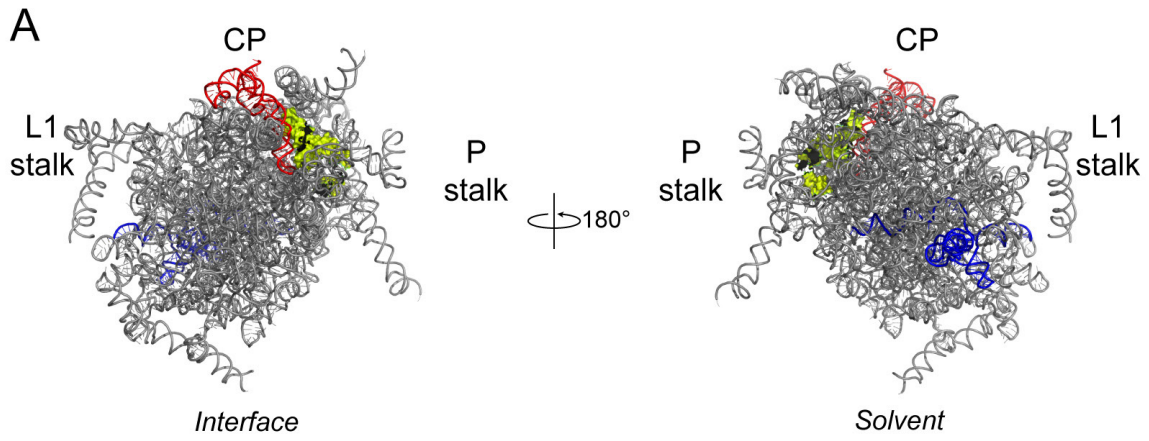
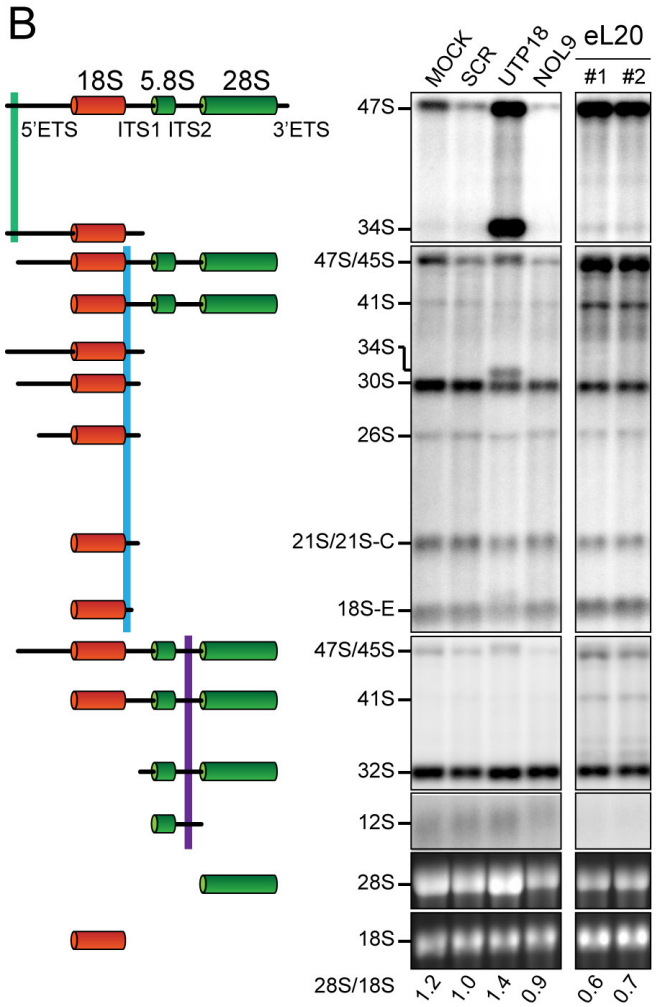
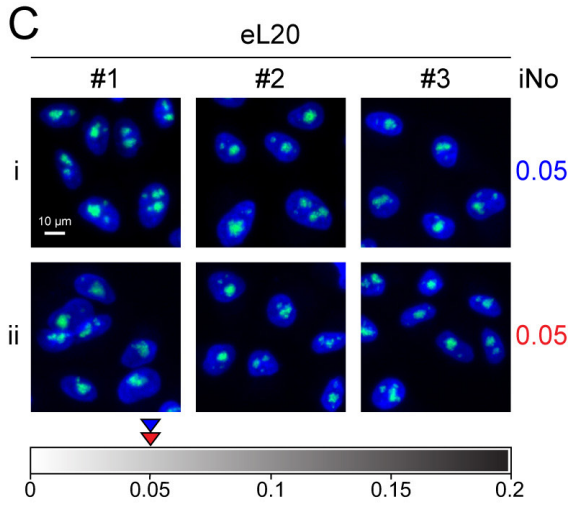
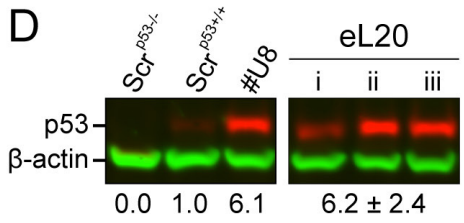
eL20 (RpL18a)









Individual data sheets for all eighty human r-proteins, showing positions on mature subunits (A), impacts on pre-rRNA processing and mature rRNA accumulation (B), nucleolar structure (C), and 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 Fig S11).

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 Figs S6 and S7) is included for reference. Schematics representing the RNAs detected are shown to the left. Quantifications are available in Fig 2 and Figs S6-S7.

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 4 for details). A calibration set (described in Fig 4) is included for reference..