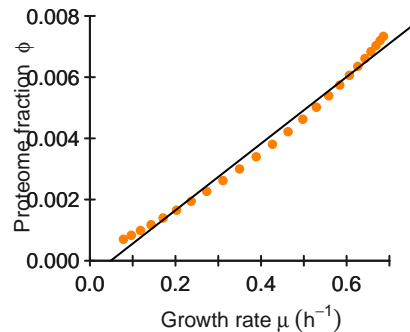
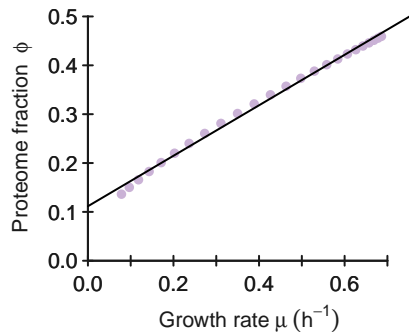
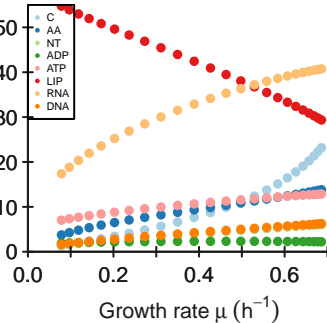
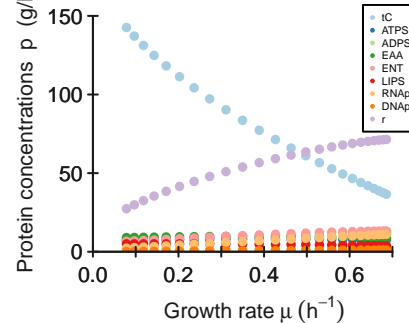
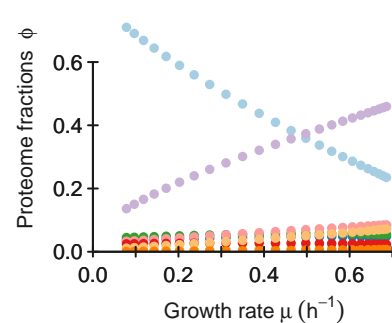
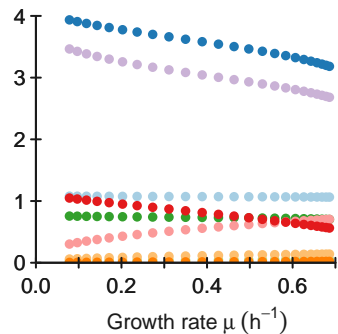
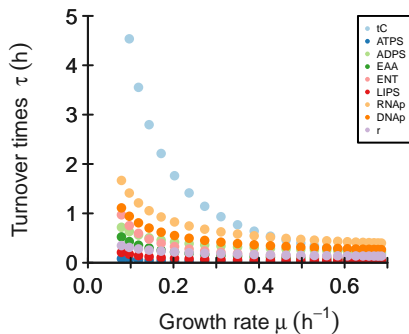
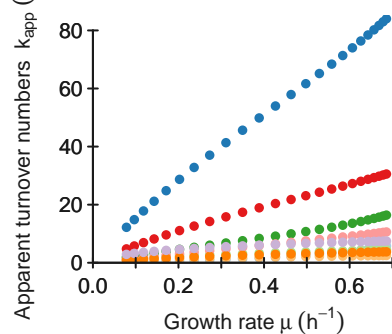
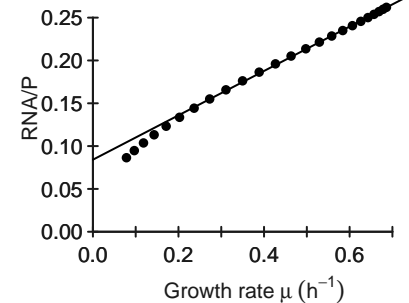
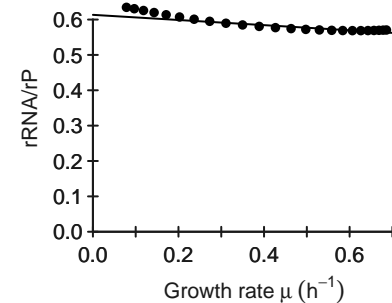
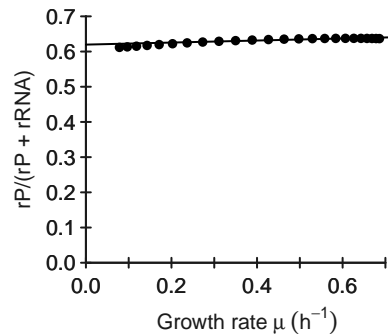
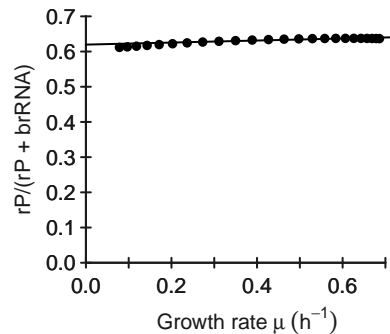


