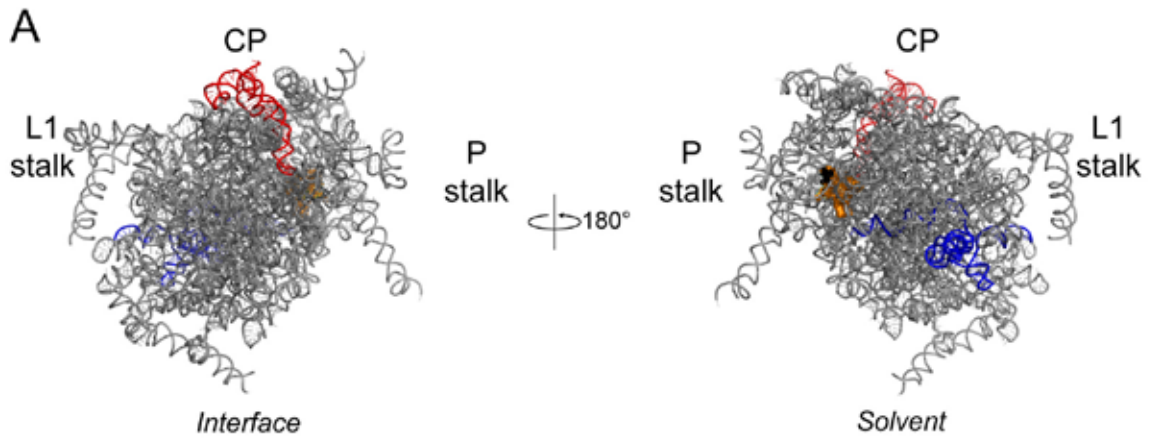
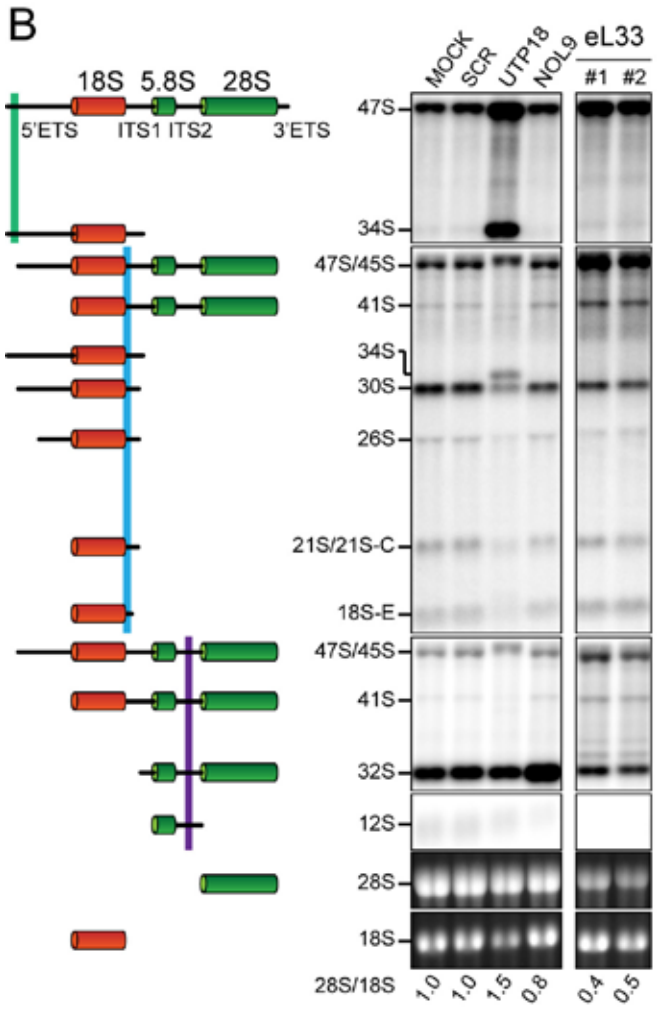
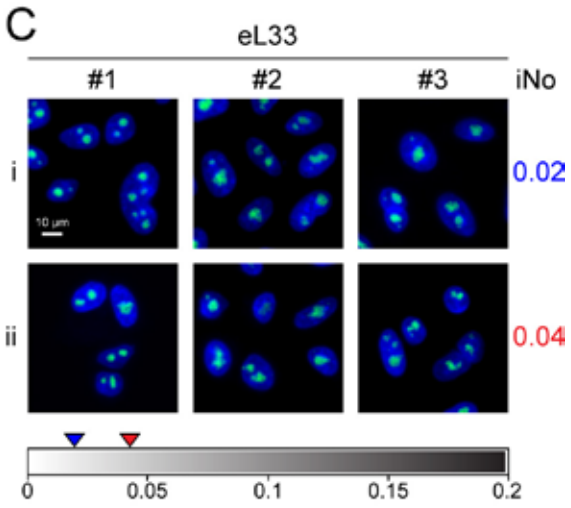
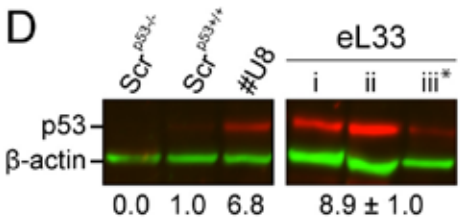
eL33 (RpL35a)









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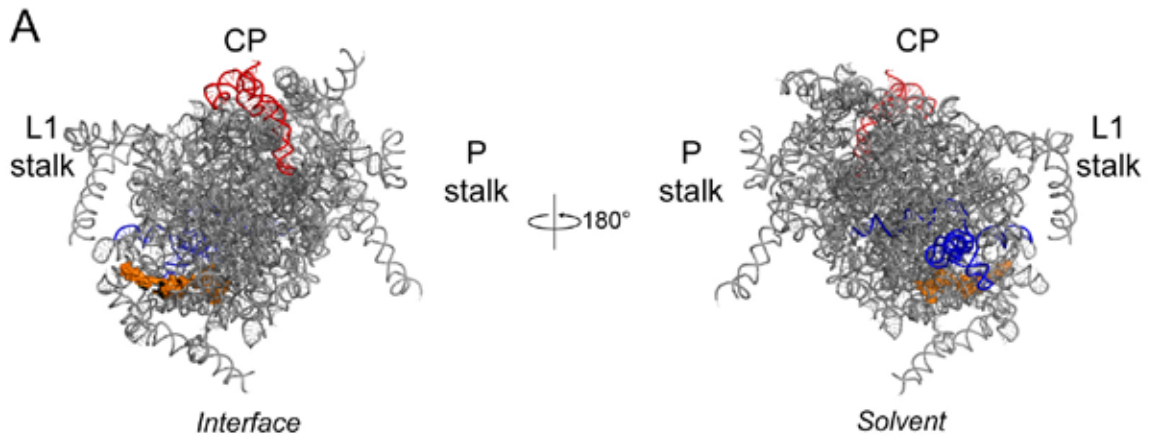
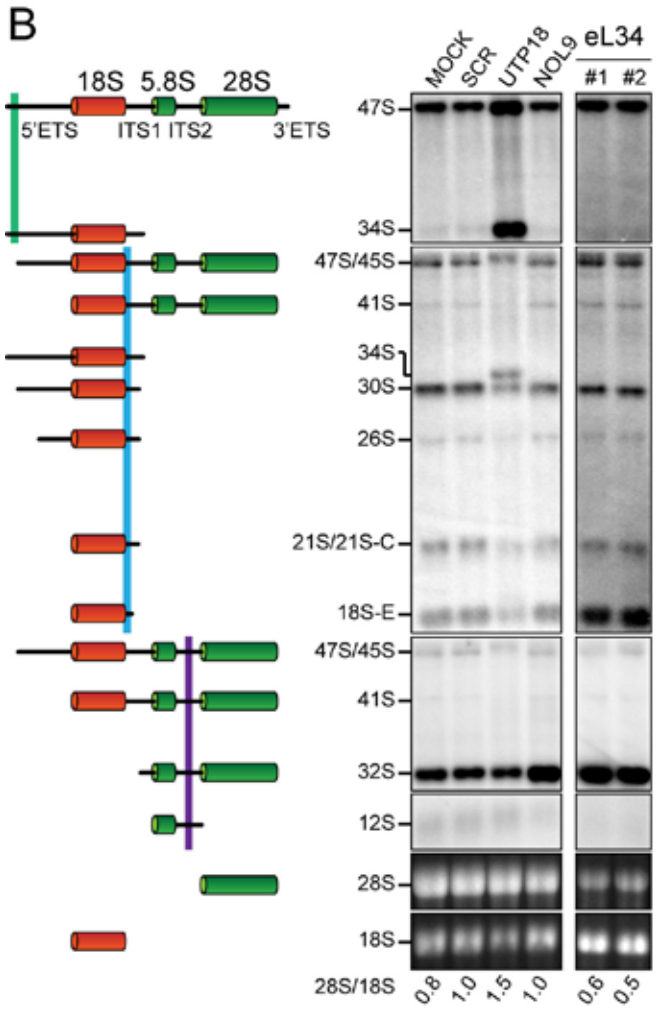
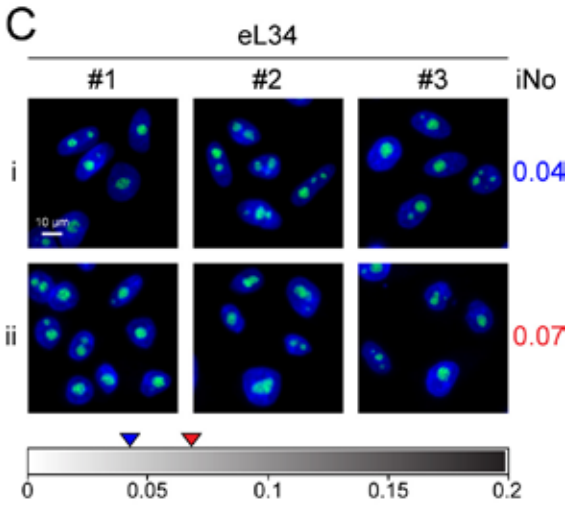
