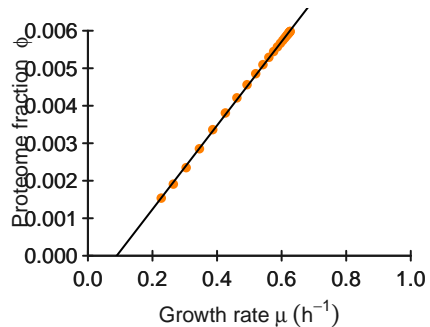
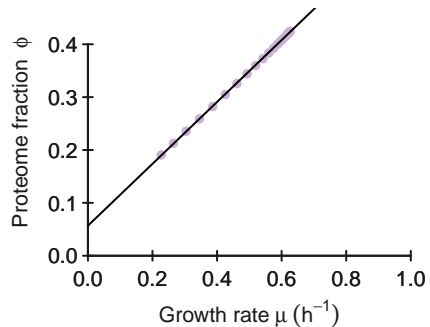


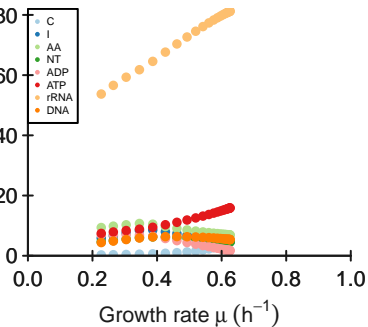
**DNAp**



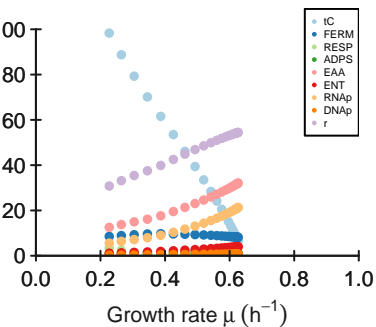
**r**



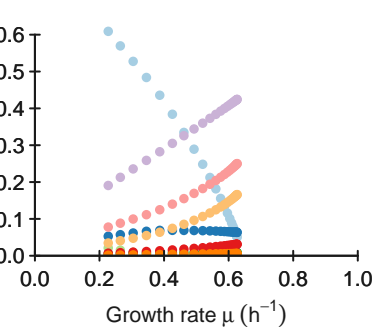
Metabolite concentrations  $c^m$  (g/L)



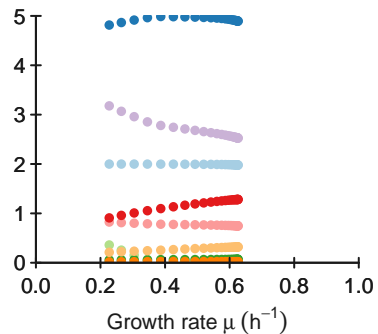
Protein concentrations  $p$  (g/L)



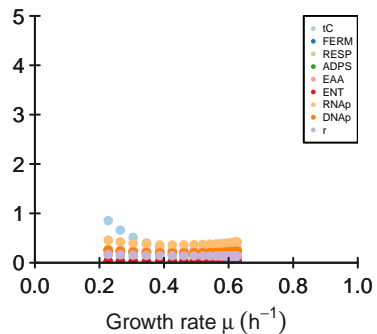
Proteome fractions  $\phi$



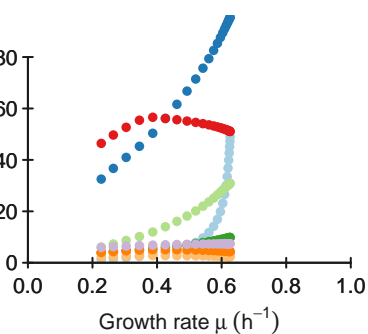
Flux fractions  $f$



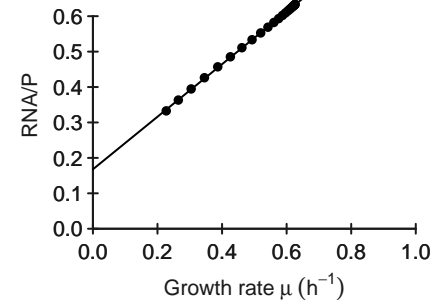
Turnover times  $\tau$  (h)