**DNAp****r**Metabolite concentrations  $c^m$  (g/L)Protein concentrations  $p$  (g/L)Proteome fractions  $\phi$ Flux fractions  $f$ Turnover times  $\tau$  (h)Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )**RNA/P****rRNA/rP**

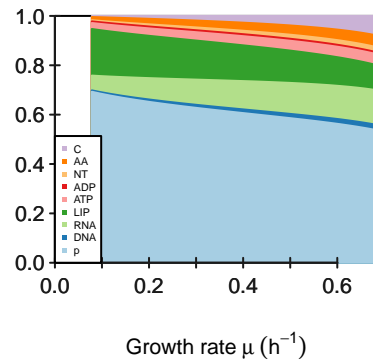
$rP/(rP + rRNA)$



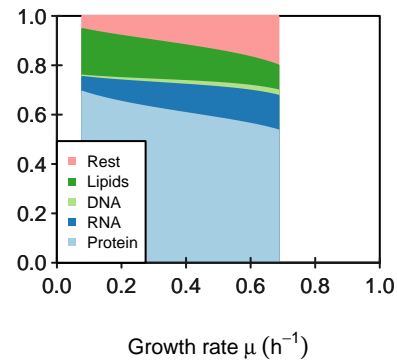
Protein mass fraction in ribosome



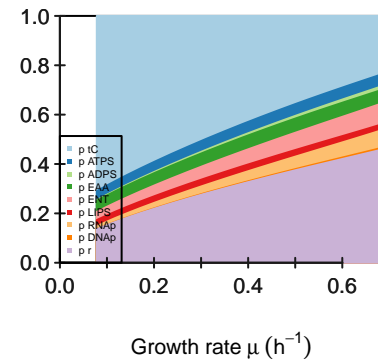
Relative biomass composition



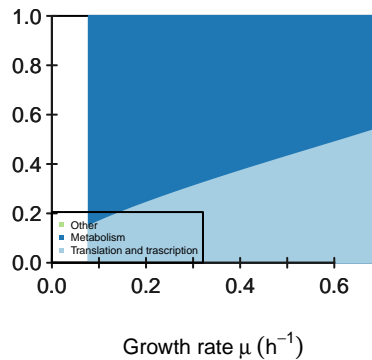
Predicted biomass



Proteome composition



Proteome sectors









# kcat

	tC	ATPS	ADPS	EAA	ENT	LIPS	RNAp	DNAp	r
kcatf	14	201	10	41	20	49	6	9	22
kcatb	1	20	1	4	2	0	0	0	0

## Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
3640	134	5	6.833333333333333	1.666666666666667	Inf	Inf	Inf	Inf	



## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	0.147	0.031	0.006	0.043	0.21	0.04	0.11	0.003	0.41

**average saturation input**

3

### minimal phi constraint

[illegible]

