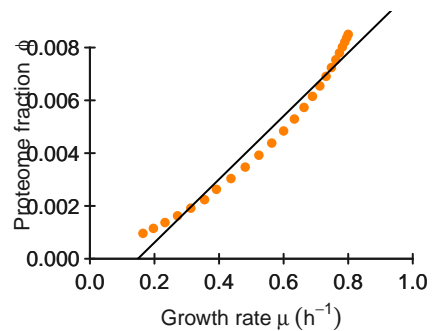
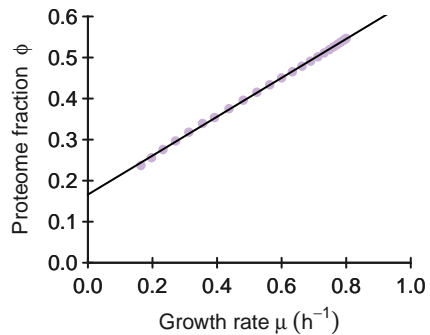


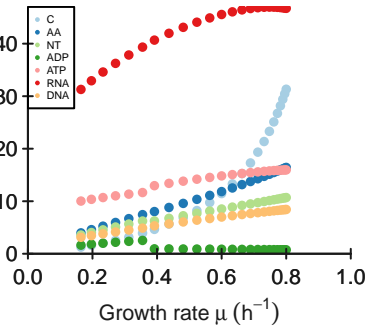
**DNAP**



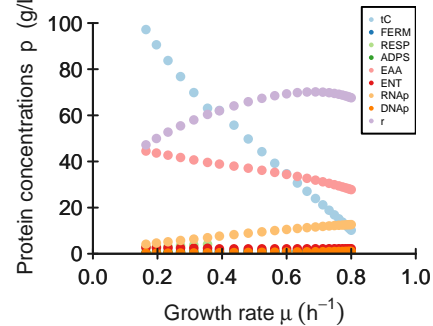
**r**



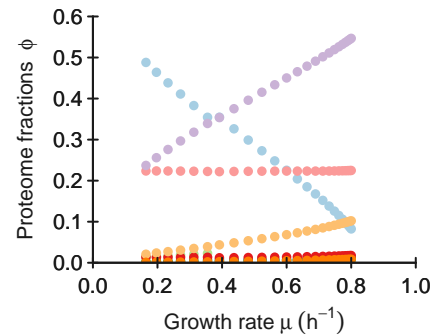
Metabolite concentrations  $c^m$  (g/L)



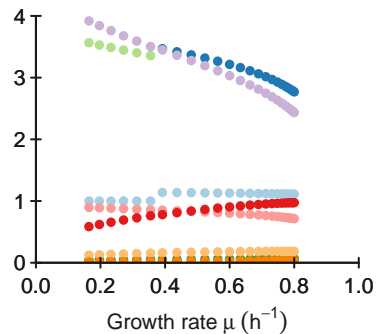
Protein concentrations  $p$  (g/L)



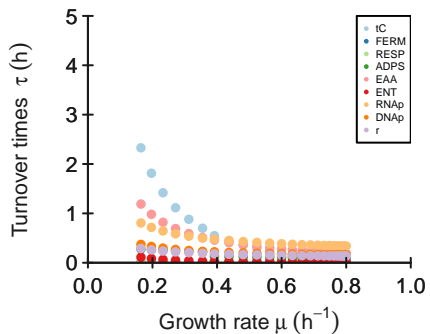
Proteome fractions  $\phi$



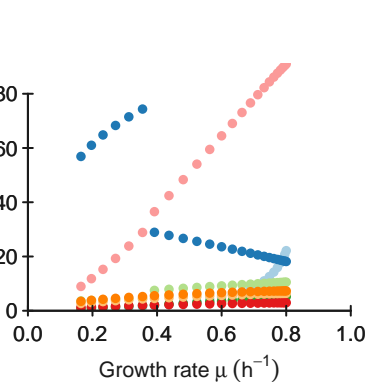
Flux fractions  $f$



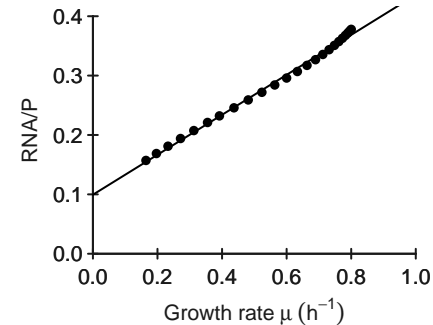
Turnover times  $\tau$  (h)



