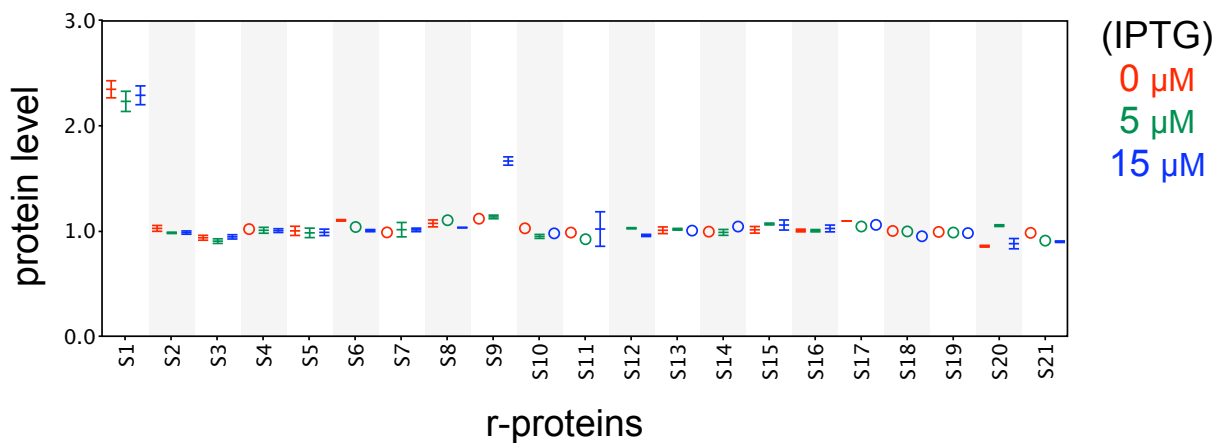
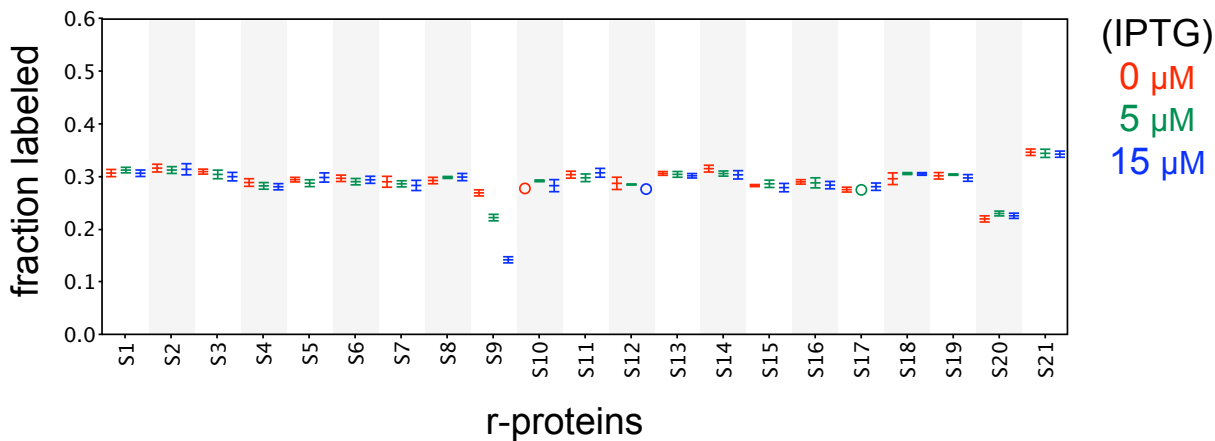


Fig. S1 Simulations of labeling kinetics for different relative precursor pools \mathbf{P} and exchange rates ϵ . Lines represent calculated labeling kinetics from Equations S7 and S8 (see Electronic Supplementary Information), for growth rate $k = 0.019254$ and $d = 0$. (a) From top to bottom: $\mathbf{P} = 0, 0.05, 0.1, 0.2$; $\epsilon = 0$ (b) From bottom to top: $\epsilon = 0, k, 5k, 50k$; $\mathbf{P} = 0.2$. Dotted line in both plots represent $\mathbf{P} = 0.2$ and $\epsilon = 0$.

a)



b)



c)

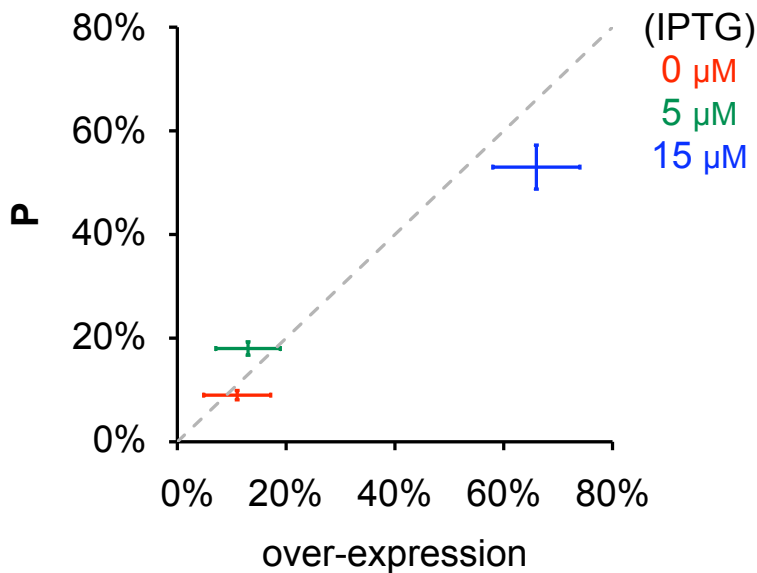


Fig. S2 Whole-cell lysate protein level and labeling kinetics of S9 over-expression experiments. Cells carrying an inducible S9 plasmid were grown in the presence of 0 μM (red), 5 μM (green), and 15 μM (blue) IPTG. (a) Protein levels of 30S r-proteins in whole-cell lysates relative to a 70S spike, defined as the ratio of r-protein in the whole cell lysate versus that of the 70S spike, normalized to the median of all 30S r-proteins except S1 and S9. (b) Pulse-labeling kinetics of 30S r-proteins in dissociated 30S subunits. (c) Plot of S9 over-expression (percent increase over 100%) versus calculated precursor pool size **P** (doubling time = 54 minutes, pulse time = 30 minutes).