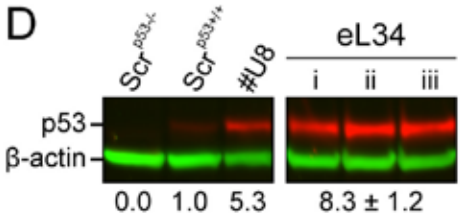
eL34 (RpL34)









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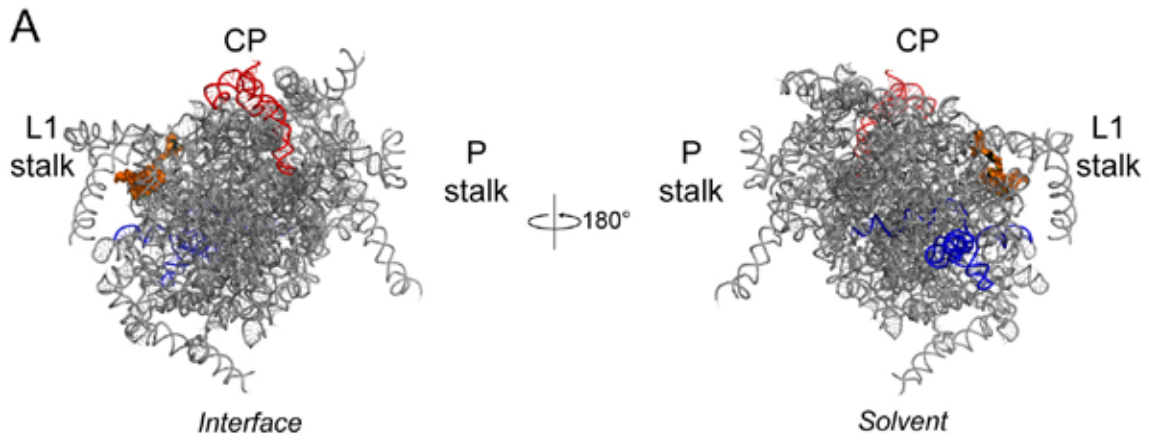
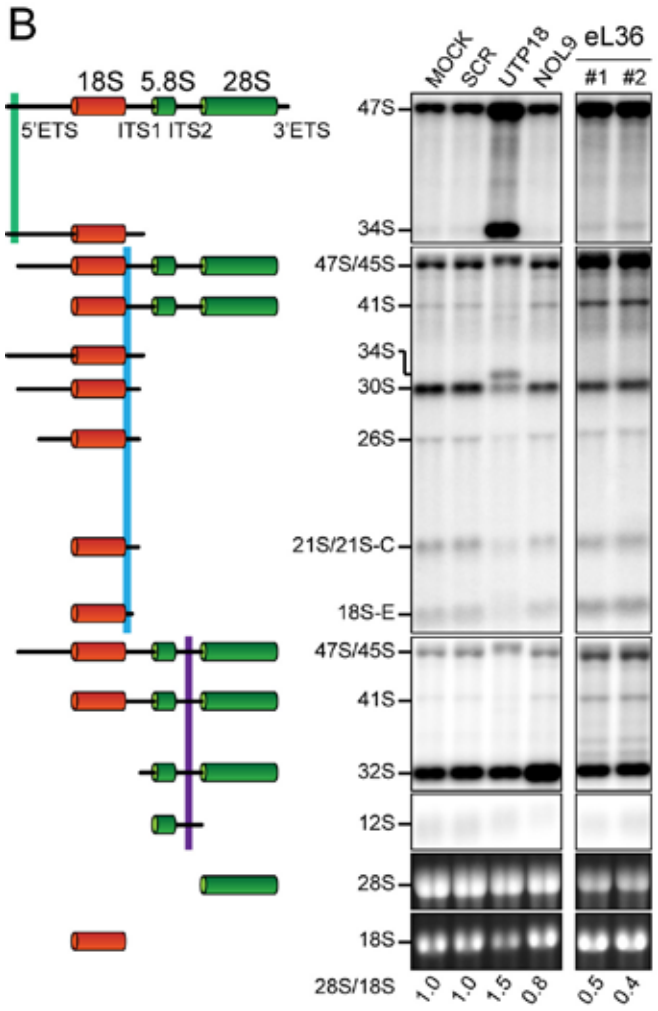
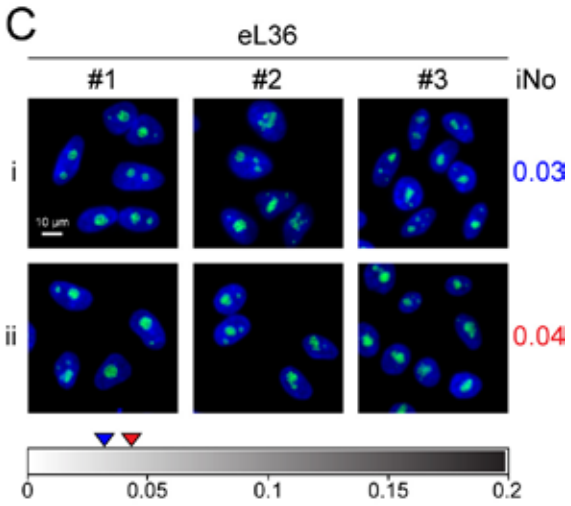
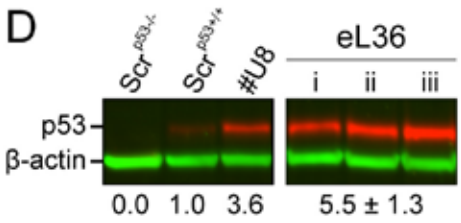
eL36 (RpL36)









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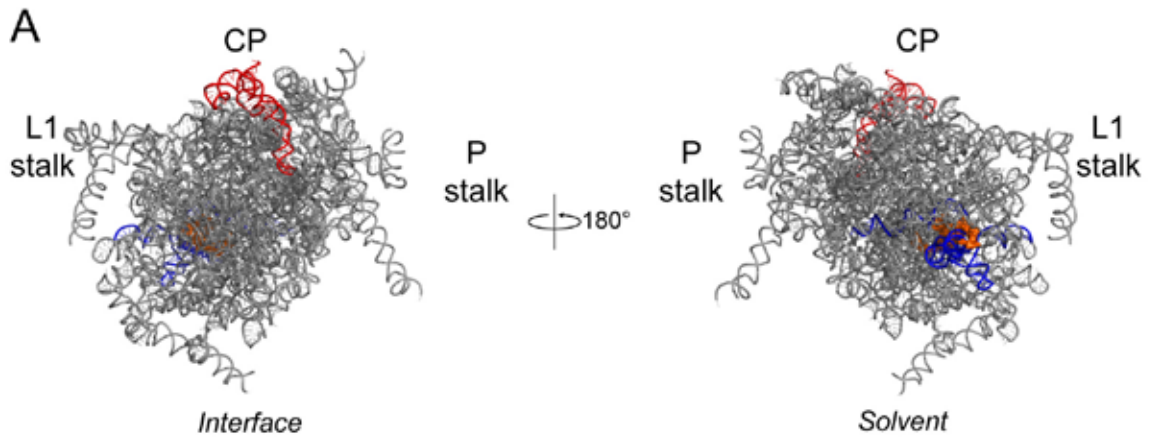