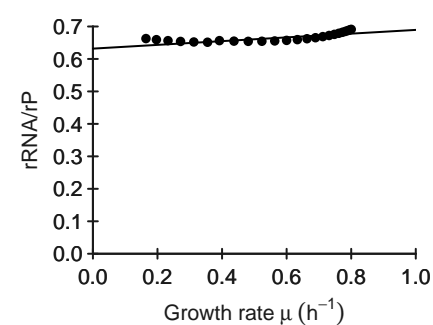
Apparent turnover numbers  $k_{app}$  ( $h^{-1}$ )



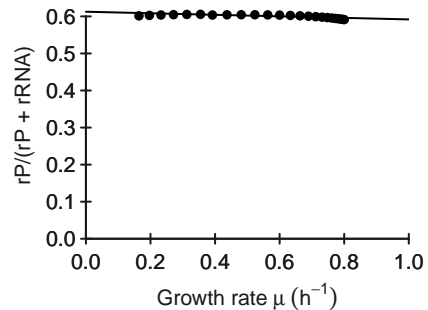
**RNA/P**



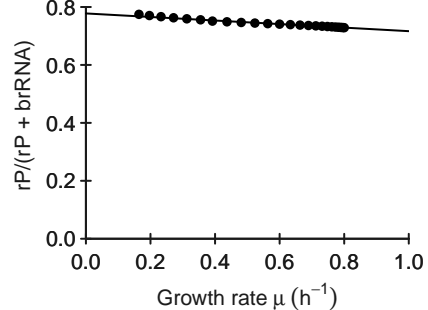
**rRNA/rP**



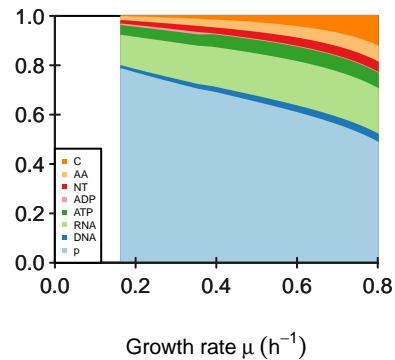
$rP/(rP + rRNA)$



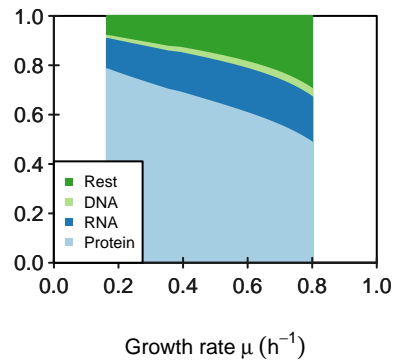
Protein mass fraction in ribosome



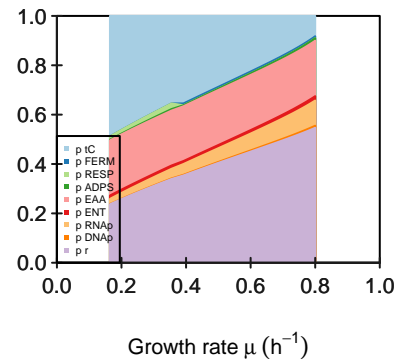
Relative biomass composition



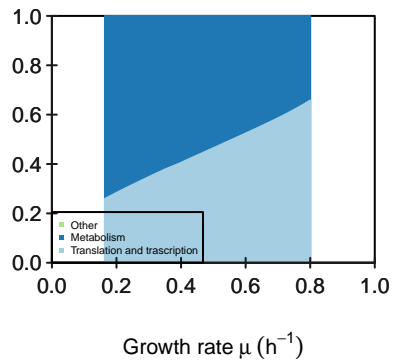
Predicted biomass



Proteome composition



Proteome sectors



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

# M

[illegible]





# kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAp	r
kcatf	29	2060	206	18	8	153	6	13	19
kcatb	3	206	21	2	1	15	0	0	0



## Keq

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
[1,]	1643.33333333333	100	58.8571428571429	2.25	14.6666666666667	2.3375	Inf	Inf	Inf

## phi input

[1,]	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]
	0.065	0.035	0.035	0.003	0.248	0.032	0.119	0.003	0.46

**average saturation input**

3



### minimal f constraint

[illegible]