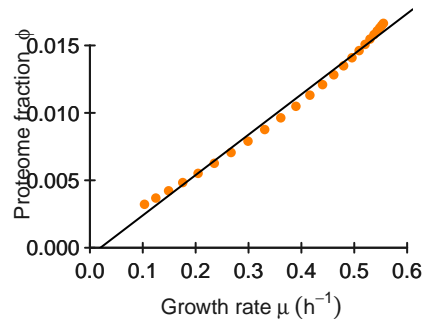
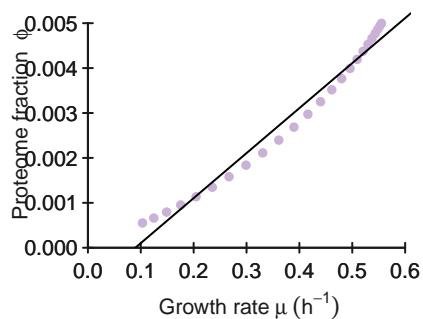
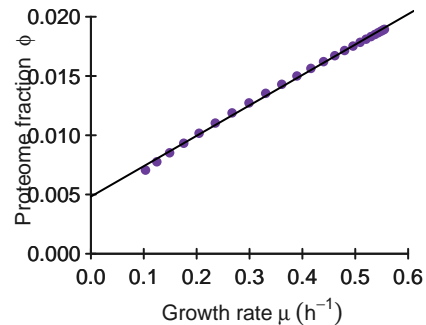
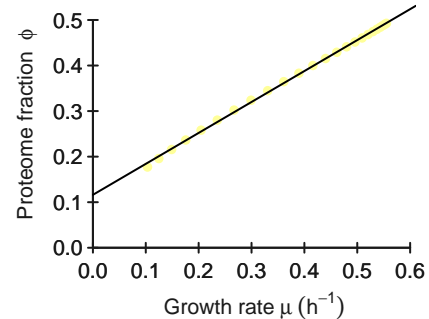
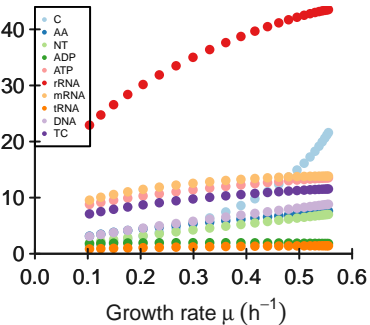
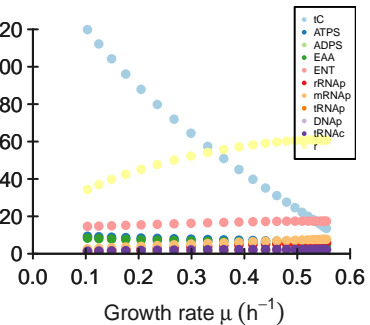
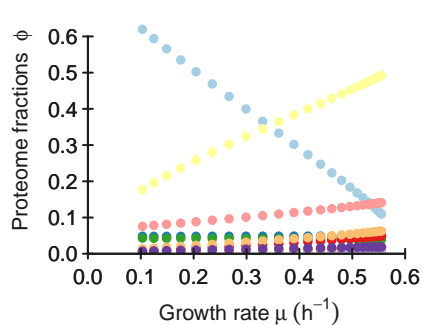
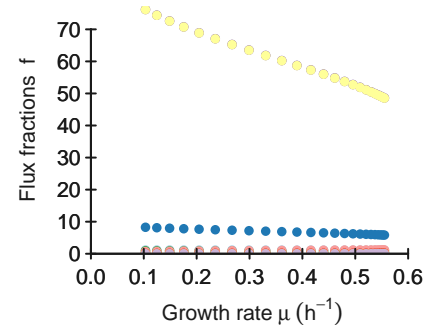
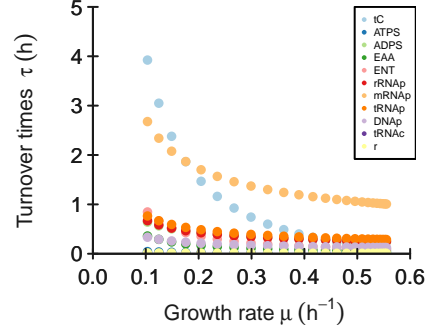
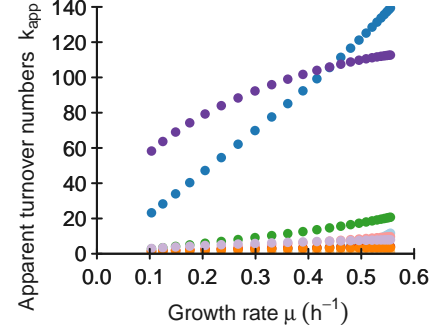
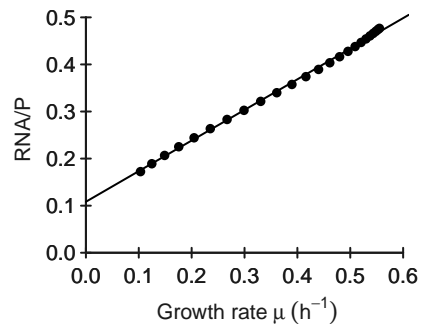


tRNA<sub>p</sub>DNA<sub>p</sub>tRNA<sub>c</sub>

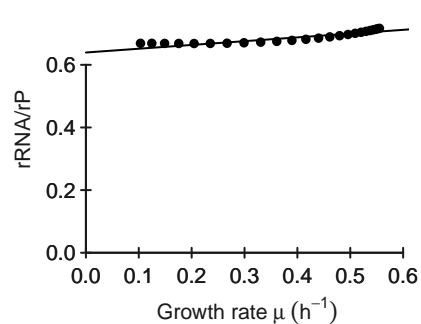
r

Metabolite concentrations  $c^m$  (g/L)Protein concentrations  $p$  (g/L)Proteome fractions  $\phi$ Flux fractions  $f$ Turnover times  $\tau$  (h)Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )