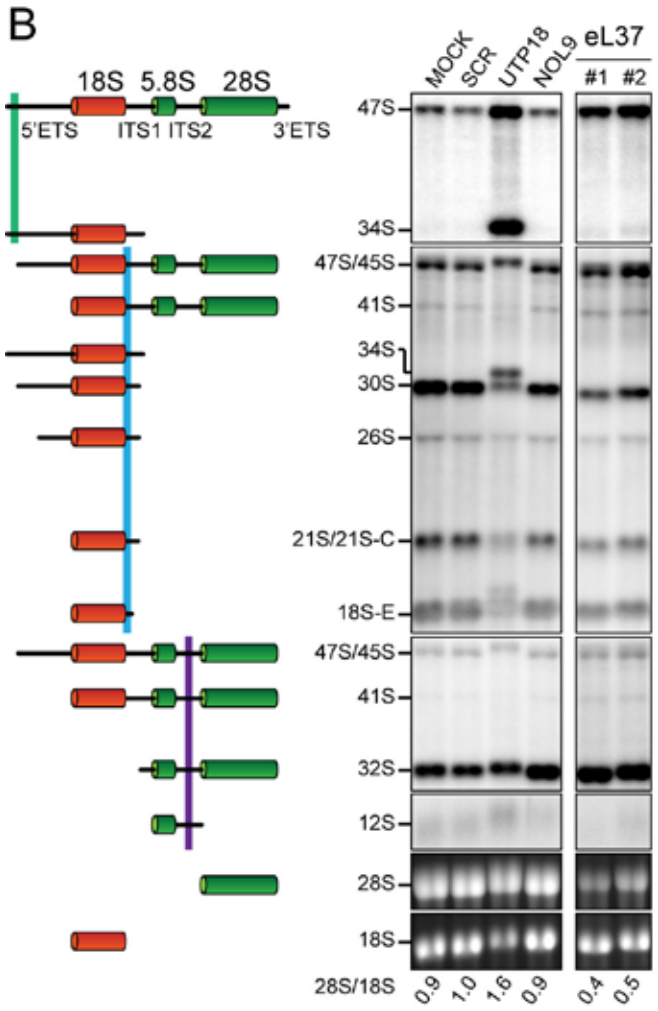
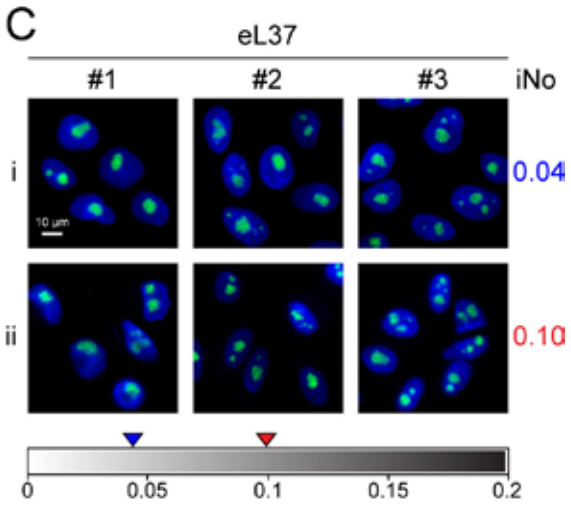
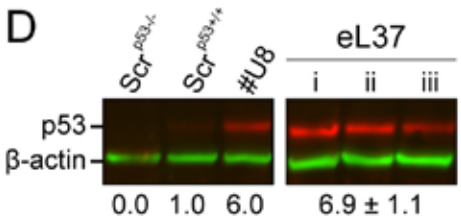
eL37 (RpL37)









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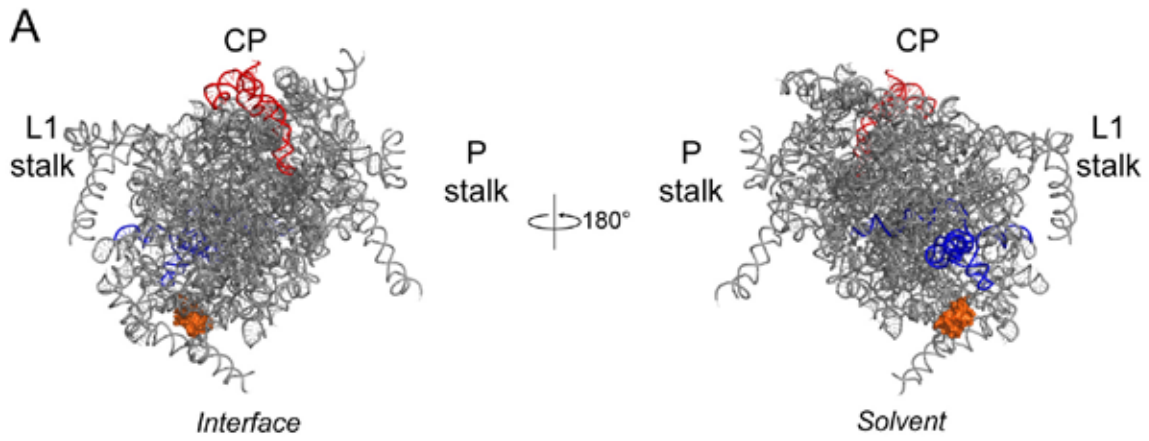
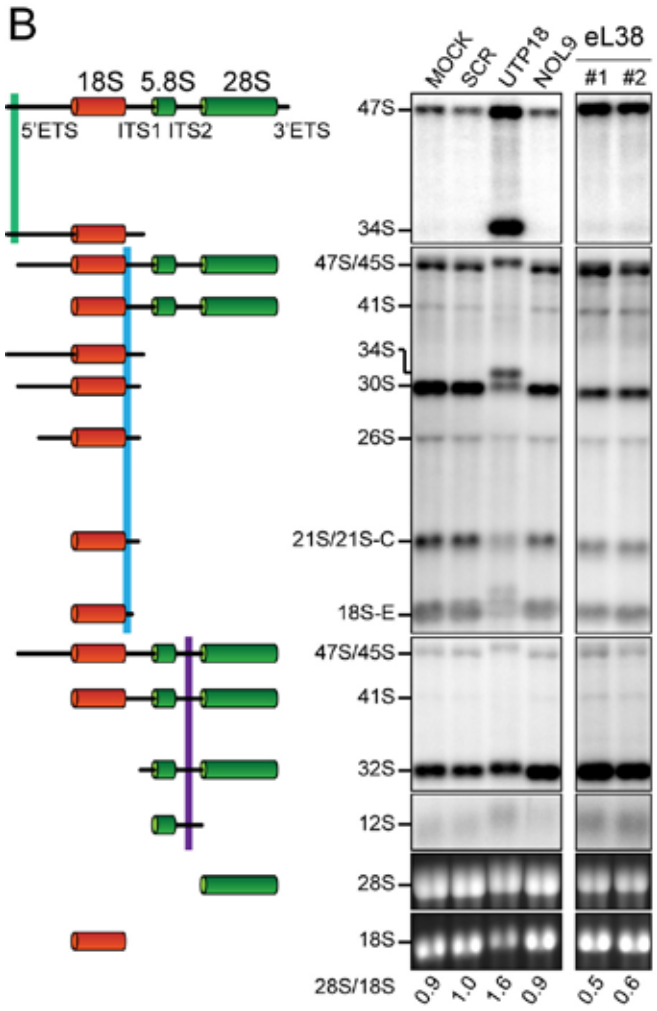
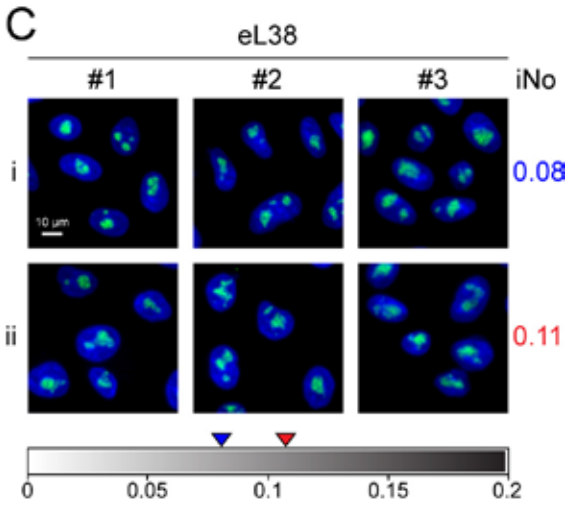