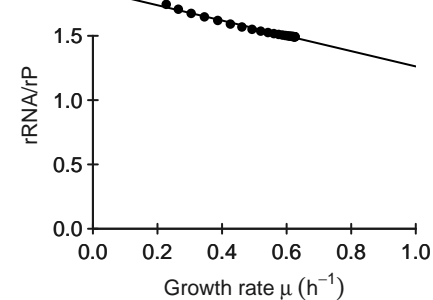
Apparent turnover numbers  $k_{app}$  ( $\text{h}^{-1}$ )



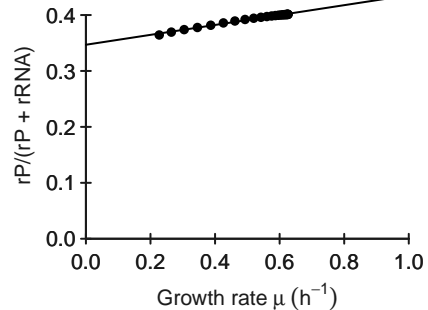
**RNA/P**



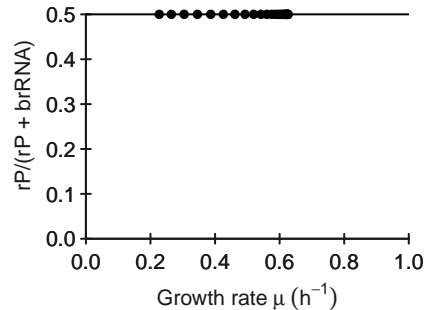
**rRNA/rP**



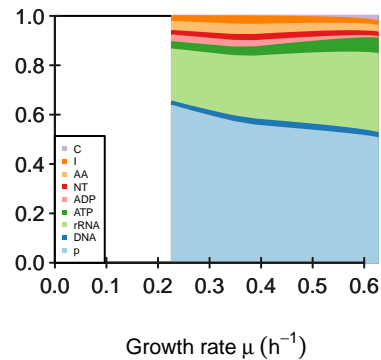
$rP/(rP + rRNA)$



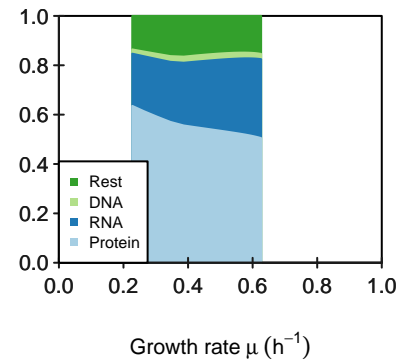
Protein mass fraction in ribosome



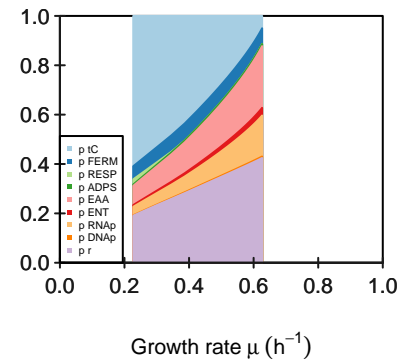
Relative biomass composition



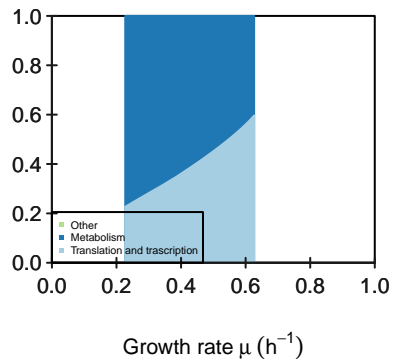
Predicted biomass



Proteome composition



Proteome sectors



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

## M

[illegible]





## kcat

	tC	FERM	RESP	ADPS	EAA	ENT	RNAp	DNAP	r
kcatf	56	177.8	118.53333333333333	23	7	109	6	11	16
kcatb	6	18	12	2	1	11	0	0	0



## Keq

[1,]	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]
	1306.66666666667	210.725925925926	210.725925925926	5.75	28	7.43181818181818	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**

5



### minimal f constraint

[illegible]