r-proteins	n ^a	pool ^b	+/- ^c	RCS ^d	turnover ^e	+/-	RCS
S1	55	0.2%	0.1%	3.0	0.12%	0.22%	3.1
S2	81	0.1%	0.1%	2.3	0.00%	0.16%	2.3
S3	96	1.1%	0.1%	2.3	0.00%	0.22%	5.6
S4	88	2.3%	0.1%	3.5	0.00%	0.43%	17.2
S5	101	1.1%	0.1%	2.0	0.00%	0.23%	5.7
S6	45	2.0%	0.1%	1.7	0.00%	0.56%	13.8
S7	56	1.9%	0.2%	3.8	0.00%	0.49%	14.2
S8	44	1.0%	0.1%	2.5	0.00%	0.33%	5.1
S9	67	0.4%	0.1%	2.0	0.00%	0.19%	2.5
S10	38	5.6%	0.1%	1.2	0.00%	1.36%	79.0
S11	28	0.0%	0.2%	4.2	0.00%	0.38%	4.2
S12	16	1.5%	0.3%	3.8	0.00%	0.74%	10.1
S13	55	0.1%	0.1%	2.4	0.00%	0.21%	2.5
S14	28	0.2%	0.3%	6.5	0.00%	0.50%	6.6
S15	51	2.2%	0.1%	2.2	0.00%	0.53%	15.9
S16	71	3.5%	0.1%	2.6	0.00%	0.71%	36.2
S17	25	2.4%	0.2%	2.3	0.00%	0.89%	19.8
S18	48	0.8%	0.1%	3.0	0.00%	0.30%	4.6
S19	28	1.2%	0.2%	3.4	0.00%	0.52%	7.6
S20L26	48	0.0%	0.6%	51.8	6.84%	0.22%	2.4
S21	56	0.0%	0.7%	75.4	8.39%	0.22%	2.9
L1	100	2.1%	0.1%	2.6	0.00%	0.37%	14.8
L2	133	1.7%	0.1%	2.1	0.00%	0.27%	10.2
L3	82	3.6%	0.1%	3.0	0.00%	0.70%	39.9
L4	140	3.8%	0.1%	2.2	0.00%	0.53%	40.2
L5	100	2.2%	0.1%	2.6	0.00%	0.37%	15.3
L6	100	1.1%	0.1%	2.0	0.00%	0.26%	5.9
L7	115	1.2%	0.1%	3.3	0.00%	0.27%	7.4
L9	83	0.7%	0.1%	3.0	0.00%	0.22%	4.3
L10	58	1.5%	0.1%	2.3	0.00%	0.38%	8.6
L11	70	3.3%	0.1%	2.7	0.00%	0.70%	33.5
L13	105	2.6%	0.1%	1.4	0.00%	0.45%	20.7
L14	72	2.5%	0.1%	2.9	0.00%	0.49%	19.0
L15	66	3.0%	0.1%	3.2	0.00%	0.61%	26.7
L16	66	3.3%	0.1%	2.0	0.00%	0.70%	33.2
L17	65	2.7%	0.2%	5.3	0.00%	0.68%	27.5
L18	90	1.0%	0.1%	2.7	0.00%	0.25%	5.5
L19	43	0.5%	0.2%	3.5	0.00%	0.29%	4.2
L20	74	2.8%	0.1%	2.6	0.00%	0.58%	25.0
L21	34	3.4%	0.2%	3.1	0.00%	0.98%	35.9
L22	63	5.4%	0.2%	3.5	0.00%	1.20%	85.0
L23	57	3.2%	0.1%	2.2	0.00%	0.75%	32.2
L24	49	5.0%	0.2%	4.3	0.00%	1.22%	73.3
L25	61	0.9%	0.1%	3.1	0.00%	0.31%	5.7
L27	38	1.0%	0.2%	4.6	0.00%	0.42%	7.5
L28	42	7.0%	0.2%	1.9	0.00%	1.70%	126.3
L29	29	4.0%	0.2%	4.5	0.00%	1.31%	50.9
L30	42	2.8%	0.2%	4.9	0.00%	0.81%	27.8
L31	18	0.0%	0.3%	5.1	0.78%	0.50%	4.5
L32	27	4.0%	0.3%	6.0	0.00%	1.38%	52.7
L33	45	0.0%	0.3%	11.1	2.75%	0.29%	3.6
L34	33	0.0%	0.2%	4.1	0.52%	0.30%	3.7
L35	26	1.6%	0.3%	5.5	0.00%	0.79%	14.1

Table S1 Fit statistics for observed r-protein pulse labeling kinetics.

^aNumber of fitted isotope distributions points observed for each r-protein in the pulse labeling timecourse.

^bFitted relative pool size **P**, reported values highlighted in bold.

^cEstimated s.d. of the parameter.

^dReduced chi-squares values for the fits, calculated from an estimated error of 0.4% s.d. and $n - 2$ degrees of freedom.

^eTurnover rate per generation, reported values are highlighted in bold.