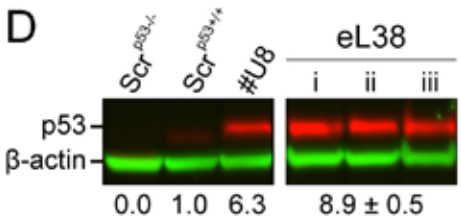
eL38 (RpL38)









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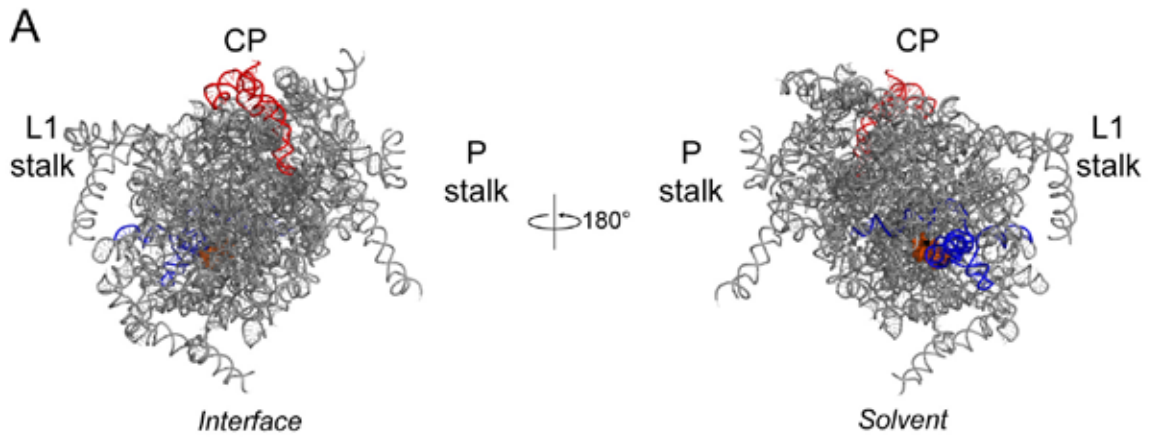
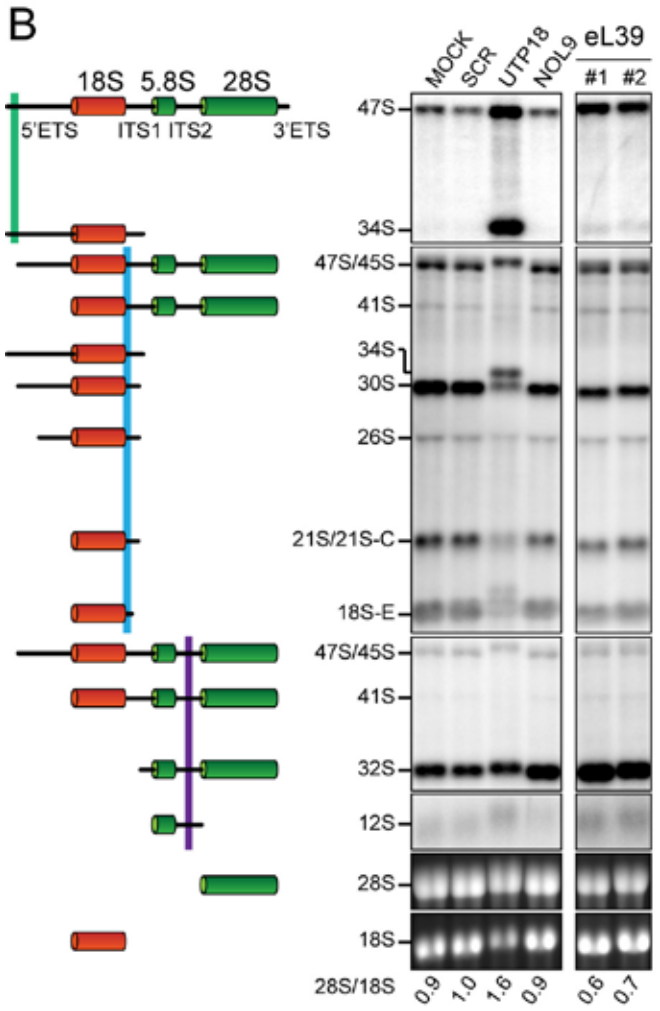
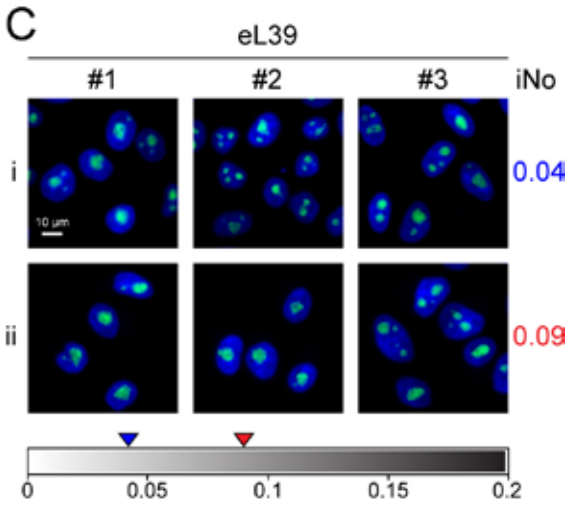
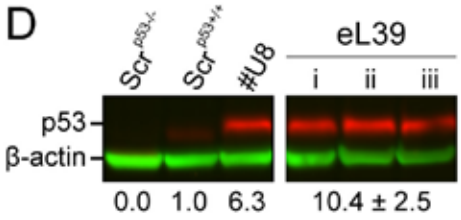
eL39 (RpL39)









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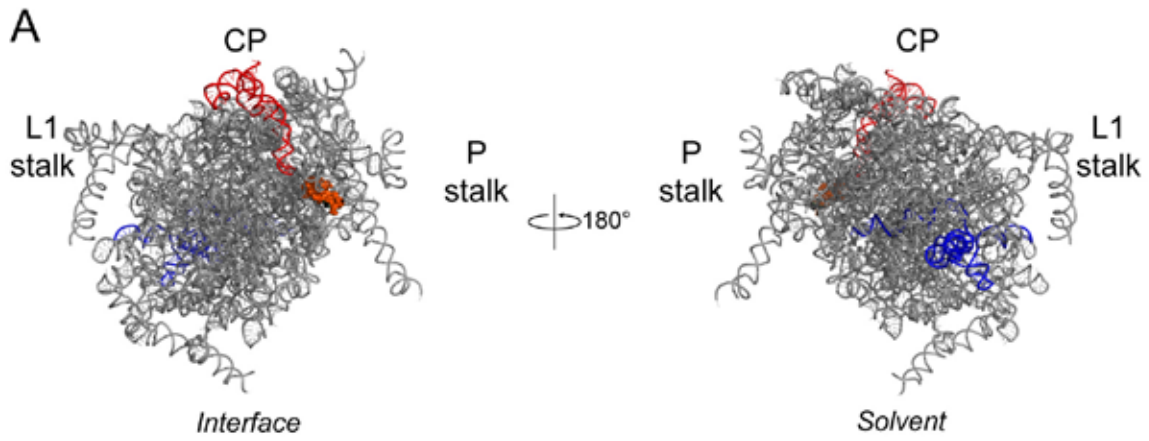