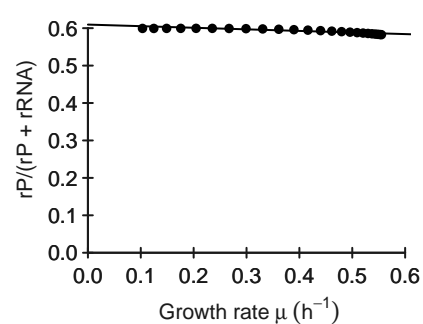
RNA/P



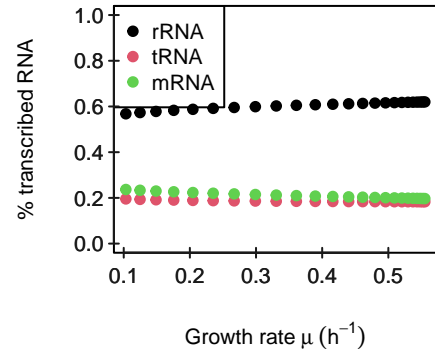
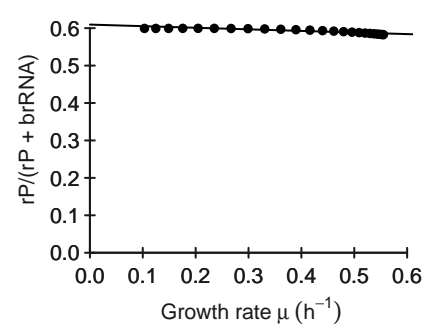
rRNA/rP



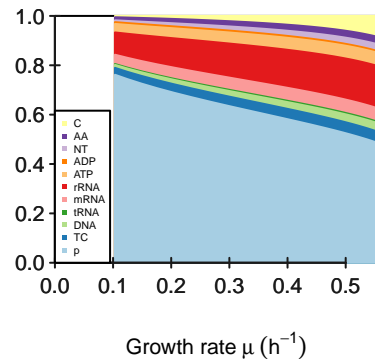
rP/(rP + rRNA)



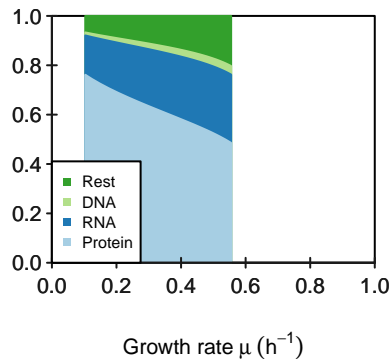
Protein mass fraction in ribosome



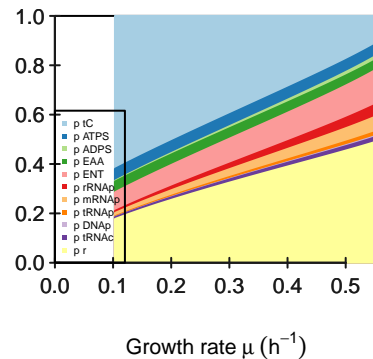
Relative biomass composition



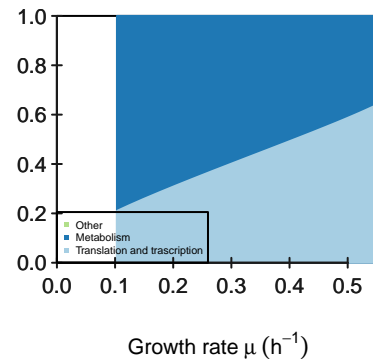
Predicted biomass



Proteome composition



Proteome sectors



# M

[illegible]

**K**

[illegible]

**KA**[illegible]

# kcat

	tC	ATPS	ADPS	EAA	ENT	rRNAp	mRNAp	tRNAp	DNAp	tRNAc	r
kcatf	14	360	8	40	20	8	2	7	16	7904	444
kcatb	1	36	1	4	2	0	0	0	0	790	0

## Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
	3220	150	4	7.5	1.875	Inf	Inf	Inf	Inf	15.0075949367089	Inf



## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]	[,11]
	0.15	0.032	0.007	0.045	0.223	0.07	0.03	0.01	0.003	0.03	0.4

**average saturation input**

3

### minimal phi constraint

[1,]	[,1] 0	[,2] 0	[,3] 0	[,4] 0	[,5] 0	[,6] 0	[,7] 0	[,8] 0	[,9] 0	[,10] 0	[,11] 0
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## minimal f constraint

[1,]	[,1] 0	[,2] 0	[,3] 0	[,4] 0	[,5] 0	[,6] 0	[,7] 0	[,8] 0	[,9] 0	[,10] 0	[,11] 0
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