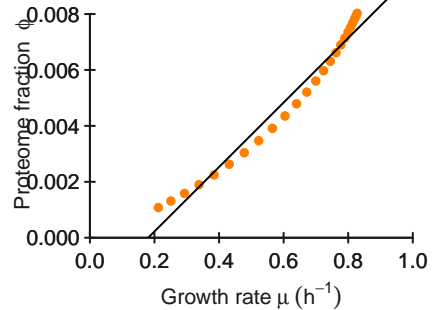
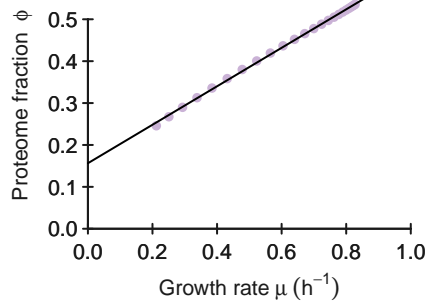
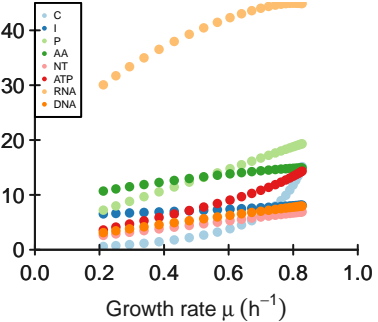
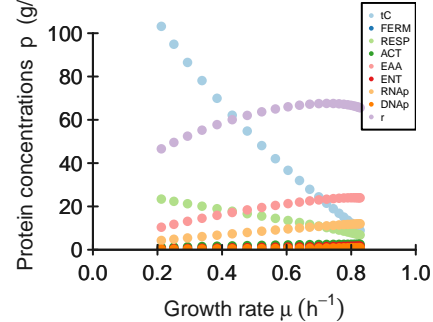
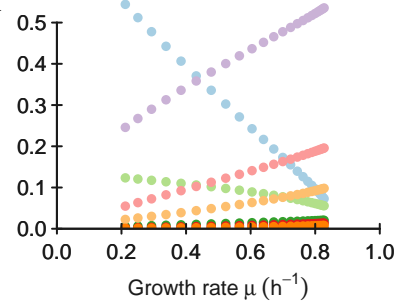
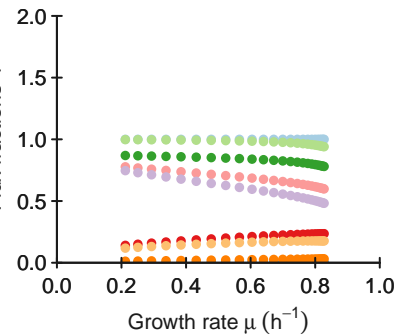
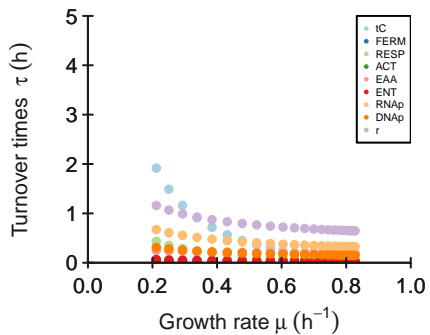
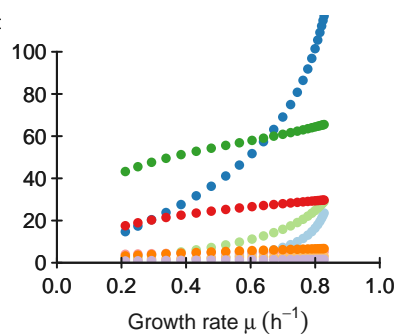
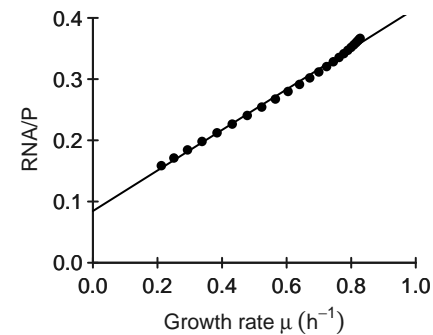
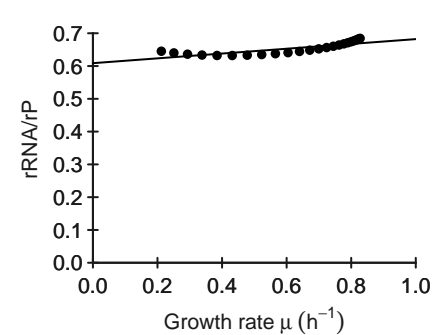
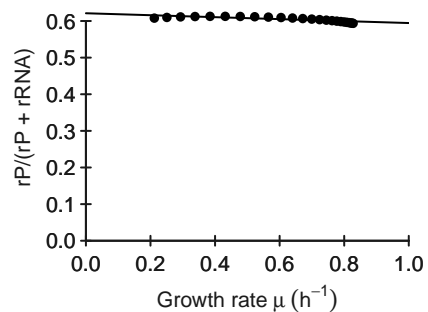
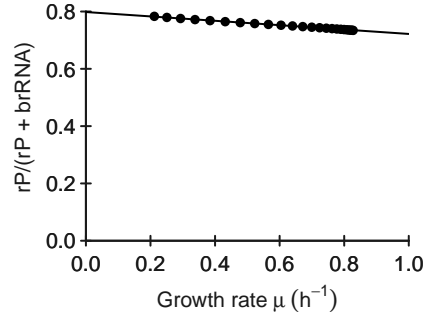