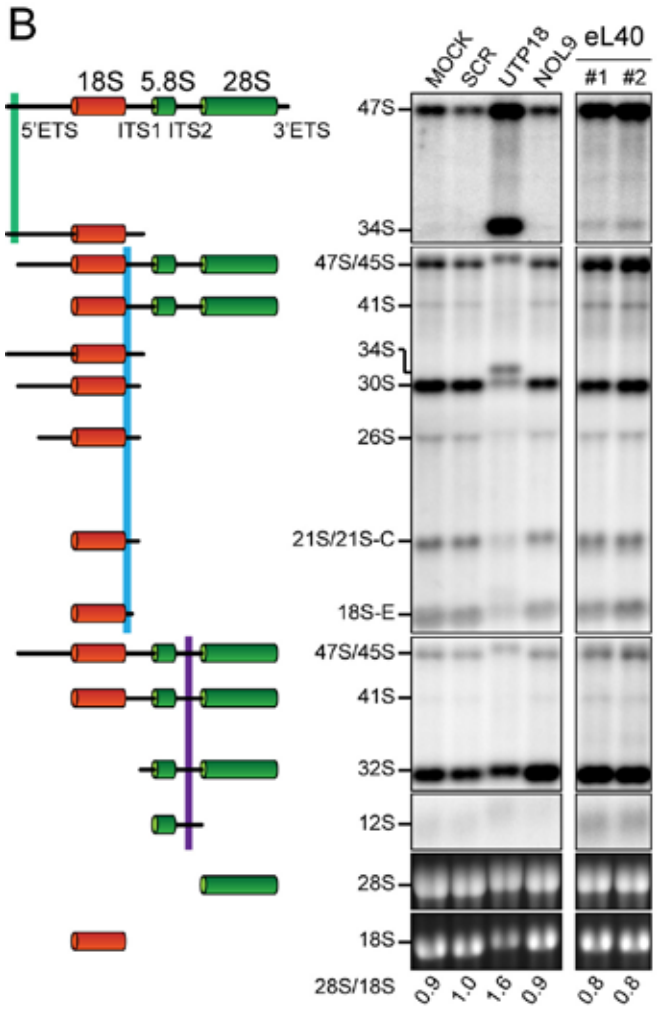
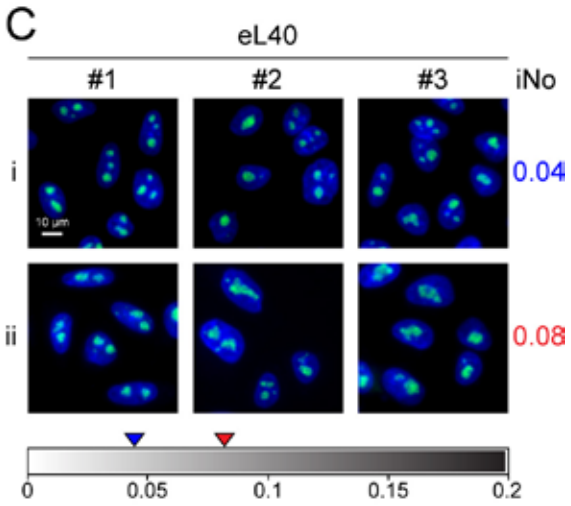
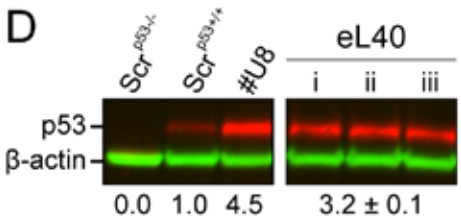
eL40 (RpL40)









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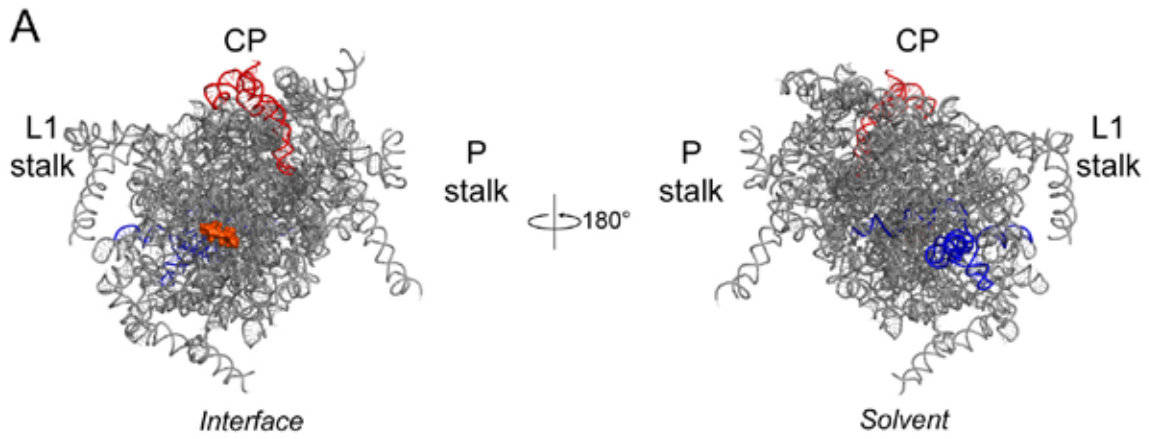
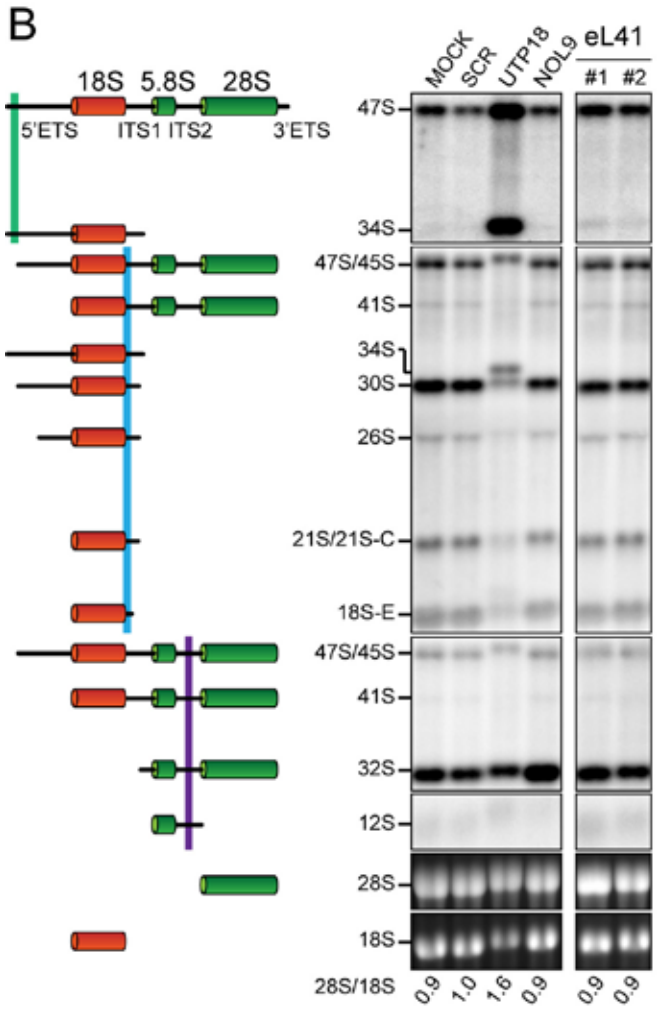
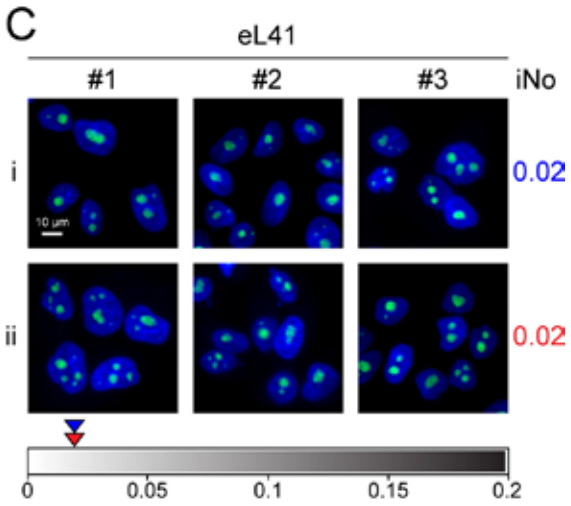
