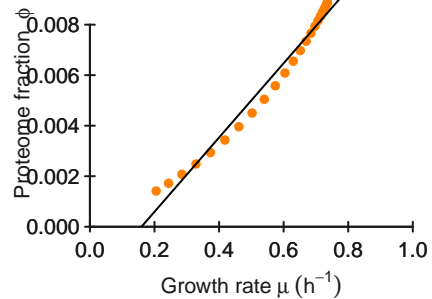
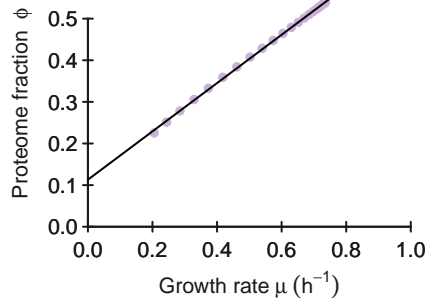
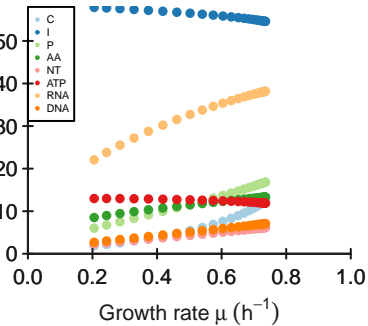
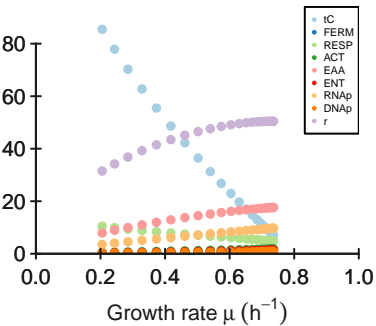
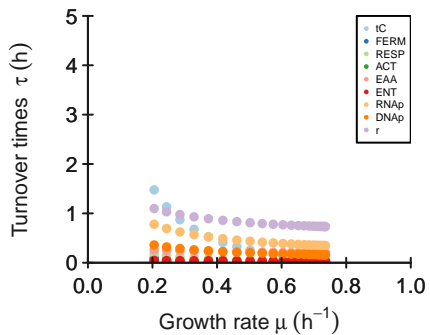
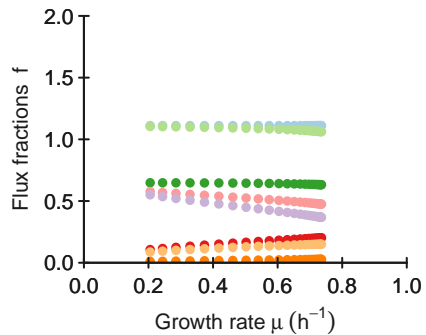
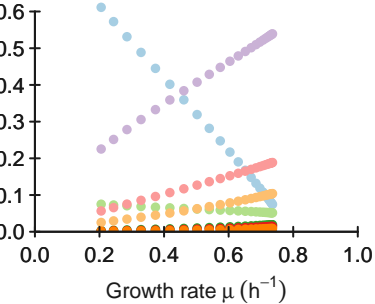
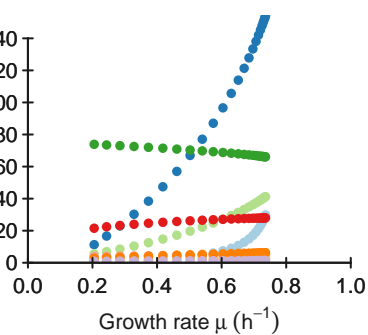
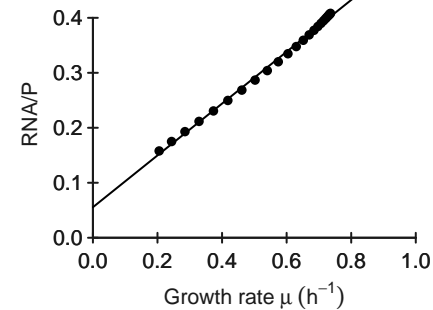
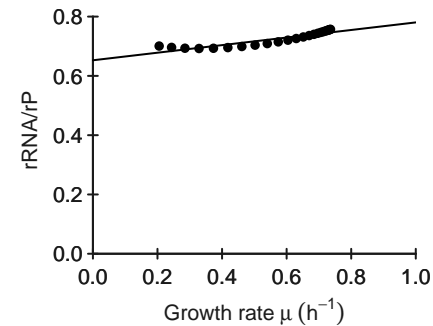
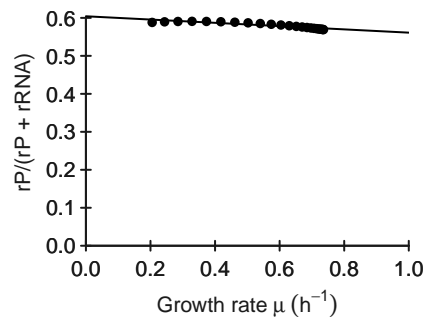
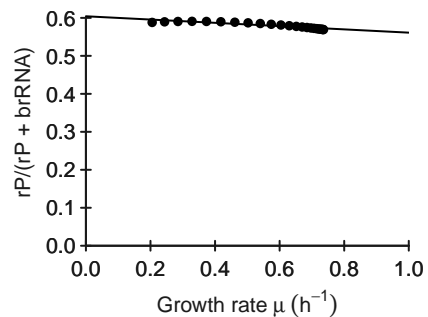