**DNAp****r**Metabolite concentrations  $c^m$  (g/L)Protein concentrations  $p$  (g/L)Proteome fractions  $\phi$ Flux fractions  $f$ Turnover times  $\tau$  (h)Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )**RNA/P****rRNA/rP**

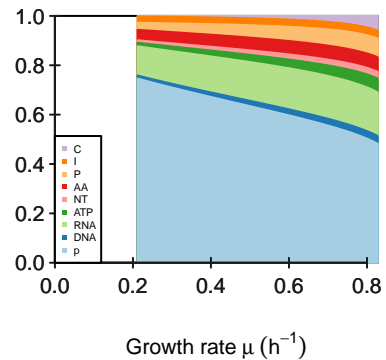
$rP/(rP + rRNA)$



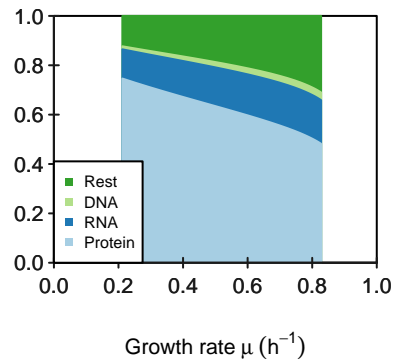
Protein mass fraction in ribosome



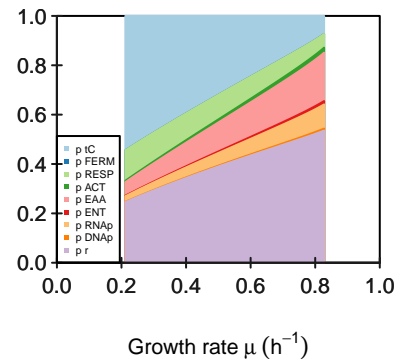
Relative biomass composition



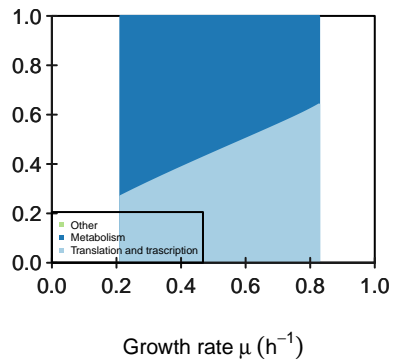
Predicted biomass



Proteome composition



Proteome sectors



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





**KA**[illegible]

# kcat

	tC	FERM	RESP	ACT	EAA	ENT	RNAp	DNAp	r
kcatf	29	400	100	115	7	45	6	13	4
kcatb	3	40	10	12	1	4	0	0	0



## Keq

[1,]	1256.666666666667	[,1]	[,2]	[,3]	9.583333333333333	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
		840	168		28	5.625	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]