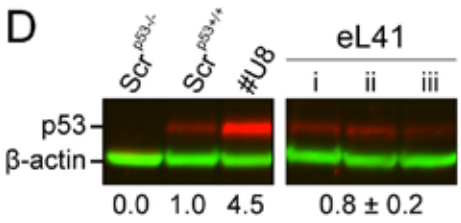
eL41 (RpL41)









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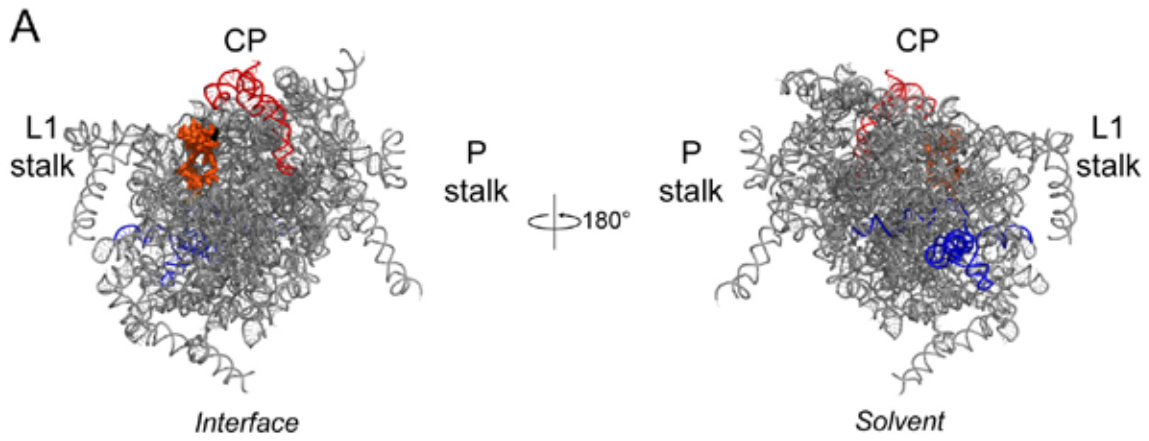
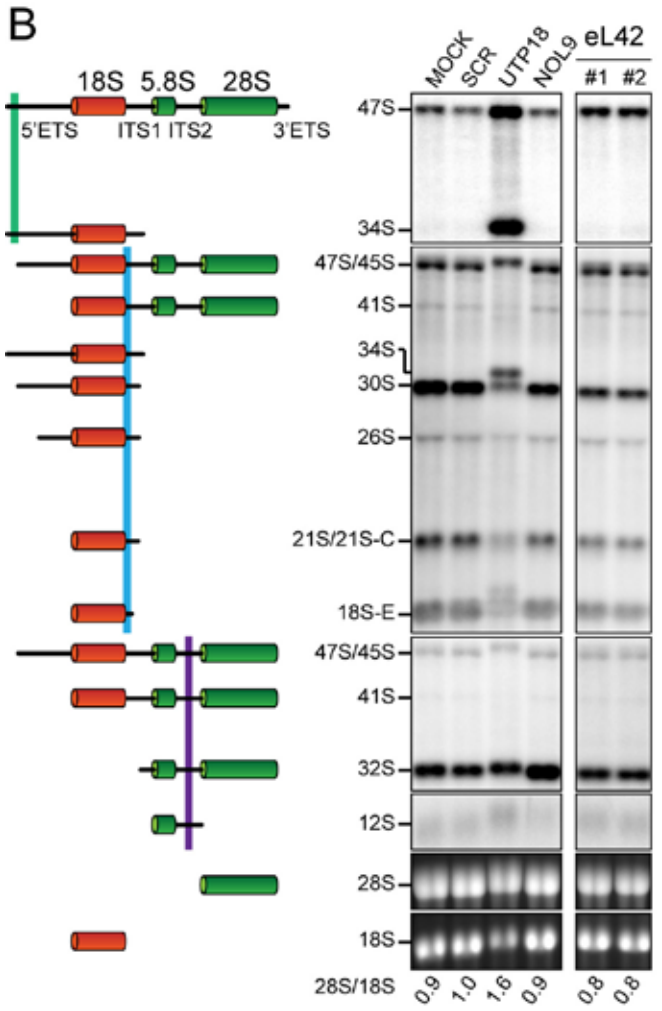
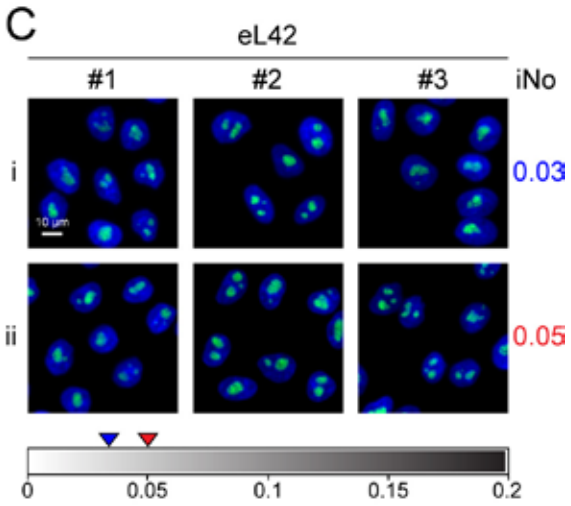
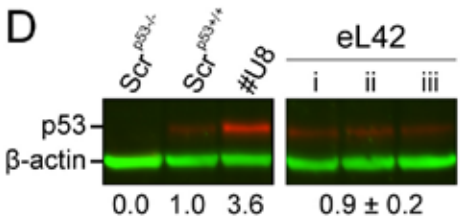
eL42 (RpL36a)