**DNAp****r**Metabolite concentrations  $c^m$  (g/L)Protein concentrations  $p$  (g/L)Proteome fractions  $\phi$ Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )**RNA/P****rRNA/rP**

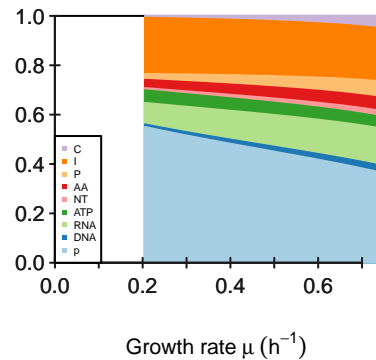
$rP/(rP + rRNA)$



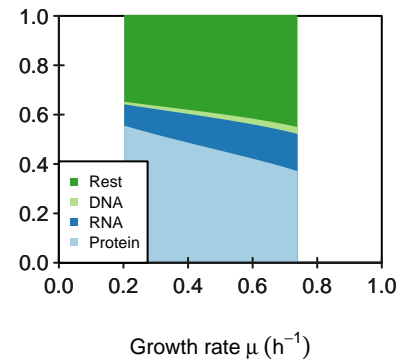
Protein mass fraction in ribosome



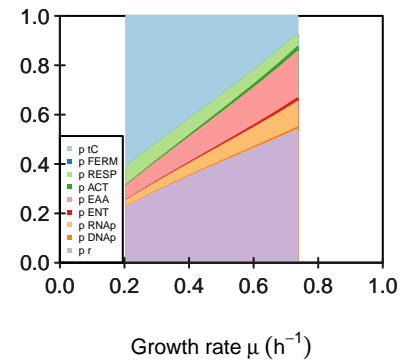
Relative biomass composition



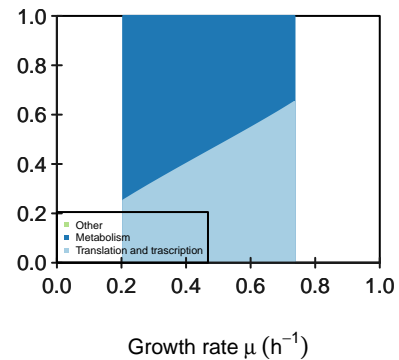
Predicted biomass



Proteome composition



Proteome sectors



keep\_ribosome\_kcat FALSE  
keep\_transport\_kcat FALSE  
maintenance\_fun constant

# M

[illegible]



**KA**[illegible]

# kcat

	tC	FERM	RESP	ACT	EAA	ENT	RNAp	DNAp	r
kcatf	39	544	136	115	7	45	6	13	4
kcatb	4	54	14	12	1	4	0	0	0



Keq

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
487.5	642.222222222222	1238.57142857143	1.4093137254902	24.5	4.6875	Inf	Inf	Inf	

## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	0.065	0.024	0.024	0.024	0.248	0.032	0.12	0.003	0.46

**average saturation input**

3

### minimal phi constraint

[illegible]

### minimal f constraint

[illegible]