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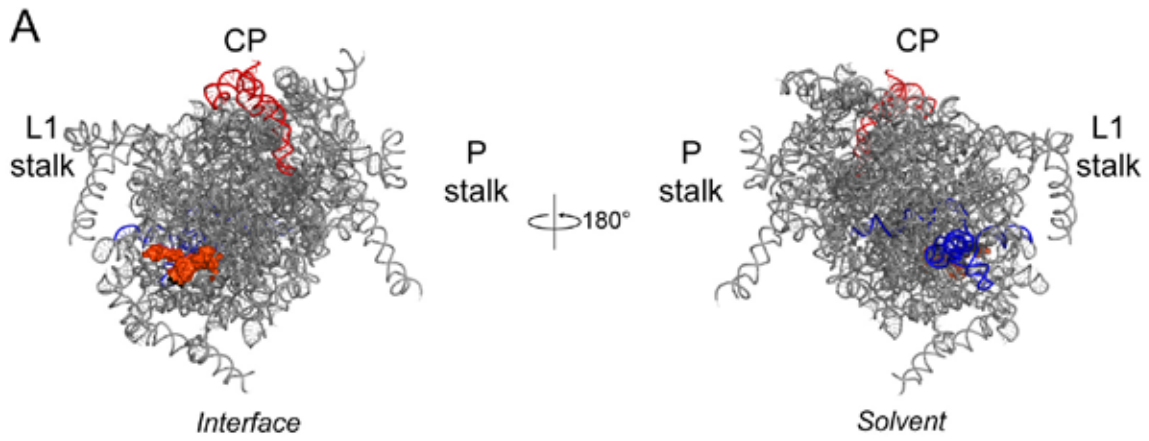
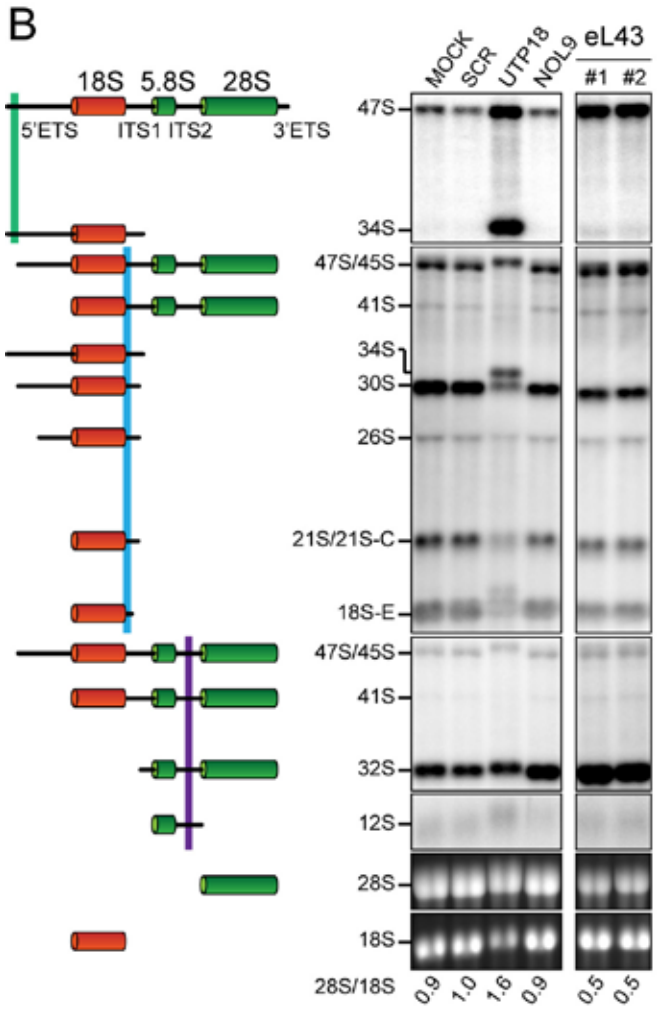
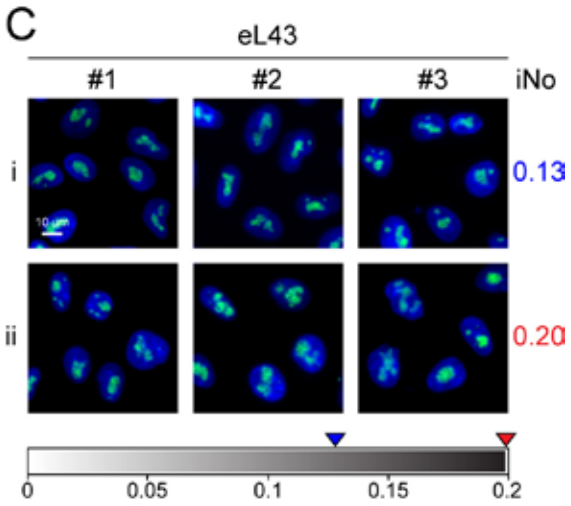
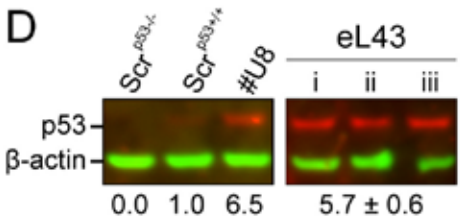
eL43 (RpL37a)









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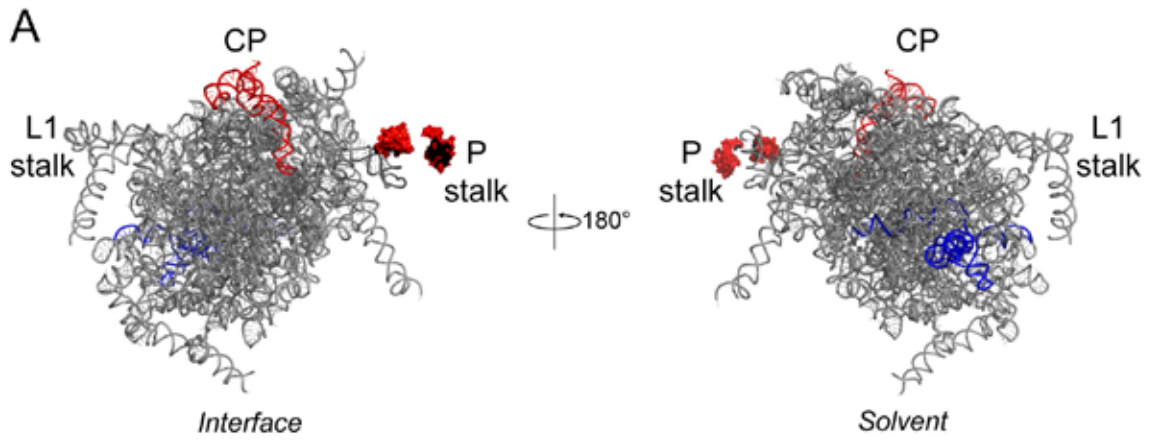
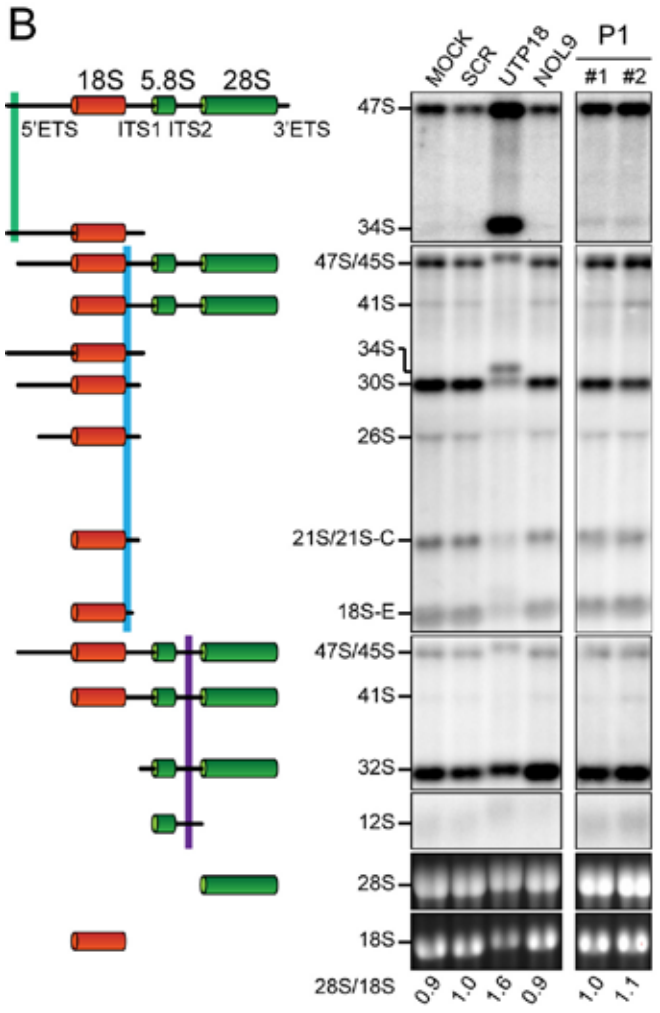
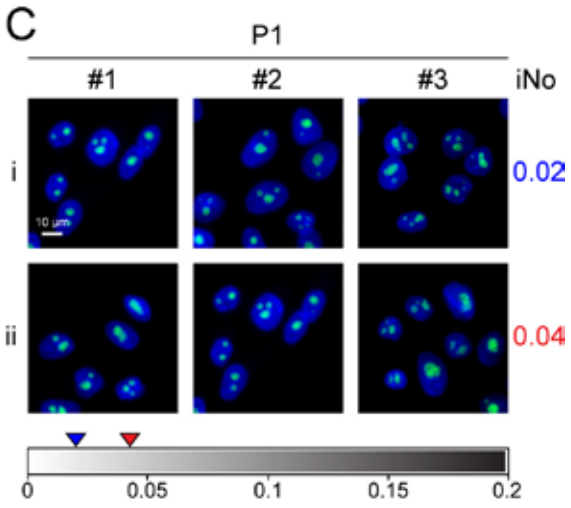
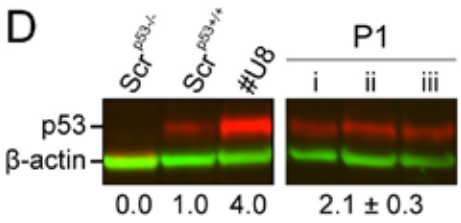
P1 (P1)









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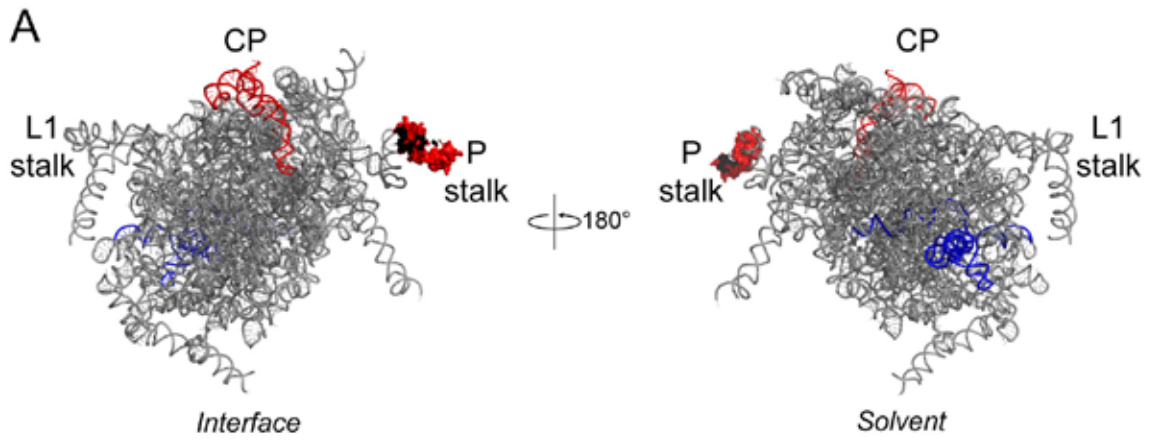
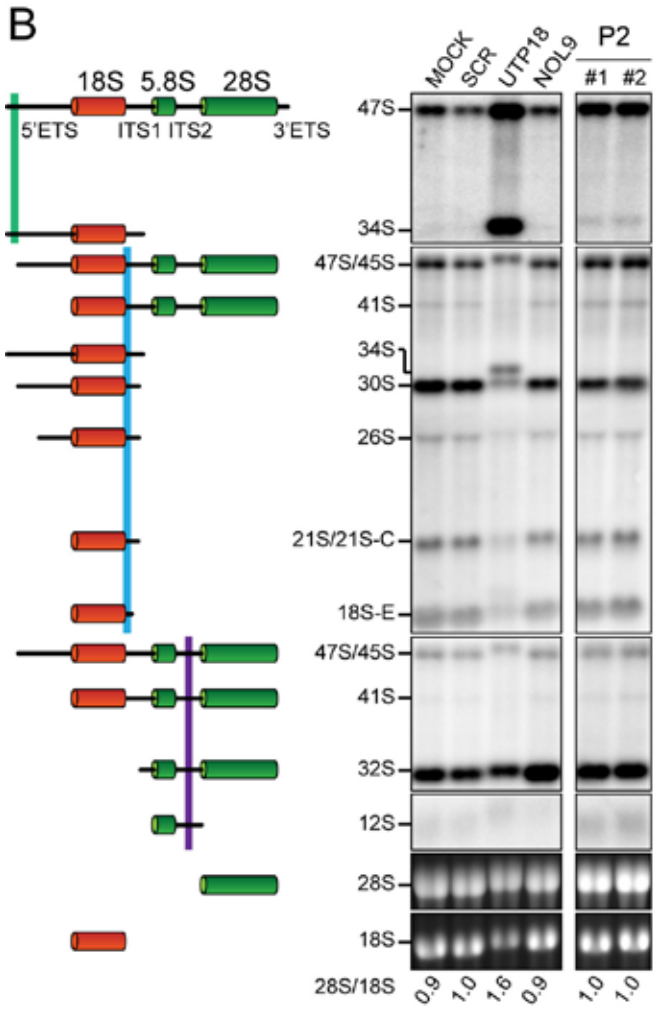
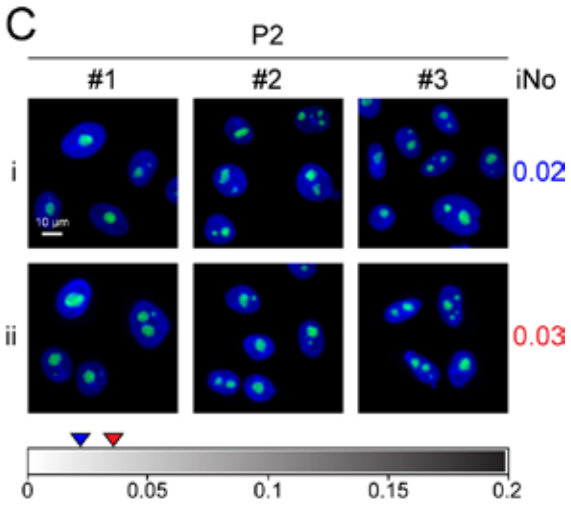
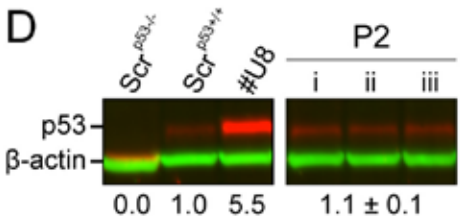
P2 (P2)









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